



Query Match 11.9%; Score 77.5; DB 2; Length 401;  
Best Local Similarity 25.0%; Pred. No. 0.65;  
Matches 30; Conservative 24; Mismatches 39; Indels 27; Gaps 5;

QY 8 FGKVVYFISAIENFGPRYLHVHGYPP-YELILVR-----IISFLIGDMEDVLLNCTLL 58  
Db 103 FFWW-YFLNWFILNFKNIYFPYFVSVIHLAVGVVYCLISWTVGLPKRAPIDSTQL 161  
QY 59 KRSRFRFGALVCSMDSCRSRVAVTY-----RFITLLNIPSPAVWMA 102  
Db 162 KLLTPVAFCHALGHVTNSVFAAVAVSFTHIKALEPFFNVSASQFILGQIPL-ALWLS 220

RESULT 3  
H75194  
hypothetical protein PAB0044 - Pyrococcus abyssi (strain Orsay)  
C/Species: Pyrococcus abyssi  
C/Date: 20-Aug-1999 #sequence\_revision 20-Aug-1999 #text\_change 09-Jul-2004  
C/Accession: H75194  
R;anonymous, Genoscope  
submitted to the EMBL Data Library, July 1999  
A/Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome structure  
A/Reference number: A75001  
A/Accession: H75194  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-280 <KAW>  
A/Cross-references: UNIPROT:Q9V2J1; GB:AJ248283; GB:AL096836; NID:g5457433; PIDN:CAB4900  
A/Experimental source: strain Orsay  
C/Genetics:  
A/Gene: PAB0044  
C/Superfamily: Pyrococcus abyssi hypothetical protein PAB0044

Query Match 11.8%; Score 77; DB 2; Length 280;  
Best Local Similarity 23.7%; Pred. No. 0.51;  
Matches 33; Conservative 26; Mismatches 36; Indels 44; Gaps 9;

QY 3 VCVNRFCKW-----VVFISAIENFGPRYLHVHGYPPYFELILVRIISFLI--GDMEVDLLN 54  
Db 70 VLVDKYPWQLIRSVLIIIAI-----LLVSVLSFYIPFGKGYIFR 113  
QY 55 CTLKRSSRF-FWGALVCSMDSC-----RFSRVAVTYR---FITLLNIP-SPA 98  
Db 114 --IRTEKFRFLGWACYRQCYAFAKALLNARFPGIAITRDPPEVFRGKLNHLTPV 170

QY 99 VVMARNTIDQOVLRSIKLE 117  
Db 171 IWISK-VKHEEAVSPTRL 188

RESULT 4  
T45037  
hypothetical protein Y39B6B.k [imported] - Caenorhabditis elegans  
C/Species: Caenorhabditis elegans  
C/Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 21-Jul-2000  
C/Accession: T45037  
R;Wilson, R.; Ainscough, R.; Anderson, K.; Baynes, C.; Berks, M.; Bonfield, J.; Burton, R.; Faser, A.; Fulton, L.; Gardner, A.; Green, P.; Hawkins, T.; Hillier, L.; Jiet, M.; Johnson, B.; O'Callaghan, M.; Parsons, J.; Percy, C.; Rifkin, L.; Roopra, A.; Saunders, D. Nature 368, 32-38, 1994  
A/Authors: Showkneen, R.; Sims, M.; Smaldon, N.; Smith, A.; Smith, M.; Sonhammer, E.; S. tock, L.; Wilkinson-Sproat, J.; Wohldman, P.  
A/Title: 2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans.  
A/Reference number: S43531; MUID:94150718; PMID:7906398  
A/Accession: T45037  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-1132 <WIL>  
A/Cross-references: EMBL:AL132896; NID:g6434440; PIDN:CAB60916.1; PID:g6434451  
A/Experimental source: clone Y39B6B  
C/Genetics:  
A/Map position: 3

A; Introns: 9/2; 63/3; 124/3; 152/2; 229/3; 270/3; 429/3; 490/3; 527/3; 554/2; 609/3; 645/3; 654/3; 655/3; 656/3; 657/3; 658/3; 659/3; 660/3; 661/3; 662/3; 663/3; 664/3; 665/3; 666/3; 667/3; 668/3; 669/3; 670/3; 671/3; 672/3; 673/3; 674/3; 675/3; 676/3; 677/3; 678/3; 679/3; 680/3; 681/3; 682/3; 683/3; 684/3; 685/3; 686/3; 687/3; 688/3; 689/3; 690/3; 691/3; 692/3; 693/3; 694/3; 695/3; 696/3; 697/3; 698/3; 699/3; 700/3; 701/3; 702/3; 703/3; 704/3; 705/3; 706/3; 707/3; 708/3; 709/3; 710/3; 711/3; 712/3; 713/3; 714/3; 715/3; 716/3; 717/3; 718/3; 719/3; 720/3; 721/3; 722/3; 723/3; 724/3; 725/3; 726/3; 727/3; 728/3; 729/3; 730/3; 731/3; 732/3; 733/3; 734/3; 735/3; 736/3; 737/3; 738/3; 739/3; 740/3; 741/3; 742/3; 743/3; 744/3; 745/3; 746/3; 747/3; 748/3; 749/3; 750/3; 751/3; 752/3; 753/3; 754/3; 755/3; 756/3; 757/3; 758/3; 759/3; 760/3; 761/3; 762/3; 763/3; 764/3; 765/3; 766/3; 767/3; 768/3; 769/3; 770/3; 771/3; 772/3; 773/3; 774/3; 775/3; 776/3; 777/3; 778/3; 779/3; 780/3; 781/3; 782/3; 783/3; 784/3; 785/3; 786/3; 787/3; 788/3; 789/3; 790/3; 791/3; 792/3; 793/3; 794/3; 795/3; 796/3; 797/3; 798/3; 799/3; 800/3; 801/3; 802/3; 803/3; 804/3; 805/3; 806/3; 807/3; 808/3; 809/3; 810/3; 811/3; 812/3; 813/3; 814/3; 815/3; 816/3; 817/3; 818/3; 819/3; 820/3; 821/3; 822/3; 823/3; 824/3; 825/3; 826/3; 827/3; 828/3; 829/3; 830/3; 831/3; 832/3; 833/3; 834/3; 835/3; 836/3; 837/3; 838/3; 839/3; 840/3; 841/3; 842/3; 843/3; 844/3; 845/3; 846/3; 847/3; 848/3; 849/3; 850/3; 851/3; 852/3; 853/3; 854/3; 855/3; 856/3; 857/3; 858/3; 859/3; 860/3; 861/3; 862/3; 863/3; 864/3; 865/3; 866/3; 867/3; 868/3; 869/3; 870/3; 871/3; 872/3; 873/3; 874/3; 875/3; 876/3; 877/3; 878/3; 879/3; 880/3; 881/3; 882/3; 883/3; 884/3; 885/3; 886/3; 887/3; 888/3; 889/3; 890/3; 891/3; 892/3; 893/3; 894/3; 895/3; 896/3; 897/3; 898/3; 899/3; 900/3; 901/3; 902/3; 903/3; 904/3; 905/3; 906/3; 907/3; 908/3; 909/3; 910/3; 911/3; 912/3; 913/3; 914/3; 915/3; 916/3; 917/3; 918/3; 919/3; 920/3; 921/3; 922/3; 923/3; 924/3; 925/3; 926/3; 927/3; 928/3; 929/3; 930/3; 931/3; 932/3; 933/3; 934/3; 935/3; 936/3; 937/3; 938/3; 939/3; 940/3; 941/3; 942/3; 943/3; 944/3; 945/3; 946/3; 947/3; 948/3; 949/3; 950/3; 951/3; 952/3; 953/3; 954/3; 955/3; 956/3; 957/3; 958/3; 959/3; 960/3; 961/3; 962/3; 963/3; 964/3; 965/3; 966/3; 967/3; 968/3; 969/3; 970/3; 971/3; 972/3; 973/3; 974/3; 975/3; 976/3; 977/3; 978/3; 979/3; 980/3; 981/3; 982/3; 983/3; 984/3; 985/3; 986/3; 987/3; 988/3; 989/3; 990/3; 991/3; 992/3; 993/3; 994/3; 995/3; 996/3; 997/3; 998/3; 999/3; 1000/3; 1001/3; 1002/3; 1003/3; 1004/3; 1005/3; 1006/3; 1007/3; 1008/3; 1009/3; 1010/3; 1011/3; 1012/3; 1013/3; 1014/3; 1015/3; 1016/3; 1017/3; 1018/3; 1019/3; 1020/3; 1021/3; 1022/3; 1023/3; 1024/3; 1025/3; 1026/3; 1027/3; 1028/3; 1029/3; 1030/3; 1031/3; 1032/3; 1033/3; 1034/3; 1035/3; 1036/3; 1037/3; 1038/3; 1039/3; 1040/3; 1041/3; 1042/3; 1043/3; 1044/3; 1045/3; 1046/3; 1047/3; 1048/3; 1049/3; 1050/3; 1051/3; 1052/3; 1053/3; 1054/3; 1055/3; 1056/3; 1057/3; 1058/3; 1059/3; 1060/3; 1061/3; 1062/3; 1063/3; 1064/3; 1065/3; 1066/3; 1067/3; 1068/3; 1069/3; 1070/3; 1071/3; 1072/3; 1073/3; 1074/3; 1075/3; 1076/3; 1077/3; 1078/3; 1079/3; 1080/3; 1081/3; 1082/3; 1083/3; 1084/3; 1085/3; 1086/3; 1087/3; 1088/3; 1089/3; 1090/3; 1091/3; 1092/3; 1093/3; 1094/3; 1095/3; 1096/3; 1097/3; 1098/3; 1099/3; 1100/3; 1101/3; 1102/3; 1103/3; 1104/3; 1105/3; 1106/3; 1107/3; 1108/3; 1109/3; 1110/3; 1111/3; 1112/3; 1113/3; 1114/3; 1115/3; 1116/3; 1117/3; 1118/3; 1119/3; 1120/3; 1121/3; 1122/3; 1123/3; 1124/3; 1125/3; 1126/3; 1127/3; 1128/3; 1129/3; 1130/3; 1131/3; 1132/3; 1133/3; 1134/3; 1135/3; 1136/3; 1137/3; 1138/3; 1139/3; 1140/3; 1141/3; 1142/3; 1143/3; 1144/3; 1145/3; 1146/3; 1147/3; 1148/3; 1149/3; 1150/3; 1151/3; 1152/3; 1153/3; 1154/3; 1155/3; 1156/3; 1157/3; 1158/3; 1159/3; 1160/3; 1161/3; 1162/3; 1163/3; 1164/3; 1165/3; 1166/3; 1167/3; 1168/3; 1169/3; 1170/3; 1171/3; 1172/3; 1173/3; 1174/3; 1175/3; 1176/3; 1177/3; 1178/3; 1179/3; 1180/3; 1181/3; 1182/3; 1183/3; 1184/3; 1185/3; 1186/3; 1187/3; 1188/3; 1189/3; 1190/3; 1191/3; 1192/3; 1193/3; 1194/3; 1195/3; 1196/3; 1197/3; 11



QY	59	KRSSRFRFGALVCSMDSCRSRVAVTY-----RFTLLNIPSPAVWMA	102
Db	175	KLLTPVAFCHALGHVTSNAGFAVRVSFTTHVKALEBFFFNAAASQFILGQQIPL-ALWLS	233
RESULT 7			
Db	833934	hypothetical protein BH2276 [imported] - Bacillus halodurans (strain C-125)	
C	Species:	Bacillus halodurans	
C	Date:	01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004	
C	Accession:	D83934	
R	Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira		
Nucleic Acids Res.	28,	4317-4331, 2000	
A	Title:	Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and	
A	Reference number:	A83650; MUID:20512582; PMID:11058132	
A	Accession:	D83934	
A	Status:	preliminary	
A	Molecule type:	DNA	
A	Residues:	1-392 <S70>	
A	Cross-references:	UNIPROT:Q9KAL1; GB:BA001515; GB:BA000004; NID:gl0174886; PIDN:BA8059	
A	Experimental source:	strain C-125	
A	Genetics:		
A	Gene:	BH2276	
Query Match 11.0%; Score 71.5; DB 2; Length 392;			
Best Local Similarity 26.8%; Pred. No. 3; Mismatches 47; Indels 25; Gaps 6;			
Matches 33; Conservative 18; Mismatches 47; Indels 25; Gaps 6;			
QY	15	ISALFNFGPRYLXGVPFYFLVRIISFL-----IGDMEDVLLNCTLLKRSSRF---RF	66
Db	82	IVAIFAFMGAASFAG---YFIMFVLFLSPPTALGDS---LAQKTAINRRLSFGKIRM	135
QY	67	WGAUVCSMDSCR-----FSRVAVTVRFTLLNIPSPAVWM-----ARNTIDQOVLRIK	115
Db	136	WGSGLGFTSLAVGYILAAIGVTYIMVPLAVTVISLWLSRGLDFDFTTKPVTLLSALK	195
QY	116	LEI 118	
Db	196	LAI 198	
RESULT 8			
Db	H81040	penicillin-binding protein 1 NMB1807 [imported] - Neisseria meningitidis (strain MC58 se	
C	Species:	Neisseria meningitidis	
C	Date:	31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004	
C	Accession:	H81040; F81985	
R	Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A		
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.			
ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scariato, V.; Massignani, V.; Pizza, M.			
Science	287,	1809-1815, 2000	
A	Authors:	Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve	
A	Title:	Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.	
A	Reference number:	A81000; MUID:20175755; PMID:10710307	
A	Accession:	H81040	
A	Status:	preliminary	
A	Molecule type:	DNA	
A	Residues:	1-798 <TET>	
A	Cross-references:	UNIPROT:O05194; GB:AE002530; GB:AE002098; NID:g7227054; PIDN:AAF4214	
A	Experimental source:	serogroup B, strain MC58	
R	Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel		
i Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,			
Nature	404,	502-506, 2000	
A	Title:	Complete DNA sequence of a serogroup A strain of Neisseria meningitidis 22491.	
A	Reference number:	A81775; MUID:20222556; PMID:10761919	
A	Accession:	F81985	
A	Status:	preliminary	
A	Molecule type:	DNA	
A	Residues:	1-798 <PAR>	
A	Cross-references:	GB:AL162753; GB:AL157959; NID:g7379120; PIDN:CAB83943.1; PID:g737938	
A	Experimental source:	serogroup A, strain 22491	
A	Genetics:		
A	Gene:	ponA; NMB1807; NMA0655	

C;Superfamily: penicillin-binding protein			
Query Match 11.0%; Score 71.5; DB 2; Length 798;			
Best Local Similarity 31.2%; Pred. No. 6.4; Mismatches 9; Indels 13; Gaps 3;			
Matches 24; Conservative 9; Mismatches 31; Indels 13; Gaps 3;			
RESULT 9			
Db	45	IGDMEDVLLNCTLLKRSSRF-RFWGALVCSMDSCRSRVAVTVRFTLLNIPSPAVWMAR	103
Db	73	IGDFPEVLRNAVTAEDKRFYRHG-----VDVMGVARAAVG-----NWVSGSVQSGA	120
QY	104	NTIDQOVLRIKLEIKR	120
Db	121	STITQOVAKNFYLSSEK	137
nitrate ABC transporter, permease protein (nrtB-1) homolog - Archaeoglobus fulgidus			
C	Species:	Archaeoglobus fulgidus	
C	Date:	05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004	
C	Accession:	F69260	
R	Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson		
.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.			
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.			
Nature	390,	364-370, 1997	
A	Authors:	Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.	
Smith, H.O.; Woese, C.R.; Venter, J.C.			
A	Title:	The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo	
A	Reference number:	A69250; MUID:98049343; PMID:9389475	
A	Accession:	F69260	
A	Status:	preliminary; nucleic acid sequence not shown; translation not shown	
A	Molecule type:	DNA	
A	Residues:	1-244 <KLE>	
A	Cross-references:	UNIPROT:O30150; GB:AE001100; GB:AE000782; NID:g2689423; PIDN:AAB9111	
C	Superfamily:	Synechococcus nitrate transport protein nrtB	
Query Match 10.9%; Score 71; DB 2; Length 244;			
Best Local Similarity 25.6%; Pred. No. 2.1; Mismatches 35; Indels 10; Gaps 2;			
Matches 23; Conservative 22; Mismatches 35; Indels 10; Gaps 2;			
QY	25	YLXGVFPFYFLVRIISFLIGDMEDVLLNCTLLKRSSRFRFGALVCSMDSCRSRVAV	84
Db	93	YLLVPIPHIVLLPLYILLFGDLSRVLLIATIL-----FFQIAVTRDA---AKQVS	142
QY	85	TYRFTLLNIPSPAVWMARNTIDQOVLRSI	114
Db	143	DYVYVSILSGASKIDIYRHIIPAVMPKI	172
RESULT 10			
Db	C69120	conserved hypothetical protein MTH1898 - Methanobacterium thermoautotrophicum (strain De	
C	Species:	Methanobacterium thermoautotrophicum	
C	Date:	05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004	
C	Accession:	C69120	
R	Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;		
Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.			
ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.			
J. Bacteriol.	179,	7135-7155, 1997	
A	Title:	Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct	
A	Reference number:	A69000; MUID:98037514; PMID:9371463	
A	Accession:	C69120	
A	Status:	preliminary; nucleic acid sequence not shown; translation not shown	
A	Molecule type:	DNA	
A	Residues:	1-672 <MTH>	
A	Cross-references:	UNIPROT:O27920; GB:AE000941; GB:AE000666; NID:g2623025; PIDN:AAB8635	
A	Experimental source:	strain Delta H	
C	Genetics:		
A	Gene:	MTH1898	
A	Start codon:	TTG	
Query Match 10.8%; Score 70.5; DB 2; Length 672;			
Best Local Similarity 27.5%; Pred. No. 6.9;			



C;Accession: H89103  
R;anonymous, The C. elegans Sequencing Consortium.  
Science 282, 2012-2018, 1998  
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biological processes  
A;Reference number: A75000; MUID:99069613; PMID:9851916  
A;Note: see websites genome.wustl.edu/gsc/C\_elegans/ and www.sanger.ac.uk/Projects/C\_elegans/  
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and Science 283, 2103, 1999; and  
A;Accession: H89103  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-297 <STO>  
A;Cross-references: UNIPROT:P91077; GB:chr\_V; PIDN:AAC25812.1; PID:g3294493; GSPDB:GN000  
C;Genetics:  
A;Gene: C18810.1  
A;Map position: 5

Query Match 10.5%; Score 68.5; DB 2; Length 297;  
Best Local Similarity 30.4%; Pred. No. 4.9;  
Matches 21; Conservative 18; Mismatches 19; Indels 11; Gaps 3;  
Qy 36 ILVRIISFLIGDMEDVLL--NCTLLKSSRRFRFWGALVCSMDSCRFS-----RVAVT 85  
Db 136 VIVILAILSLGTLENLVLFQSC-TLNLSPKNGVLRCAVDACFFSYWASDRSAMPALN 194  
Qy 86 YRFITLNI 94  
Db 195 FIFGGLLSI 203

Search completed: October 11, 2005, 07:01:32  
Job time : 21.9198 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 11, 2005, 06:57:07 ; Search time 73.2326 Seconds  
(without alignments)  
853.085 Million cell updates/sec

Title: US-10-092-934-2  
Perfect score: 651  
Sequence: 1 MMVCWRFRFGKWYFSAIFN.....RNTIDQQVLSRIKLEIKRCL 122

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	88	13.5	282	2	Q57787
2	79.5	12.2	417	2	Q9FTT3
3	78	12.0	417	2	Q9ARH5
4	77.5	11.9	401	2	O40568
5	77	11.8	280	2	Q9V2J1
6	76.5	11.8	265	2	Q8MYN2
7	75	11.5	295	2	Q8PS42
8	75	11.5	402	2	Q9ATY2
9	74.5	11.4	178	2	Q8IF34
10	74.5	11.4	320	2	Q8LA34
11	74.5	11.4	380	2	Q75FMI
12	74.5	11.4	380	2	Q8EXK4
13	74.5	11.4	449	2	Q8W47
14	74.5	11.4	462	2	Q7R1C2
15	74	11.4	347	1	QPSV_XENLA
16	73.5	11.3	515	2	Q8OWT4
17	73	11.2	463	2	Q8G4Y8
18	73	11.2	483	2	Q64017
19	72.5	11.1	268	2	Q97C97
20	72.5	11.1	384	2	Q8Z40
21	72.5	11.1	790	2	Q6DHES
22	72	11.1	263	2	Q6CS38
23	72	11.1	447	2	Q63231
24	72	11.1	1008	2	Q9VQZ8
25	71.5	11.0	392	2	Q8KAT1
26	71.5	11.0	394	2	Q8Z49
27	71.5	11.0	797	1	PBPA_NEIGO
28	71.5	11.0	798	1	PBPA_NEIMA
29	71.5	11.0	1278	2	Q9U8G3
30	71	10.9	244	2	O30150
31	71	10.9	783	1	CRSB_XENLA

32	70.5	10.8	314	2	Q8E427
33	70.5	10.8	672	2	O27920
34	70	10.8	394	2	Q6VV64
35	70	10.8	409	1	CPTX_MAIZE
36	70	10.8	492	2	Q83E30
37	70	10.8	581	2	Q6CUT8
38	70	10.8	634	2	Q8S298
39	70	10.8	855	2	Q9AW68
40	70	10.8	1564	2	Q8ISW4
41	69.5	10.7	148	1	NU3M_HANWI
42	69	10.6	205	1	CYOC_BUCAI
43	69	10.6	353	2	Q6FTC4
44	69	10.6	421	2	Q98IA5
45	68.5	10.5	297	2	P91077

ALIGNMENTS

RESULT 1

O57787 ID O57787 PRELIMINARY; PRT; 282 AA.  
AC O57787;  
DT 01-AUG-1998 (TrEMBLrel. 07, Created)  
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Hypothetical protein PH0076.  
GN OrderedLocusNames=PH0076;  
OS Pyrococcus horikoshii.  
OC Archaea; Euryarchaeota; Thermococci; Thermococcaceae;  
OC Pyrococcus.  
OX NCBI\_TaxID=53953;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=OT3;  
RX MEDLINE=98344137; PubMed=9679194;  
RA Kawarabayashi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y., Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y., Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y., Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K., Mauchli Y., Shizuya H., Kikuchi H.;  
RT "Complete sequence and gene organization of the genome of a hyper-thermophilic archaeobacterium, Pyrococcus horikoshii OT3.";  
RL DNA Res. 5:55-76(1998).  
DR EMBL; AP000001; BAA29145.1; -.  
DR PIR; B71227; B71227.  
DR InterPro; IPR008553; DUF835.  
DR Pfam; PF05763; DUF835; 1.  
KW Complete proteome; Hypothetical protein.  
SQ SEQUENCE 282 AA; 32359 MW; C960845D3B178747 CRC64;

Query Match 13.5%; Score 88; DB 2; Length 282;  
Best Local Similarity 27.4%; Pred. No. 0.34;  
Matches 31; Conservative 16; Mismatches 42; Indels 24; Gaps 6;

Qy	6	NREKQWYFSAIFNFGPRVLYHGVFYLIVRIISFLI--GDMDVLNCTLLKSSR 63
Db	73	NQYETWQFFRSIFITMAA-----FFLLASVLSFYVFGKKRYVFK--VVSEAKL 120
Qy	64	FRFWGALVCSMDSCFRSRVAVYRFTILNIPSPAVVMARNTIDQVLSRIKL 116
Db	121	SKLGWGYCDRNSC-----YAV---FKALLNARLPGLAIAR---DPPEIFREKL 163

RESULT 2

O9FTT3 ID O9FTT3 PRELIMINARY; PRT; 417 AA.  
AC O9FTT3;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
DE Putative triose phosphate/phosphate translocator.

```

GN Name=OSJNBa0086P08.23; Synonyms=OSJNBa0010K01.4;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=12474738; DOI=10.1038/nature01184;
RA Sasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y.,
RA Wu J., Niimura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H.,
RA Hosokawa S., Masukawa M., Arikawa K., Chiden Y., Hayashi M.,
RA Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C.,
RA Hijiishi S., Honda M., Ichikawa Y., Idonuma A., Iijima M., Ikeda M.,
RA Ikeno M., Itoh S., Itoh Y., Itoh Y., Iwabuchi A., Kamiya K.,
RA Karasawa W., Katagiri S., Kikuta A., Kobayashi N., Kono I.,
RA Machita K., Maehara T., Mizuno H., Mizubayashi T., Mukai Y.,
RA Nagasaki H., Nakashima M., Nakama Y., Nakamichi Y., Nakamura M.,
RA Namiki N., Negishi M., Ohta I., Ono N., Saji S., Sakai K., Shibata M.,
RA Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Tsuji K.,
RA Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K.,
RA Zhong H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.I., Eun M.Y.,
RA Yano M., Jiang J., Gojobori T.;
RT "The genome sequence and structure of rice chromosome 1.";
RL Nature 420:312-316(2002).
DR EMBL; AP002855; BAB17213.1; -.
DR EMBL; AP003210; BAB40092.1; -.
DR Gramene; Q9FTT3; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; F:transport; IEA.
DR InterPro; IPR004853; DUF250.
DR InterPro; IPR004696; Tpt_PEP_transl.
DR Pfam; PF03151; DUF250; 1.
DR TIGRFAMS; TIGR00817; tpt; 1.
SQ SEQUENCE 417 AA; 44643 MW; 32B4E1930715E38B CRC64;

Query Match 12.2%; Score 79.5; DB 2; Length 417;
Best Local Similarity 23.3%; Pred. No. 4.1;
Matches 28; Conservative 25; Mismatches 40; Indels 27; Gaps 5;

QY 8 FGKWWYFISAIENFGPRYLHGVPF-YFLILVR-----IISFLIGMEDVLLNCTLL 58
DB 120 FFMW-YFLNVIFENILNKIYNYPYPYFVSVIHLVGWVYCLVSWTGLPKRAPINSTLL 178

QY 59 KRSSRRFRFGALVCSMDSCFRSRAVAVTY 86
DB 179 KLLFPVALCHALGHVTSNVSFATVAVSF 206

RESULT 3
ID Q9ARH5 PRELIMINARY; PRT; 417 AA.
AC Q9ARH5
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE Triose phosphate/phosphate translocator.
OS Oryza sativa (rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RX Wang Q., Chen J., Wang X., Sun J., Sha W.;
RT "Molecular cloning and expression analysis of the rice triose
phosphate/phosphate translocator gene.";
RL Plant Sci. 162:785-790(2002).
DR EMBL; AY028422; AAK27373.1; -.
DR Gramene; Q9ARH5; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.

Query Match 12.2%; Score 79.5; DB 2; Length 417;
Best Local Similarity 23.3%; Pred. No. 4.1;
Matches 28; Conservative 25; Mismatches 40; Indels 27; Gaps 5;

QY 8 FGKWWYFISAIENFGPRYLHGVPF-YFLILVR-----IISFLIGMEDVLLNCTLL 58
DB 120 FFMW-YFLNVIFENILNKIYNYPYPYFVSVIHLVGWVYCLVSWTGLPKRAPINSTLL 178

QY 59 KRSSRRFRFGALVCSMDSCFRSRAVAVTY 86
DB 179 KLLFPVALCHALGHVTSNVSFATVAVSF 206

RESULT 4
ID Q40568 PRELIMINARY; PRT; 401 AA.
AC Q40568
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE Phosphate translocator precursor.
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Leaf;
RC MEDLINE=94166771; PubMed=8121415;
RA Knight J.S., Gray J.C.;
RT "Expression of genes encoding the tobacco chloroplast phosphate
translocator is not light-regulated and is repressed by sucrose.";
RL Mol. Gen. Genet. 242:586-594(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Leaf;
RA Gray J.;
RL Submitted (AUG-1993) to the EMBL/GenBank/DBJ databases.
DR EMBL; X75088; CAAS2979.1; -.
DR PIR; S42583; S42583.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; F:transport; IEA.
DR InterPro; IPR004853; DUF250.
DR InterPro; IPR004696; Tpt_PEP_transl.
DR Pfam; PF03151; DUF250; 1.
DR TIGRFAMS; TIGR00817; tpt; 1.
KW Signal.
FT SIGNAL 1 73 Potential phosphate translocator.
FT CHAIN 74 401
SQ SEQUENCE 401 AA; 43705 MW; 36CC6B5859A45035 CRC64;

Query Match 11.9%; Score 77.5; DB 2; Length 401;
Best Local Similarity 25.0%; Pred. No. 6.5;
Matches 30; Conservative 24; Mismatches 39; Indels 27; Gaps 5;

QY 8 FGKWWYFISAIENFGPRYLHGVPF-YFLILVR-----IISFLIGMEDVLLNCTLL 58
DB 103 FFMW-YFLNVIFENILNKIYNYPYPYFVSVIHLVGWVYCLVSWTGLPKRAPIDSTQL 161

QY 59 KRSSRRFRFGALVCSMDSCFRSRAVAVTY 86
DB 162 KLLTPVAFCHALGHVTSNVSFATVAVSFTHTIKALEPFFNFASQFILGQQLPL-ALWLS 220

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RA Ferro E.S., Ferro M.I.T., Furlan L.R., Gamberini M., Gigliotti E.A.,
RA Goeb-Neto A., Goldman G.H., Goldman M.H.S., Harakava R.,
RA Jeronimo S.M.B., Junqueira-de-Azevedo I.L.M., Kimura E.T.,
RA Kuramae E.E., Lemos E.G.M., Lemos M.V.F., Marino C.L., Nunes L.R.,
RA de Oliveira R.C., Pereira G.G., Reis M.S., Schriefer A.,
RA Siqueira W.J., Sommer P., Tsai S.M., Simpson A.J.G., Ferro J.A.,
RA Camargo L.E.A., Kitajima J.P., Setubal J.C., Van Sluys M.A.,
RT "Comparative genomics of two Leptospira interrogans serovars reveals
RT novel insights into physiology and pathogenesis.";
RL J. Bacteriol. 186:2164-2172(2004).
DR EMBL; AE016824; AAS72189.1; -.
DR GO; GO:0009058; P:biosynthesis; IEA.
DR InterPro; IPR001296; Glyco trans 1.
DR Pfam; PF00534; Glycos_transf_1; I.
KW Complete proteome.
SQ SEQUENCE 380 AA; 43772 MW; FB289EA9C63D6D6F CRC64;

Query Match 11.4%; Score 74.5; DB 2; Length 380;
Best Local Similarity 28.6%; Pred. No. 13;
Matches 28; Conservative 13; Mismatches 44; Indels 13; Gaps 5;

Qy 25 YLHGVPFYFLVRIIS-----FLIGDMEDVL-LNCTLLKRSRFR---FWGALVCSM 74
||| : : : : : : : : : : : : : : : : : : : : : : : :
Db 49 YLYSNKPIH-TVFYDILSNPNRSFFMTGKFGIILNCTVPKRISKORLDFWGTQLLP 107
||| : : : : : : : : : : : : : : : : : : : : : : : :

Qy 75 DSCFRSVAVTYRFTLLNIPSPAVWMAWNTIDQOVLS 112
||| : : : : : : : : : : : : : : : : : : : : : : : :
Db 108 LICGGALTAVNHDNLNFR--AAPXTMTTNSFWQHKILS 143

RESULT 12
Q8EXK4 PRELIMINARY; PRT; 380 AA.
AC Q8EXK4;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Mannosyltransferase A.
GN Name=ntfa; OrderedLocusNames=LB204;
OS Leptospira interrogans.
OC Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
OX NCBI_TaxID=173;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar lai;
RX MEDLINE=22598143; PubMed=12712204; DOI=10.1038/nature01597;
RA Ren S.-X., Fu G., Jiang X.-G., Zeng R., Miao Y.-G., Xu H.,
RA Zhang Y.-X., Xiong H., Lu G., Lu L.-P., Jiang H.-Q., Jia J., Tu Y.-F.,
RA Jiang J.-X., Gu W.-Y., Zhang Y.-Q., Cai Z., Sheng H.-H., Yin H.-F.,
RA Zhang Y., Zhu G.-F., Wan M., Huang H.-L., Qian Z., Wang S.-Y., Ma W.,
RA Yao Z.-J., Shen Y., Qiang B.-Q., Xia Q.-C., Guo X.-K., Danchin A.,
RA Saint Girons I., Somerville R.L., Wen Y.-M., Shi M.-H., Chen Z.,
RA Xu J.-G., Zhao G.-P.;
RT "Unique physiological and pathogenic features of Leptospira
RT interrogans revealed by whole-genome sequencing.";
RL Nature 422:888-893(2003).
DR EMBL; AE011608; AAN51763.1; -.
DR GO; GO:0009058; P:biosynthesis; IEA.
KW Complete proteome.
SQ SEQUENCE 380 AA; 43772 MW; FB289EA9C63D6D6F CRC64;

Query Match 11.4%; Score 74.5; DB 2; Length 380;
Best Local Similarity 28.6%; Pred. No. 13;
Matches 28; Conservative 13; Mismatches 44; Indels 13; Gaps 5;

Qy 25 YLHGVPFYFLVRIIS-----FLIGDMEDVL-LNCTLLKRSRFR---FWGALVCSM 74
||| : : : : : : : : : : : : : : : : : : : : : : : :
Db 49 YLYSNKPIH-TVFYDILSNPNRSFFMTGKFGIILNCTVPKRISKORLDFWGTQLLP 107
||| : : : : : : : : : : : : : : : : : : : : : : : :

Qy 75 DSCFRSVAVTYRFTLLNIPSPAVWMAWNTIDQOVLS 112
||| : : : : : : : : : : : : : : : : : : : : : : : :
Db 108 LICGGALTAVNHDNLNFR--AAPXTMTTNSFWQHKILS 143

RESULT 13
Q88W47 PRELIMINARY; PRT; 449 AA.
AC Q88W47;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Integral membrane protein.
GN OrderedLocusNames=lp_1815;
OS Lactobacillus plantarum.
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OX NCBI_TaxID=1590;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCIMB 8826 / WCFS1;
RX MEDLINE=22480296; PubMed=12566566; DOI=10.1073/pnas.0337704100;
RA Kleerebezem M., Boekhorst J., van Kranenburg R., Molenaar D.,
RA Kuipers O.P., Leer R., Tarchini R., Peters S.A., Sandbrink H.M.,
RA Fiers M.W.E.J., Stiekema W., Klein Lankhorst R.M., Bron P.A.,
RA Hoffer S.M., Nierop Groot M.N., Kerkhoven R., De Vries M., Ursing B.,
RA De Vos W.M., Siezen R.J.;
RT "Complete genome sequence of Lactobacillus plantarum WCFS1.";
RL Proc. Natl Acad. Sci. U.S.A. 100:1990-1995(2003).
DR EMBL; AL935257; CAB64224.1; -.
KW Complete proteome.
SQ SEQUENCE 449 AA; 50073 MW; 59A911D45E3E474B CRC64;

Query Match 11.4%; Score 74.5; DB 2; Length 449;
Best Local Similarity 22.5%; Pred. No. 15;
Matches 32; Conservative 23; Mismatches 40; Indels 47; Gaps 7;

Qy 8 FGKW-VYFISAFNFG-----PRLYHG-----VFFVFLI 36
||| : : : : : : : : : : : : : : : : : : : : : : : :
Db 277 FGKMGVLPFAIYLLGPGTCRPLVLLGRHDLHRTTIARGLLVGHLLVATAQPLVVA 336
||| : : : : : : : : : : : : : : : : : : : : : : : :

Qy 37 LVRIISFLIGDMEDVLLNCTL-----LKRSSRFHWGALVCSMDSCRSRVAV- 84
||| : : : : : : : : : : : : : : : : : : : : : : : :
Db 337 GLLIISLYVG-FENPAINTSVYATVNDPDLAIHKYRFTSYGGLLQCL--CFFGLLVIV 393
||| : : : : : : : : : : : : : : : : : : : : : : : :

Qy 85 -TVRFITLLNIPSPAVWMAWNT 105
||| : : : : : : : : : : : : : : : : : : : : : : : :
Db 394 SSFQQLNLLNFFNPASTALKNT 415

RESULT 14
Q7RIC2 PRELIMINARY; PRT; 462 AA.
AC Q7RIC2;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE GUP 306 47338 45950.
OS Giardia lamblia ATCC 50803.
OC Eukaryota; Diplomonadida; Hexamitidae; Giardiinae; Giardia.
OX NCBI_TaxID=184922;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WB C6;
RA Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D.,
RA Olsen G.J., Sogin M.L.;
RT "Draft sequence of the Giardia lamblia genome.";
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AACB0100028; EAA41122.1; -.
SQ SEQUENCE 462 AA; 52140 MW; 278538F81B35F016 CRC64;

Query Match 11.4%; Score 74.5; DB 2; Length 462;
Best Local Similarity 24.2%; Pred. No. 16;
Matches 36; Conservative 20; Mismatches 50; Indels 43; Gaps 8;

```



GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: October 11, 2005, 06:57:07 ; Search time 90.3583 Seconds  
(without alignments)  
522.196 Million cell updates/sec

Title: US-10-092-934-2

Perfect score: 651

Sequence: 1 MMVWNRFGKVVVFISAFN.....RNTIDQOVLSRIKLEIKRCL 122

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq16Dec04:\*

1: Geneseqp1980s:\*

2: Geneseqp1990s:\*

3: Geneseqp2000s:\*

4: Geneseqp2001s:\*

5: Geneseqp2002s:\*

6: Geneseqp2003as:\*

7: Geneseqp2003bs:\*

8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	651	100.0	122	2	AAR63237 Neural th
2	651	100.0	122	2	AAR95916 AD 3-4 hu
3	651	100.0	122	5	AAE29143 Neural th
4	651	100.0	122	6	ABR63241 122 amino
5	651	100.0	122	6	ABU02973 Human neu
6	651	100.0	122	6	ABP59924 Human 122
7	651	100.0	122	6	AAE33190 Neural th
8	651	100.0	122	6	ABJ19446 122-mer n
9	651	100.0	122	7	ADB37520 Neural th
10	651	100.0	122	7	ADL96022 Human neu
11	94	14.4	15	6	ABP59884 Human neu
12	94	14.4	15	7	ADL96030 Human neu
13	84	12.9	15	6	ABP59885 Human neu
14	84	12.9	15	7	ADL96031 Human neu
15	83	12.7	15	6	ABP59888 Human neu
16	83	12.7	15	7	ADL96034 Human neu
17	82	12.6	17	6	ABP59883 Human neu
18	82	12.6	17	7	ADB37533 Neural th
19	82	12.6	17	7	ADL96029 Human neu
20	80	12.3	15	6	ABP59890 Human neu
21	80	12.3	15	7	ADL96036 Human neu
22	78	12.0	15	6	ABP59887 Human neu
23	78	12.0	15	7	ADL96033 Human neu
24	77	11.8	15	6	ABP59889 Human neu
25	77	11.8	15	7	ADL96035 Human neu

26	76	11.7	320	6	ABP80429 N. gonorr
27	76	11.7	515	7	ABO65789 Klebsiell
28	74.5	11.4	239	3	AAQ05704 Arabidops
29	74.5	11.4	320	3	AAQ05703 Arabidops
30	74.5	11.4	321	3	AAQ05702 Arabidops
31	73.5	11.3	118	5	AAAM48171 Human dih
32	73.5	11.3	515	8	ADO28999 Mouse nov
33	73	11.2	15	6	ABP59886 Human neu
34	73	11.2	15	7	ADL96032 Human neu
35	72	11.1	345	7	ABM73876 DNA clone
36	72	11.1	347	7	ABM74181 DNA clone
37	72	11.1	1008	4	ABB70613 Drosophil
38	71.5	11.0	798	6	ABU37842 Protein e
39	71.5	11.0	805	3	AAV75603 Neisseria
40	71.5	11.0	805	3	AAV75601 Neisseria
41	71.5	11.0	805	3	AAV75602 Neisseria
42	71.5	11.0	805	6	ABP77700 N. gonorr
43	71.5	11.0	805	6	ABU37483 Protein e
44	68.5	10.5	178	2	AAV60130 Human end
45	68.5	10.5	1337	8	ADJ50050 Oil-assoc

## ALIGNMENTS

## RESULT 1

AAR63237  
ID AAR63237 standard; protein; 122 AA.

XX AAR63237;

XX AC

XX DT 25-MAR-2003 (revised)

XX DT 06-JUL-1995 (first entry)

XX DE Neural thread protein AD3-4.

XX KW Neural thread protein AD3-4; Alzheimer's; neuroectodermal tumours;

XX KW malignant astrocytomas; glioblastomas.

XX OS Rattus rattus.

XX FH Key Location/Qualifiers

XX FT Misc-difference 69..122

XX FT /note= "corresponding codons CTT TGG TCT GCT CGA TGG ATT

XX FT CTT GTC GAR TTT CTC GTG TGG CAG"

XX FN WO9423756-A1.

XX PD 27-OCT-1994.

XX PF 20-APR-1994; 94WO-US004321.

XX PR 20-APR-1993; 93US-00050559.

XX PA (GEHO ) GEN HOSPITAL CORP.

XX PI De La Monte SM, Wands JR;

XX DR WPI; 1994-341497/42.

XX DR N-PSDB; AAQ77875.

XX PT Detection of neural thread proteins - to detect sporadic and familial

XX PT Alzheimer's disease, neuroectodermal tumours, malignant astrocytomas and

XX PT glioblastomas (Eng).

XX PS Example 4; Fig 16f; 158pp; English.

XX CC AAQ77875 encodes AAR63237 the AD3-4 neural thread protein (NTP). These

XX CC sequences were used in the development of an antibody dependent method,

XX CC for the detection of NTPs. This new method could be used to diagnose

XX CC Alzheimer's disease (differentiating between sporadic and familial),

XX CC neuroectodermal tumours, malignant astrocytomas and glioblastomas.

XX CC (Updated on 25-MAR-2003 to correct FN field.)

XX SQ Sequence 122 AA;

Query Match 100.0%; Score 651; DB 2; Length 122;  
Best Local Similarity 100.0%; Pred. No. 1.9e-73;  
Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MMVWNRFKGVYFISAIENFGPRYLHGVPFYFLILVRIISFLIGDMEDVLLNCTLLKR 60  
Db 1 MMVWNRFKGVYFISAIENFGPRYLHGVPFYFLILVRIISFLIGDMEDVLLNCTLLKR 60

Qy 61 SSRFRWGALVCSMDSCRSRVAVTYRTITLINIPSPAVWMARNTIDQQVLSRKLEIKR 120  
Db 61 SSRFRWGALVCSMDSCRSRVAVTYRTITLINIPSPAVWMARNTIDQQVLSRKLEIKR 120

Qy 121 CL 122  
Db 121 CL 122

RESULT 3  
AAE29143  
ID AAE29143 standard; protein; 122 AA.  
XX AAE29143;  
AC AAE29143;  
DT 27-JAN-2003 (first entry)  
XX Neural thread protein (NTP) #1.  
DE Neural thread protein; NTP; hyperplasia; hypertrophy; arteriosclerosis;  
KW haemorrhoid; gene therapy; tumour; vascular disease; atherosclerosis;  
KW inflammatory disease; nutritional deficiency disease; genetic disease;  
KW autoimmune disease; metabolic disease; traumatic disease; intoxication;  
KW amyloid disease; fibrosis disease; storage disease; radiation disease;  
KW poisoning; environmental disease; endocrine disease; protein therapy;  
KW degenerative disease; mechanical disease.  
XX Unidentified.  
OS Unidentified.  
XX WO200274323-A2.  
PN WO200274323-A2.  
XX 26-SEP-2002.  
PD 26-SEP-2002.  
XX 08-MAR-2002; 2002WO-IB001959.  
PF 08-MAR-2001; 2001US-0273957P.  
XX 08-MAR-2001; 2001US-0273957P.  
PR (AVER/) AVERBACK P.  
PA AVERBACK P;  
XX AVERBACK P;  
PI AVERBACK P;  
XX WPI; 2002-759864/82.  
DR WPI; 2002-759864/82.  
XX Treating a condition in a patient requiring removal or destruction of  
PT cells, such as a benign or malignant tumor of a tissue or an inflammatory  
PT disease, comprises administering a neural thread protein (NTP) or a NTP  
PT gene to a mammal.

Claim 23; Fig 2; 70pp; English.

CC The invention relates to a method for treating a condition in a patient  
CC requiring removal or destruction of cells. The method involves  
CC administering to a mammal a neural thread protein (NTP), or administering  
CC to a tumour or other target cell a NTP gene, where the expression of the  
CC NTP gene is induced resulting in expression of the NTP protein. The  
CC method and NTP are useful for treating a condition in a patient requiring  
CC removal or destruction of cells, such as a benign or malignant tumour of  
CC a tissue, a hyperplasia, hypertrophy, or overgrowth of a tissue.  
CC preferably tonsillar hypertrophy or prostatic hyperplasia, a virally,  
CC bacterially, or parasitically altered tissue, or a malformation of a  
CC tissue. Other conditions include a cosmetic modification to a tissue,  
CC such as removal of unwanted facial hair warts or unwanted fatty tissue,  
CC a vascular disease, particularly atherosclerosis or arteriosclerosis,  
CC haemorrhoids, or varicose veins, an inflammatory disease, autoimmune  
CC disease, metabolic disease, hereditary/genetic disease, traumatic disease  
CC or physical injury, nutritional deficiency disease, infectious disease,  
CC congenital malformation, amyloid disease, fibrosis disease, storage  
CC

XX SQ Sequence 122 AA;

Query Match 100.0%; Score 651; DB 2; Length 122;  
Best Local Similarity 100.0%; Pred. No. 1.9e-73;  
Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MMVWNRFKGVYFISAIENFGPRYLHGVPFYFLILVRIISFLIGDMEDVLLNCTLLKR 60  
Db 1 MMVWNRFKGVYFISAIENFGPRYLHGVPFYFLILVRIISFLIGDMEDVLLNCTLLKR 60

Qy 61 SSRFRWGALVCSMDSCRSRVAVTYRTITLINIPSPAVWMARNTIDQQVLSRKLEIKR 120  
Db 61 SSRFRWGALVCSMDSCRSRVAVTYRTITLINIPSPAVWMARNTIDQQVLSRKLEIKR 120

Qy 121 CL 122  
Db 121 CL 122

RESULT 2  
AAR95916  
ID AAR95916 standard; protein; 122 AA.  
XX AAR95916;  
AC AAR95916;  
DT 14-NOV-1996 (first entry)  
XX AD 3-4 human neural thread protein clone (partial sequence).  
DE AD 3-4 human neural thread protein clone (partial sequence).  
KW Neural thread protein; NTP; diagnosis; detection; Alzheimer's disease;  
KW neuroectodermal tumour; malignant astrocytoma; monoclonal antibody;  
KW binding fragment.  
XX Homo sapiens.  
OS Homo sapiens.  
XX WO9615272-A1.  
PN WO9615272-A1.  
XX 23-MAY-1996.  
PD 23-MAY-1996.  
XX 14-NOV-1995; 95WO-US017111.  
PF 14-NOV-1994; 94US-00340426.  
XX 14-NOV-1994; 94US-00340426.  
PR (GEO ) GEN HOSPITAL CORP.  
PA De La Monte S, Wands JR;  
XX De La Monte S, Wands JR;  
PI De La Monte S, Wands JR;  
XX WPI; 1996-259865/26.  
DR WPI; 1996-259865/26.  
XX Detection of neural thread protein in diagnosis of Alzheimer's disease -  
PT also NTP DNA and protein sequences used in gene and anti-sense therapy.  
PT Example 4c; Fig 16f; 238pp; English.

CC A method for detecting the presence of neural thread protein (NTP) having  
CC a molecular weight of 8, 14, 17, 21, 26 or 42 kD in a human subject  
CC comprises (a) contacting a sample from a human subject that is suspected  
CC of containing the NTP with at least one molecule capable of binding to  
CC the protein; and (b) detecting any of the molecule bound to the protein.  
CC The binding molecule is selected from an antibody free of natural  
CC impurities, a monoclonal antibody or a binding fragment of either of  
CC these. The method may be used for diagnosing the presence of Alzheimer's  
CC disease, neuroectodermal tumours and a malignant astrocytoma in a human.  
CC A number of clones of neural thread protein were isolated from healthy 17  
CC -18 week old foetal human brain (HB) 2 year old temporal lobe neocortex  
CC and end stage Alzheimer's disease (AD) cerebral cortex. See AAT27753-75  
XX

XX SQ Sequence 122 AA;

Query Match 100.0%; Score 651; DB 2; Length 122;  
Best Local Similarity 100.0%; Pred. No. 1.9e-73;  
Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC disease, enzyme deficiency disease, poisoning, intoxication, degenerative  
CC disease, radiation disease, environmental disease, endocrine disease or  
CC mechanical disease. The invention is useful in protein therapy and gene  
CC therapy. The present sequence is NTP protein

XX SQ Sequence 122 AA;  
Query Match 100.0%; Score 651; DB 5; Length 122;  
Best Local Similarity 100.0%; Pred. No. 1.9e-73;  
Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MMVCNRFQKVVYFISAIENFGPRYLHGVPFFFLILVRIISFLIGDMEDVLLNCTLLKR 60  
Db 1 MMVCNRFQKVVYFISAIENFGPRYLHGVPFFFLILVRIISFLIGDMEDVLLNCTLLKR 60  
Qy 61 SSRFRFGALVCSMDSCRSFSAVYTFITLLNIPSPAVVMARNTIDQVLSRIKLEIKR 120  
Db 61 SSRFRFGALVCSMDSCRSFSAVYTFITLLNIPSPAVVMARNTIDQVLSRIKLEIKR 120  
Qy 121 CL 122  
Db 121 CL 122

## RESULT 4

ID ABR63241 standard; protein; 122 AA.

AC ABR63241;

XX 28-AUG-2003 (first entry)

DE 122 amino acid neural thread protein.

XX Cytostatic; Antibacterial; Immunosuppressive; Antiinflammatory;  
KW neural thread protein; NTP; tumour.

XX Unidentified.

XX WO2003008443-A2.

XX 30-JAN-2003.

XX 19-JUL-2002; 2002WO-CA001105.

XX 19-JUL-2001; 2001US-0306150P.

XX 19-JUL-2001; 2001US-0306161P.

XX 16-NOV-2001; 2001US-0331477P.

XX (NTMO-) NYMOX CORP.

XX Averbak PA;

XX WPI; 2003-247999/24.

XX Novel neural thread protein peptide, referred as cell death peptide,  
PT useful for treating prostatic hyperplasia, psoriasis, eczema, dermatosis,  
PT atherosclerosis, cosmetic modification to skin, throat, mouth, muscle.

XX Disclosure; Fig 2; 77pp; English.

XX The present invention relates to a neural thread protein (NTP) peptide  
CC referred to as cell death peptide. Thought to be cytostatic,  
CC antibacterial, immunosuppressive and antiinflammatory. It is useful for  
CC treating a condition in a patient requiring removal or destruction of  
CC cells, for treating a condition such as benign or malignant tumor.  
CC inflammatory disease, autoimmune disease and infectious disease. The  
CC peptide useful for treatment is derived from the amino acid sequence for  
CC a pancreatic thread protein. The peptide is conjugated, linked or bound  
CC to a molecule chosen from antibody or its fragment, antibody-like binding  
CC molecule, where the molecule has a higher affinity for binding to a tumor  
CC or other target than binding to other cells. Treatment using NTP peptides  
CC can remove benign tumors with less risk and fewer of the undesirable side

CC effects of surgery. The present sequence is an NTP amino acid sequence  
XX SQ Sequence 122 AA;

Query Match 100.0%; Score 651; DB 6; Length 122;  
Best Local Similarity 100.0%; Pred. No. 1.9e-73;  
Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MMVCNRFQKVVYFISAIENFGPRYLHGVPFFFLILVRIISFLIGDMEDVLLNCTLLKR 60  
Db 1 MMVCNRFQKVVYFISAIENFGPRYLHGVPFFFLILVRIISFLIGDMEDVLLNCTLLKR 60  
Qy 61 SSRFRFGALVCSMDSCRSFSAVYTFITLLNIPSPAVVMARNTIDQVLSRIKLEIKR 120  
Db 61 SSRFRFGALVCSMDSCRSFSAVYTFITLLNIPSPAVVMARNTIDQVLSRIKLEIKR 120  
Qy 121 CL 122  
Db 121 CL 122

## RESULT 5

ID ABU02973 standard; protein; 122 AA.

AC ABU02973;

XX 20-JAN-2003 (first entry)

DE Human neural thread protein AD7C-NTP, protein fragment #1.

XX Neural thread protein; NTP-peptide; AD7C-NTP; surgical excision;  
KW transplantation; grafting; chemotherapy; immunotherapy; vaccination;  
KW ablation; cryotherapy; laser therapy; phototherapy; gene therapy;  
KW radiation; tumour; hyperplasia; hypertrophy; overgrowth of tissue;  
KW malformation of tissue; tonsillary hypertrophy; prostatic hyperplasia;  
KW cosmetic modification; vascular disease; atherosclerosis;  
KW arteriosclerosis; haemorrhoid; varicose vein; inflammatory disease;  
KW autoimmune disease; metabolic disease; traumatic disease;  
KW physical injury; nutritional deficiency disease; infectious disease;  
KW amyloid disease; fibrosis disease; storage disease;  
KW congenital malformation; enzyme deficiency disease; poisoning;  
KW intoxication; environmental disease; radiation disease;  
KW endocrine disease; degenerative disease; mechanical disease.

XX Homo sapiens.

XX WO200297030-A2.

XX 05-DEC-2002.

XX 24-MAY-2002; 2002WO-CA000759.

XX 25-MAY-2001; 2001US-0293156P.

XX (NTMO-) NYMOX CORP.

XX Averbak PA;

XX WPI; 2003-041406/03.

XX Novel peptides similar in amino acid sequence to neural thread proteins  
PT (NTP), useful for treating unwanted cellular proliferations such as  
PT malignant tumors and prostatic hyperplasia.

XX Disclosure; Fig 2; 78pp; English.

XX The invention describes an NTP-peptide (I) comprising at least one amino  
CC acid sequence corresponding to part of the amino acid sequence of a  
CC neural thread protein, AD7C-NTP. The invention provides a method of  
CC treating a condition requiring removal or destruction of cells of a  
CC mammal comprising administering to a mammal, a therapeutic amount of (I).  
CC The treatment is administered to the mammal before, during or after

CC surgical excision, transplantation, grafting, chemotherapy,  
 CC immunotherapy, vaccination, thermal or electrical ablation, cryotherapy,  
 CC laser therapy, phototherapy, gene therapy and/or radiation. The method is  
 CC useful for treatment of benign or malignant tumour; hyperplasia,  
 CC hypertrophy or overgrowth of tissue; virally, bacterially or  
 CC parasitically altered tissue; malformation of tissue selected from lung,  
 CC breast, stomach, pancreas, prostate, bladder, bone, ovary, skin, kidney,  
 CC sinus, colon, intestine, rectum, esophagus, heart, spleen, salivary  
 CC gland, blood, brain and its coverings, spinal cord, muscle, connective  
 CC tissue, adrenal, parathyroid, thyroid, uterus, testis, pituitary,  
 CC reproductive organs, liver, hair, gall bladder, eye, ear, nose, throat,  
 CC tonsils, mouth and lymph nodes and lymphoid system; tonsillary  
 CC hypertrophy; prostatic hyperplasia; cosmetic modification to a tissue;  
 CC vascular disease (atherosclerosis or arteriosclerosis); haemorrhoids;  
 CC varicose veins; inflammatory disease; autoimmune disease; metabolic  
 CC disease; hereditary/genetic disease; traumatic disease; physical injury;  
 CC nutritional deficiency disease; infectious disease; amyloid disease;  
 CC fibrosis disease; storage disease; congenital malformation; enzyme  
 CC deficiency disease; poisoning; intoxication; environmental disease;  
 CC radiation disease; endocrine disease; degenerative disease and mechanical  
 CC disease. This is the amino acid sequence of a human neural thread protein  
 CC AD7C-NTP protein fragment  
 XX  
 SQ Sequence 122 AA;

Query Match 100.0%; Score 651; DB 6; Length 122;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-73;  
 Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MMVCNRFQKWWYFISAIENFGPRYLHGVPFFLLVRIISFLIGDMEDVLLNCTLLKR 60  
 DB 1 MMVCNRFQKWWYFISAIENFGPRYLHGVPFFLLVRIISFLIGDMEDVLLNCTLLKR 60  
 QY 61 SSRFRFWGALVCSMDSCRSRVAVTYRFTLLNIPSPAVWMAARNTIDQQVLSRIKLEIKR 120  
 DB 61 SSRFRFWGALVCSMDSCRSRVAVTYRFTLLNIPSPAVWMAARNTIDQQVLSRIKLEIKR 120  
 QY 121 CL 122  
 DB 121 CL 122

RESULT 6  
 ABP5924  
 ID ABP5924 standard; protein; 122 AA.  
 XX  
 AC ABP5924;  
 XX  
 DT 08-SEP-2003 (first entry)  
 XX  
 DE Human 122 amino acid neural thread protein.  
 XX  
 KW Human; tumour; cancer; neural thread protein; NTP; cell removal;  
 KW cell destruction; antipsoriatic; antimicrobial; immunosuppressive;  
 KW antiinflammatory; dermatological; antiarteriosclerotic; vasotropic;  
 KW gene therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 PN W02003044053-A2.  
 XX  
 PD 30-MAY-2003.  
 XX  
 PF 18-NOV-2002; 2002WO-CA001757.  
 XX  
 PR 16-NOV-2001; 2001US-0331477P.  
 XX  
 PA (NYMO-) NYMOX CORP.  
 XX  
 PI Averbach P, Gemmell J;  
 XX  
 DR WPI; 2003-457592/43.  
 XX

PT New neural thread protein (NTP), useful for preparing a composition for  
 PT treating or preventing a condition in a mammal requiring removal or  
 PT destruction of cells, e.g. psoriasis, eczema, atherosclerosis or  
 PT inflammatory disease.  
 XX  
 PS Disclosure; Fig 1; 98pp; English.  
 XX  
 CC The present invention relates to peptides derived from the human neural  
 CC thread protein (NTP). The peptides are useful for preparing a composition  
 CC for treating or preventing a condition in a mammal requiring removal or  
 CC destruction of cells, comprising tonsillary hypertrophy, prostatic  
 CC hyperplasia, psoriasis, eczema, dermatosis, cosmetic modification to a  
 CC breast, connective, skin, eye, ear, nose, throat, mouth or muscle tissue,  
 CC varicose veins, atherosclerosis, inflammatory, metabolic, infectious,  
 CC fibrosis, endocrine or autoimmune disease, or stenosis, restenosis,  
 CC occlusion or blockage of an artery or of a stent placed or implanted in  
 CC an artery. The present sequence is an NTP protein used to produce  
 CC peptides of the invention  
 XX  
 SQ Sequence 122 AA;

Query Match 100.0%; Score 651; DB 6; Length 122;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-73;  
 Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MMVCNRFQKWWYFISAIENFGPRYLHGVPFFLLVRIISFLIGDMEDVLLNCTLLKR 60  
 DB 1 MMVCNRFQKWWYFISAIENFGPRYLHGVPFFLLVRIISFLIGDMEDVLLNCTLLKR 60  
 QY 61 SSRFRFWGALVCSMDSCRSRVAVTYRFTLLNIPSPAVWMAARNTIDQQVLSRIKLEIKR 120  
 DB 61 SSRFRFWGALVCSMDSCRSRVAVTYRFTLLNIPSPAVWMAARNTIDQQVLSRIKLEIKR 120  
 QY 121 CL 122  
 DB 121 CL 122

RESULT 7  
 AAE33190  
 ID AAE33190 standard; protein; 122 AA.  
 XX  
 AC AAE33190;  
 XX  
 DT 16-APR-2003 (first entry)  
 XX  
 DE Neural thread protein (NTP) #1.  
 XX  
 KW Cell death; tissue necrosis; neural thread protein; NTP; amyloidosis;  
 KW stroke; brain tumour; Pick's disease; Parkinson's disease; glaucoma;  
 KW Alzheimer's disease; gene therapy.  
 XX  
 OS Unidentified.  
 XX  
 PN W0200289841-A2.  
 XX  
 PD 14-NOV-2002.  
 XX  
 PF 06-MAY-2002; 2002WO-CA000681.  
 XX  
 PR 04-MAY-2001; 2001US-0288463P.  
 XX  
 PA (NYMO-) NYMOX CORP.  
 XX  
 PI Averbach PA;  
 XX  
 DR WPI; 2003-120506/11.  
 XX  
 PT Preventing, controlling, modulating, ameliorating and/or treating cell  
 PT death or tissue necrosis using antibodies to neural thread proteins,  
 PT useful in disorders such as stroke, brain tumor, glaucoma and Alzheimer's  
 PT disease.  
 XX



PS Disclosure; Fig 5; 60pp; English.

XX The invention relates to a method of preventing, and/or inhibiting cell

CC death and/or tissue necrosis in live tissue containing neural thread

CC proteins (NTP). The method involves contacting the live tissue with at

CC least one antibody, fragment or derivative that recognises NTP, where the

CC antibody, fragment or derivative is present to prevent, control,

CC ameliorate and/or inhibit cell death and/or tissue necrosis caused by the

CC presence of NTP. Methods and compositions of the invention are useful for

CC preventing, modulating, controlling and/or treating disorders associated

CC with cell death and/or tissue necrosis such as stroke, brain tumour,

CC Pick's disease, Parkinson's disease, amyloidosis, glaucoma and

CC Alzheimer's disease. The invention is useful in gene therapy. The present

CC sequence is NTP protein

XX

SQ Sequence 122 AA;

Query Match 100.0%; Score 651; DB 6; Length 122;

Best Local Similarity 100.0%; Pred. No. 1.9e-73;

Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MMVCNRFKQWYFISAIENFGPRYLHGVPFFYLILVRIISFLIGMEDVLLNCTLLKR 60

Db 1 MMVCNRFKQWYFISAIENFGPRYLHGVPFFYLILVRIISFLIGMEDVLLNCTLLKR 60

Qy 61 SSRFRFGALVCSMDSCRSFSAVTVYRFTLLNIPSPAVVMARNTIDQOVLRSRIKLEIKR 120

Db 61 SSRFRFGALVCSMDSCRSFSAVTVYRFTLLNIPSPAVVMARNTIDQOVLRSRIKLEIKR 120

Qy 121 CL 122

Db 121 CL 122

RESULT 8

ABJ19446

ID ABJ19446 standard; protein; 122 AA.

AC ABJ19446;

XX

XX 27-MAR-2003 (first entry)

DE 122-mer neural thread protein.

XX

KW Nootropic; neuroprotective; cell death; tissue necrosis; NTP;

KW neural thread protein; neurodegenerative disorder; Alzheimer's disease.

XX

OS Unidentified.

XX

PN WO200292115-A2.

XX

XX 21-NOV-2002.

XX

XX 16-MAY-2002; 2002WO-CA000712.

XX

PR 16-MAY-2001; 2001US-0290971P.

XX

PA (NYMO-) NYMOX CORP.

XX

PI Averbach PA;

XX

XX WPI; 2003-129234/12.

DR

XX Preventing and/or inhibiting cell death and/or tissue necrosis in a

XX tissue for treating a neurodegenerative disorder, e.g. Alzheimer's

PT disease, by contacting the live tissue with at least one segment of

PT neural thread proteins (NTP).

XX

XX Disclosure; Fig 2; 60pp; English.

PS

XX The invention relates to a novel method for preventing and/or inhibiting

CC cell death and/or tissue necrosis in a tissue comprising contacting the

CC live tissue with at least one segment of neural thread proteins (NTP).

CC

CC The methods are composition are useful for treating a neurodegenerative

CC disorder, such as Alzheimer's disease. This sequence represents an NTP

CC protein of the invention

XX

SQ Sequence 122 AA;

Query Match 100.0%; Score 651; DB 6; Length 122;

Best Local Similarity 100.0%; Pred. No. 1.9e-73;

Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MMVCNRFKQWYFISAIENFGPRYLHGVPFFYLILVRIISFLIGMEDVLLNCTLLKR 60

Db 1 MMVCNRFKQWYFISAIENFGPRYLHGVPFFYLILVRIISFLIGMEDVLLNCTLLKR 60

Qy 61 SSRFRFGALVCSMDSCRSFSAVTVYRFTLLNIPSPAVVMARNTIDQOVLRSRIKLEIKR 120

Db 61 SSRFRFGALVCSMDSCRSFSAVTVYRFTLLNIPSPAVVMARNTIDQOVLRSRIKLEIKR 120

Qy 121 CL 122

Db 121 CL 122

RESULT 9

ADB37520

ID ADB37520 standard; protein; 122 AA.

XX

AC ADB37520;

XX

XX 04-DEC-2003 (first entry)

DT

XX Neural thread protein #1.

DE

XX Cytostatic; Antitumour; Antipsoriatic; Dermatological;

KW Antiatherosclerotic; Antiarteriosclerotic; Vasotropic; Antiinflammatory;

KW Immunosuppressive; Tranquillizer; Antiemetic; Virucide; AD7c-NTP;

KW neural thread protein; neuritic sprouting.

XX

OS Unidentified.

XX

XX WO2003008444-A2.

XX

XX 30-JAN-2003.

XX

XX 19-JUL-2002; 2002WO-CA001106.

PF

XX

PR 19-JUL-2001; 2001US-0306150P.

XX

PR 19-JUL-2001; 2001US-0306161P.

XX

PR 16-NOV-2001; 2001US-0331477P.

XX

XX (NYMO-) NYMOX CORP.

PA

XX Averbach PA, Gemmell J;

PI

XX WPI; 2003-248000/24.

XX

XX Novel Related peptide or AD7c-neural thread peptide, useful for treating

PT unwanted cellular proliferations, glandular hyperplasia, unwanted facial

PT hair, warts and unwanted fatty tissue.

XX

XX Disclosure; Fig 2; 109pp; English.

PS

XX The present invention relates to AD7c-neural thread protein (NTP) and

CC related proteins and peptides (I; ADB37528-ADB37641). The sequences are

CC useful for treating a condition in a patient requiring removal or

CC destruction of cells. The condition can be selected from benign or

CC malignant tumour of a tissue, hyperplasia, hypertrophy or overgrowth of a

CC tissue, virally, bacterially or parasitically altered tissue, or

CC malformation of a tissue, where the tissue is selected from lung, breast,

CC stomach, pancreas, prostate, bladder, bone, ovary, kidney, sinus,

CC colon, intestine, stomach, rectum, oesophagus, heart, spleen, salivary

CC gland, blood, brain and its coverings, spinal cord and its coverings,

CC muscle, connective tissue, adrenal, parathyroid, thyroid, uterus, testis,

CC

CC pituitary, reproductive organs, liver, gall bladder, eye, ear, nose,  
 CC throat, tonsils, mouth, lymph nodes and lymphoid tissue. The condition is  
 CC preferably tonsillary hypertrophy, prostatic hyperplasia, psoriasis,  
 CC eczema, dermatosis, cosmetic modification to a tissue (skin, eye, ear,  
 CC nose, throat, mouth, muscle, connective, hair or breast tissue), vascular  
 CC disease (atherosclerosis or arteriosclerosis), haemorrhoids, varicose  
 CC veins, inflammatory disease, autoimmune disease, metabolic disease,  
 CC hereditary/genetic disease, traumatic disease or physical injury,  
 CC nutritional deficiency disease, infectious disease, amyloid disease,  
 CC fibrosis disease, storage disease, congenital malformation, enzyme  
 CC deficiency disease, poisoning, intoxication, environmental disease,  
 CC radiation disease, endocrine disease, degenerative disease and mechanical  
 CC disease. The peptides are useful for treating unwanted cellular  
 CC proliferations, glandular (e.g. prostate) hyperplasia, unwanted facial  
 CC hair, warts and unwanted fatty tissue, or for preparing antibodies that  
 CC recognize and/or bind to Related proteins, Related peptides or NTP  
 CC peptides. The present sequence was used to illustrate the invention.  
 XX  
 SQ Sequence 122 AA;

Query Match 100.0%; Score 651; DB 7; Length 122;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-73;  
 Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVCNRRFGKVVYFISAIENFGPRYLHGVPFFLLILVRIISFLIGDMEDVLNCTLLKR 60  
 |||||  
 DB 1 MMVCNRRFGKVVYFISAIENFGPRYLHGVPFFLLILVRIISFLIGDMEDVLNCTLLKR 60  
 |||||  
 QY 61 SSRFRFGALVCSMDSCRSRVAVTYRFTLLNIPSPAVWMAENTIDQVLSRIKLEIKR 120  
 |||||  
 DB 61 SSRFRFGALVCSMDSCRSRVAVTYRFTLLNIPSPAVWMAENTIDQVLSRIKLEIKR 120  
 |||||  
 QY 121 CL 122  
 ||  
 DB 121 CL 122

RESULT 10  
 ADL96022  
 ID ADL96022 standard; protein; 122 AA.

XX AC ADL96022;  
 XX DT 20-MAY-2004 (first entry)  
 XX DE Human neural thread protein, NTP122.  
 XX KW Human; neural thread protein; NTP122; NTP112; NTP106; NTP98; NTP75;  
 KW NTP61; stenosis; stent; tumour; prostatic hyperplasia; psoriasis;  
 KW eczema; haemorrhoid; atherosclerosis; inflammatory disease;  
 KW autoimmune disease; metabolic disease; hereditary disease;  
 KW genetic disease; traumatic disease; physical injury;  
 KW nutritional deficiency disease; infectious disease; amyloid disease;  
 KW Alzheimer's disease; storage disease; congenital malformation;  
 KW enzyme deficiency disease; poisoning; intoxication;  
 KW environmental disease; radiation disease; endocrine disease;  
 KW degenerative disease; mechanical disease.

XX OS Homo sapiens.  
 XX PN US2003166569-A1.  
 XX PD 04-SEP-2003.

XX PF 15-NOV-2002; 2002US-00294891.  
 XX PR 16-NOV-2001; 2001US-0331477P.  
 XX PA (AVER/) AVERBACK P.  
 XX PA (GEMM/) GEMMELL J.  
 XX PI Averbach P, Gemmell J;  
 XX

DR WPI; 2003-898099/82.  
 XX New neural thread protein or its variants, useful for treating tumors and  
 PT other conditions requiring the removal or destruction of cells (e.g.  
 PT prostatic hyperplasia, psoriasis, eczema, hemorrhoids or  
 PT atherosclerosis).  
 XX  
 PS Disclosure; SEQ ID NO 1; 32pp; English.

XX The invention relates to a peptide, or its homologue, derivative,  
 CC fragment, variant or mimetic, comprising at least one neural thread  
 CC protein (NTP) peptide appearing as ADL96029-ADL96069, derived from  
 CC NTP122, 112, 106, 98, 75, 68 or 61. Also included are a nucleic acid  
 CC encoding an amino acid sequence corresponding to the above peptide, a  
 CC composition comprising one or more peptides or nucleic acids cited above  
 CC and a carrier, a method of treating a condition in a mammal requiring  
 CC removal or destruction of cells (comprising administering to the mammal  
 CC an amount of the peptide cited above) and a method of preventing or  
 CC inhibiting the stenosis, occlusion or blockage of a stent, comprising  
 CC coating the stent with an amount of the above peptide. The peptide  
 CC further comprises an amino acid in a reverse-D order based on the above  
 CC amino acid sequences. The composition and methods are useful in treating  
 CC tumours and other conditions requiring the removal or destruction of  
 CC cells (e.g. prostatic hyperplasia, psoriasis, eczema, haemorrhoids or  
 CC atherosclerosis). These may also be used in treating inflammatory  
 CC diseases, autoimmune diseases, metabolic diseases, hereditary/genetic  
 CC diseases, traumatic diseases or physical injuries, nutritional deficiency  
 CC diseases, infectious diseases, amyloid diseases e.g. Alzheimer's disease,  
 CC storage diseases, congenital malformation, enzyme deficiency diseases,  
 CC poisoning, intoxication, environmental diseases, radiation diseases,  
 CC endocrine diseases, degenerative diseases or mechanical diseases. The  
 CC present sequence is a human NTP protein from which the peptides of the  
 CC invention are derived.

XX SQ Sequence 122 AA;

Query Match 100.0%; Score 651; DB 7; Length 122;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-73;  
 Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVCNRRFGKVVYFISAIENFGPRYLHGVPFFLLILVRIISFLIGDMEDVLNCTLLKR 60  
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 DB 1 MMVCNRRFGKVVYFISAIENFGPRYLHGVPFFLLILVRIISFLIGDMEDVLNCTLLKR 60  
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 QY 61 SSRFRFGALVCSMDSCRSRVAVTYRFTLLNIPSPAVWMAENTIDQVLSRIKLEIKR 120  
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 DB 61 SSRFRFGALVCSMDSCRSRVAVTYRFTLLNIPSPAVWMAENTIDQVLSRIKLEIKR 120  
 |||||  
 QY 121 CL 122  
 ||  
 DB 121 CL 122

RESULT 11  
 ABP59884

ID ABP59884 standard; peptide; 15 AA.

XX AC ABP59884;  
 XX DT 28-AUG-2003 (first entry)  
 XX DE Human neural thread protein NTP(122) peptide #2.

XX KW Human; tumour; cancer; neural thread protein; NTP; cell removal;  
 KW cell destruction; antipsoriatic; antimicrobial; immunosuppressive;  
 KW antiinflammatory; dermatological; antiarteriosclerotic; vasotropic;  
 KW gene therapy.

XX OS Homo sapiens.  
 XX PN WO2003044053-A2.  
 XX PD 30-MAY-2003.

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XX 18-NOV-2002; 2002WO-CA001757.
XX
XX 16-NOV-2001; 2001US-0331477P.
XX
XX (NYMO-) NYMOX CORP.
XX
XX Averbach P, Gemmell J;
XX
XX WPI; 2003-457592/43.
XX
XX New neural thread protein (NTP), useful for preparing a composition for
XX treating or preventing a condition in a mammal requiring removal or
XX destruction of cells, e.g. psoriasis, eczema, atherosclerosis or
XX inflammatory disease.
XX
XX Claim 1; Page 31; 98pp; English.
XX
XX The present invention relates to peptides derived from the human neural
XX thread protein (NTP). The peptides are useful for preparing a composition
XX for treating or preventing a condition in a mammal requiring removal or
XX destruction of cells, comprising tonsillary hypertrophy, prostatic
XX hyperplasia, psoriasis, eczema, dermatosis, cosmetic modification to a
XX breast, connective, skin, eye, ear, nose, throat, mouth or muscle tissue,
XX varicose veins, atherosclerosis, inflammatory, metabolic, infectious,
XX fibrosis, endocrine or autoimmune disease, or stenosis, restenosis,
XX occlusion or blockage of an artery or of a stent placed or implanted in
XX an artery. The present sequence is a peptide of the invention
XX
XX Sequence 15 AA;
XX
XX Query Match 14.4%; Score 94; DB 6; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 0.00016;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 MMVCNRFQKQWYFI 15
XX Db 1 MMVCNRFQKQWYFI 15
XX
XX RESULT 12
XX ADL96030
XX ID ADL96030 standard; peptide; 15 AA.
XX
XX AC ADL96030;
XX
XX 20-MAY-2004 (first entry)
XX
XX Human neural thread protein, NTP122, peptide #2.
XX
XX Human; neural thread protein; NTP122; NTP106; NTP98; NTP75;
XX NTP68; NTP61; stenosis; stent; tumour; prostatic hyperplasia; psoriasis;
XX eczema; haemorrhoid; atherosclerosis; inflammatory disease;
XX autoimmune disease; metabolic disease; hereditary disease;
XX genetic disease; traumatic disease; physical injury;
XX nutritional deficiency disease; infectious disease; amyloid disease;
XX Alzheimer's disease; storage disease; congenital malformation;
XX enzyme deficiency disease; poisoning; intoxication;
XX environmental disease; radiation disease; endocrine disease;
XX degenerative disease; mechanical disease.
XX
XX Homo sapiens.
XX
XX US2003166569-A1.
XX
XX 04-SEP-2003.
XX
XX 15-NOV-2002; 2002US-00294891.
XX
XX 16-NOV-2001; 2001US-0331477P.
XX
XX (AVER/) AVERBACK P.
XX (GEMM/) GEMMELL J.
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```
XX Averbach P, Gemmell J;
XX
XX WPI; 2003-898099/82.
XX
XX New neural thread protein or its variants, useful for treating tumors and
XX other conditions requiring the removal or destruction of cells (e.g.
XX prostatic hyperplasia, psoriasis, eczema, haemorrhoids or
XX atherosclerosis).
XX
XX Claim 1; SEQ ID NO 9; 32pp; English.
XX
XX The invention relates to a peptide, or its homologue, derivative,
XX fragment, variant or mimetic, comprising at least one neural thread
XX protein (NTP) peptide appearing as ADL96030-ADL96069, derived from
XX NTP122, 112, 106, 98, 75, 68 or 61. Also included are a nucleic acid
XX encoding an amino acid sequence corresponding to the above peptide, a
XX composition comprising one or more peptides or nucleic acids cited above
XX and a carrier, a method of treating a condition in a mammal requiring
XX removal or destruction of cells (comprising administering to the mammal
XX an amount of the peptide cited above) and a method of preventing or
XX inhibiting the stenosis, occlusion or blockage of a stent, comprising
XX coating the stent with an amount of the above peptide. The peptide
XX further comprises an amino acid in a reverse-D order based on the above
XX amino acid sequences. The composition and methods are useful in treating
XX tumours and other conditions requiring the removal or destruction of
XX cells (e.g. prostatic hyperplasia, psoriasis, eczema, haemorrhoids or
XX atherosclerosis). These may also be used in treating inflammatory
XX diseases, autoimmune diseases, metabolic diseases, hereditary/genetic
XX diseases, traumatic diseases or physical injuries, nutritional deficiency
XX diseases, infectious diseases, amyloid diseases e.g. Alzheimer's disease,
XX storage diseases, congenital malformation, enzyme deficiency diseases,
XX poisoning, intoxication, environmental diseases, radiation diseases,
XX endocrine diseases, degenerative diseases or mechanical diseases. The
XX present sequence is a NTP peptide of the invention.
XX
XX Sequence 15 AA;
XX
XX Query Match 14.4%; Score 94; DB 7; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 0.00016;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 MMVCNRFQKQWYFI 15
XX Db 1 MMVCNRFQKQWYFI 15
XX
XX RESULT 13
XX ABP59885
XX ID ABP59885 standard; peptide; 15 AA.
XX
XX AC ABP59885;
XX
XX 28-AUG-2003 (first entry)
XX
XX Human neural thread protein NTP(122) peptide #3.
XX
XX Human; tumour; cancer; neural thread protein; NTP; cell removal;
XX cell destruction; antipsoriatic; antimicrobial; immunosuppressive;
XX antiinflammatory; dermatological; antiarteriosclerotic; vasotropic;
XX gene therapy.
XX
XX Homo sapiens.
XX
XX WO2003044053-A2.
XX
XX 30-MAY-2003.
XX
XX 18-NOV-2002; 2002WO-CA001757.
XX
XX 16-NOV-2001; 2001US-0331477P.
XX
XX (NYMO-) NYMOX CORP.
```

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XX Averback P, Gemmell J;
XX WPI; 2003-457592/43.
XX
XX New neural thread protein (NTP), useful for preparing a composition for
XX treating or preventing a condition in a mammal requiring removal or
XX destruction of cells, e.g. psoriasis, eczema, atherosclerosis or
XX inflammatory disease.
XX
XX Claim 1; Page 31; 98pp; English.
XX
XX The present invention relates to peptides derived from the human neural
XX thread protein (NTP). The peptides are useful for preparing a composition
XX for treating or preventing a condition in a mammal requiring removal or
XX destruction of cells, comprising tonsillary hypertrophy, prostatic
XX hyperplasia, psoriasis, eczema, dermatosis, cosmetic modification to a
XX breast, connective, skin, eye, ear, nose, throat, mouth or muscle tissue,
XX varicose veins, atherosclerosis, inflammatory, metabolic, infectious,
XX fibrosis, endocrine or autoimmune disease, or stenosis, restenosis,
XX occlusion or blockage of an artery or of a stent placed or implanted in
XX an artery. The present sequence is a peptide of the invention
XX
XX Sequence 15 AA;
XX
XX Query Match 12.9%; Score 84; DB 6; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 0.0029;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 16 SAIFNFGPRYLXGV 30
XX DB 1 SAIFNFGPRYLXGV 15
XX
XX RESULT 14
XX ADL96031
XX ID ADL96031 standard; peptide; 15 AA.
XX AC
XX ADL96031;
XX
XX 20-MAY-2004 (first entry)
XX
XX Human neural thread protein, NTP122, peptide #3.
XX
XX Human; neural thread protein; NTP122; NTP106; NTP98; NTP75;
XX NTP68; NTP61; stenosis; stent; tumour; prostatic hyperplasia; psoriasis;
XX eczema; haemorrhoid; atherosclerosis; inflammatory disease;
XX autoimmune disease; metabolic disease; hereditary disease;
XX genetic disease; traumatic disease; physical injury;
XX nutritional deficiency disease; infectious disease; amyloid disease;
XX Alzheimer's disease; storage disease; congenital malformation;
XX enzyme deficiency disease; poisoning; intoxication;
XX environmental disease; radiation disease; endocrine disease;
XX degenerative disease; mechanical disease.
XX
XX Homo sapiens.
XX
XX US2003166569-A1.
XX
XX 04-SEP-2003.
XX
XX 15-NOV-2002; 2002US-00294891.
XX
XX 16-NOV-2001; 2001US-0331477P.
XX
XX (AVER/) AVERBACK P.
XX (GEMM/) GEMMELL J.
XX
XX Averback P, Gemmell J;
XX WPI; 2003-898099/82.
XX
XX New neural thread protein or its variants, useful for treating tumors and

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PT other conditions requiring the removal or destruction of cells (e.g.
PT prostatic hyperplasia, psoriasis, eczema, hemorrhoids or
PT atherosclerosis).
XX
XX Claim 1; SEQ ID NO 10; 32pp; English.
XX
XX The invention relates to a peptide, or its homologue, derivative,
XX fragment, variant or mimetic, comprising at least one neural thread
XX protein (NTP) peptide appearing as ADL96029-ADL96069, derived from
XX NTP122, 112, 106, 98, 75, 68 or 61. Also included are a nucleic acid
XX encoding an amino acid sequence corresponding to the above peptide, a
XX composition comprising one or more peptides or nucleic acids cited above
XX and a carrier, a method of treating a condition in a mammal requiring
XX removal or destruction of cells (comprising administering to the mammal
XX an amount of the peptide cited above) and a method of preventing or
XX inhibiting the stenosis, occlusion or blockage of a stent, comprising
XX coating the stent with an amount of the above peptide. The peptide
XX further comprises an amino acid in a reverse-D order based on the above
XX amino acid sequences. The composition and methods are useful in treating
XX tumours and other conditions requiring the removal or destruction of
XX cells (e.g. prostatic hyperplasia, psoriasis, eczema, haemorrhoids or
XX atherosclerosis). These may also be used in treating inflammatory
XX diseases, autoimmune diseases, metabolic diseases, hereditary/genetic
XX diseases, traumatic diseases or physical injuries, nutritional deficiency
XX storage diseases, congenital malformation, enzyme deficiency diseases,
XX poisoning, intoxication, environmental diseases, radiation diseases,
XX endocrine diseases, degenerative diseases or mechanical diseases. The
XX present sequence is a NTP peptide of the invention.
XX
XX Sequence 15 AA;
XX
XX Query Match 12.9%; Score 84; DB 7; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 0.0029;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 16 SAIFNFGPRYLXGV 30
XX DB 1 SAIFNFGPRYLXGV 15
XX
XX RESULT 15
XX ABP59888
XX ID ABP59888 standard; peptide; 15 AA.
XX AC
XX ABP59888;
XX
XX 28-AUG-2003 (first entry)
XX
XX Human neural thread protein NTP(122) peptide #6.
XX
XX Human; tumour; cancer; neural thread protein; NTP; cell removal;
XX cell destruction; antipsoriatic; antimicrobial; immunosuppressive;
XX antiinflammatory; dermatological; antiarteriosclerotic; vasotropic;
XX gene therapy.
XX
XX Homo sapiens.
XX
XX WO2003044053-A2.
XX
XX 30-MAY-2003.
XX
XX 18-NOV-2002; 2002WO-CA001757.
XX
XX 16-NOV-2001; 2001US-0331477P.
XX
XX (NYMO-) NYMOX CORP.
XX
XX Averback P, Gemmell J;
XX WPI; 2003-457592/43.
XX
XX New neural thread protein (NTP), useful for preparing a composition for

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PT treating or preventing a condition in a mammal requiring removal or  
PT destruction of cells, e.g. psoriasis, eczema, atherosclerosis or  
PT inflammatory disease.  
XX  
PS Claim 1; Page 32; 98pp; English.  
XX  
CC The present invention relates to peptides derived from the human neural  
CC thread protein (NTP). The peptides are useful for preparing a composition  
CC for treating or preventing a condition in a mammal requiring removal or  
CC destruction of cells, comprising tonsillary hypertrophy, prostatic  
CC hyperplasia, psoriasis, eczema, dermatosis, cosmetic modification to a  
CC breast, connective, skin, eye, ear, nose, throat, mouth or muscle tissue,  
CC varicose veins, atherosclerosis, inflammatory, metabolic, infectious,  
CC fibrosis, endocrine or autoimmune disease, or stenosis, restenosis,  
CC occlusion or blockage of an artery or of a stent placed or implanted in  
CC an artery. The present sequence is a peptide of the invention  
XX  
SQ Sequence 15 AA;

Query Match 12.7%; Score 83; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.0038;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 61 SSRFRFWGALVCSMD 75  
Db 1 SSRFRFWGALVCSMD 15  
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Job time : 94.3583 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 11, 2005, 06:57:16 ; Search time 204.529 Seconds  
(without alignment)  
248.149 Million cell updates/sec

Title: US-10-092-934-2

Perfect score: 651

Sequence: 1 MMVCNRFKGVYFISAFIN.....RNTIDQVLSRIKLEIKRCL 122

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1854112 seqs, 416015017 residues

Total number of hits satisfying chosen parameters: 1854112

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

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- 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*
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- 21: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*
- 22: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	651	100.0	122	14	US-10-138-516-1
2	651	100.0	122	14	US-10-146-130-3
3	651	100.0	122	14	US-10-092-934-2
4	651	100.0	122	14	US-10-153-334-2
5	651	100.0	122	14	US-10-198-069-2
6	651	100.0	122	14	US-10-198-070-2
7	651	100.0	122	14	US-10-294-891-1
8	651	100.0	122	17	US-10-920-313-1
9	94	14.4	15	14	US-10-294-891-9
10	94	14.4	15	17	US-10-920-313-9
11	84	12.9	15	14	US-10-294-891-10

12	84	12.9	15	17	US-10-920-313-10	Sequence 10, Appl
13	83	12.7	15	14	US-10-294-891-13	Sequence 13, Appl
14	83	12.7	15	17	US-10-920-313-13	Sequence 13, Appl
15	82	12.6	17	14	US-10-198-070-15	Sequence 15, Appl
16	82	12.6	17	14	US-10-294-891-8	Sequence 8, Appl
17	82	12.6	17	17	US-10-920-313-8	Sequence 15, Appl
18	80	12.3	15	14	US-10-294-891-15	Sequence 15, Appl
19	80	12.3	15	17	US-10-920-313-15	Sequence 15, Appl
20	78	12.0	15	14	US-10-294-891-12	Sequence 12, Appl
21	78	12.0	15	17	US-10-920-313-12	Sequence 12, Appl
22	77	11.8	15	14	US-10-294-891-14	Sequence 14, Appl
23	77	11.8	15	17	US-10-920-313-14	Sequence 14, Appl
24	75	11.5	402	16	US-10-739-930-10886	Sequence 10886, A
25	73	11.2	15	14	US-10-294-891-11	Sequence 11, Appl
26	73	11.2	15	17	US-10-920-313-11	Sequence 11, Appl
27	72	11.1	1008	20	US-11-097-143-38631	Sequence 38631, A
28	71.5	11.0	124	15	US-10-424-599-153047	Sequence 153047, A
29	71.5	11.0	798	15	US-10-282-122A-65766	Sequence 65766, A
30	71.5	11.0	805	15	US-10-282-122A-65407	Sequence 65407, A
31	71	10.9	204	15	US-10-425-114-37820	Sequence 37820, A
32	70	10.8	405	16	US-10-425-115-300362	Sequence 300362, A
33	70	10.8	410	16	US-10-425-115-291572	Sequence 291572, A
34	70	10.8	416	15	US-10-425-114-68863	Sequence 68863, A
35	69.5	10.7	311	15	US-10-424-599-191606	Sequence 191606, A
36	69	10.6	229	15	US-10-424-599-248193	Sequence 248193, A
37	68.5	10.5	1337	15	US-10-389-566-2054	Sequence 2054, Ap
38	68	10.4	104	17	US-10-732-923-12543	Sequence 12543, A
39	68	10.4	233	9	US-09-886-319A-11	Sequence 11, Appl
40	68	10.4	233	14	US-10-376-564-11	Sequence 11, Appl
41	68	10.4	929	15	US-10-436-323-3	Sequence 3, Appl
42	67.5	10.4	414	14	US-10-083-357-1274	Sequence 1274, Ap
43	67.5	10.4	645	16	US-10-437-963-182845	Sequence 182845, A
44	67	10.3	66	16	US-10-425-115-185032	Sequence 185032, A
45	67	10.3	340	16	US-10-437-963-129129	Sequence 129129, A

#### ALIGNMENTS

##### RESULT 1

US-10-138-516-1  
; Sequence 1, Application US/10138516  
; Publication No. US20030003445A1  
; GENERAL INFORMATION:  
; APPLICANT: AVERBACK, PAUL  
; TITLE OF INVENTION: METHOD OF PREVENTING CELL DEATH USING ANTIBODIES TO  
; TITLE OF INVENTION: NEURAL THREAD PROTEINS  
; FILE REFERENCE: 59003.000004  
; CURRENT APPLICATION NUMBER: US/10/138.516  
; CURRENT FILING DATE: 2002-07-23  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 122  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-138-516-1

Query Match 100.0%; Score 651; DB 14; Length 122;  
Best Local Similarity 100.0%; Pred. No. 9.6e-70;  
Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MMVCNRFKGVYFISAFINFGPRYLHGVFPFYLLVRIISFLIGDMEDVLLNCTLLKR	60
Db	1	MMVCNRFKGVYFISAFINFGPRYLHGVFPFYLLVRIISFLIGDMEDVLLNCTLLKR	60
Qy	61	SSRFRFGALVCSMDSCRSFSAVYTFITLNTSPSAVWVWNTIDQVLSRIKLEIKR	120
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Qy	121	CL 122	
Db	121	CL 122	



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RESULT 2
US-10-146-130-3
; Sequence 3, Application US/10146130
; Publication No. US20030004107A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; TITLE OF INVENTION: METHOD OF PREVENTING CELL DEATH USING SEGMENTS OF
; FILE REFERENCE: 59003.000007
; CURRENT APPLICATION NUMBER: US/10/146,130
; CURRENT FILING DATE: 2002-08-06
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-146-130-3

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Best Local Similarity 100.0%; Pred. No. 9.6e-70;
Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1  MMVCNRFCKWVYFISAIENFGPRYLHGVPFFFLILVRIISFLIGDMEDVLLNCTLLKR 60

Qy      61  SSRFRFGALVCSMDSCRSRVAVTYRFTITLLNIPSPAVVMARNTIDQQVLSRIKLEIKR 120
Db      61  SSRFRFGALVCSMDSCRSRVAVTYRFTITLLNIPSPAVVMARNTIDQQVLSRIKLEIKR 120

Qy      121  CL 122
Db      121  CL 122

RESULT 3
US-10-092-934-2
; Sequence 2, Application US/10092934
; Publication No. US20030054990A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; TITLE OF INVENTION: METHODS OF USING NEURAL THREAD PROTEINS TO TREAT TUMORS
; TITLE OF INVENTION: AND CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 018792-0199
; CURRENT APPLICATION NUMBER: US/10/092,934
; CURRENT FILING DATE: 2002-06-05
; PRIOR APPLICATION NUMBER: 60/273,957
; PRIOR FILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Neural thread
US-10-092-934-2

Query Match      100.0%; Score 651; DB 14; Length 122;
Best Local Similarity 100.0%; Pred. No. 9.6e-70;
Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1  MMVCNRFCKWVYFISAIENFGPRYLHGVPFFFLILVRIISFLIGDMEDVLLNCTLLKR 60

Qy      61  SSRFRFGALVCSMDSCRSRVAVTYRFTITLLNIPSPAVVMARNTIDQQVLSRIKLEIKR 120
Db      61  SSRFRFGALVCSMDSCRSRVAVTYRFTITLLNIPSPAVVMARNTIDQQVLSRIKLEIKR 120

Qy      121  CL 122
Db      121  CL 122

RESULT 4
US-10-153-334-2
; Sequence 2, Application US/10153334
; Publication No. US20030096350A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 59003-000006
; CURRENT APPLICATION NUMBER: US/10/153,334
; CURRENT FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: 60/293,156
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-153-334-2

Query Match      100.0%; Score 651; DB 14; Length 122;
Best Local Similarity 100.0%; Pred. No. 9.6e-70;
Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  MMVCNRFCKWVYFISAIENFGPRYLHGVPFFFLILVRIISFLIGDMEDVLLNCTLLKR 60
Db      1  MMVCNRFCKWVYFISAIENFGPRYLHGVPFFFLILVRIISFLIGDMEDVLLNCTLLKR 60

Qy      61  SSRFRFGALVCSMDSCRSRVAVTYRFTITLLNIPSPAVVMARNTIDQQVLSRIKLEIKR 120
Db      61  SSRFRFGALVCSMDSCRSRVAVTYRFTITLLNIPSPAVVMARNTIDQQVLSRIKLEIKR 120

Qy      121  CL 122
Db      121  CL 122

RESULT 5
US-10-198-069-2
; Sequence 2, Application US/10198069
; Publication No. US20030096756A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 59003.000009
; CURRENT APPLICATION NUMBER: US/10/198,069
; CURRENT FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/306,161
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/306,150
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/331,477
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Unknown NTP
; OTHER INFORMATION: peptide

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## US-10-198-069-2

Query Match 100.0%; Score 651; DB 14; Length 122;  
Best Local Similarity 100.0%; Pred. No. 9.6e-70;  
Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 MMVCNRFKGVYFISAIENFGPRYLHGVPFYFLILVRIISFLIGDMEDVLLNCTLLKR 60  
Db 1 MMVCNRFKGVYFISAIENFGPRYLHGVPFYFLILVRIISFLIGDMEDVLLNCTLLKR 60  
  
Qy 61 SSRFRFGALVCSMDSCRSFSAVYRFTILLNIPSPAVVMARNTIDQOVLRSRIKLEIKR 120  
Db 61 SSRFRFGALVCSMDSCRSFSAVYRFTILLNIPSPAVVMARNTIDQOVLRSRIKLEIKR 120  
  
Qy 121 CL 122  
Db 121 CL 122

## RESULT 6

US-10-198-070-2  
; Sequence 2, Application US/10198070  
; Publication No. US20030109437A1  
; GENERAL INFORMATION:  
; APPLICANT: AVERBACK, PAUL  
; APPLICANT: GEMMEL, JACK  
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER  
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF  
; TITLE OF INVENTION: CELLS  
; FILE REFERENCE: 59003.000008  
; CURRENT APPLICATION NUMBER: US/10/198,070  
; CURRENT FILING DATE: 2002-07-19  
; PRIOR FILING DATE: 2002-07-19  
; PRIOR FILING DATE: 2001-07-19  
; PRIOR APPLICATION NUMBER: 60/306,150  
; PRIOR FILING DATE: 2001-07-19  
; PRIOR APPLICATION NUMBER: 60/331,477  
; PRIOR FILING DATE: 2001-11-16  
; NUMBER OF SEQ ID NOS: 125  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 122  
; TYPE: PRT  
; ORGANISM: Unknown Organism  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: Unknown NTP  
; OTHER INFORMATION: peptide  
US-10-198-070-2

Query Match 100.0%; Score 651; DB 14; Length 122;  
Best Local Similarity 100.0%; Pred. No. 9.6e-70;  
Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 MMVCNRFKGVYFISAIENFGPRYLHGVPFYFLILVRIISFLIGDMEDVLLNCTLLKR 60  
Db 1 MMVCNRFKGVYFISAIENFGPRYLHGVPFYFLILVRIISFLIGDMEDVLLNCTLLKR 60  
  
Qy 61 SSRFRFGALVCSMDSCRSFSAVYRFTILLNIPSPAVVMARNTIDQOVLRSRIKLEIKR 120  
Db 61 SSRFRFGALVCSMDSCRSFSAVYRFTILLNIPSPAVVMARNTIDQOVLRSRIKLEIKR 120  
  
Qy 121 CL 122  
Db 121 CL 122

## RESULT 7

US-10-294-891-1  
; Sequence 1, Application US/10294891  
; Publication No. US20030166569A1  
; GENERAL INFORMATION:  
; APPLICANT: AVERBACK, PAUL  
; APPLICANT: GEMMEL, JACK

; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER  
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF CELLS  
; FILE REFERENCE: 59003.000010  
; CURRENT APPLICATION NUMBER: US/10/294,891  
; CURRENT FILING DATE: 2002-11-15  
; PRIOR FILING DATE: 2001-11-15  
; PRIOR APPLICATION NUMBER: 60/331,447  
; PRIOR FILING DATE: 2001-11-16  
; NUMBER OF SEQ ID NOS: 49  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1  
; LENGTH: 122  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-294-891-1

Query Match 100.0%; Score 651; DB 14; Length 122;  
Best Local Similarity 100.0%; Pred. No. 9.6e-70;  
Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 MMVCNRFKGVYFISAIENFGPRYLHGVPFYFLILVRIISFLIGDMEDVLLNCTLLKR 60  
Db 1 MMVCNRFKGVYFISAIENFGPRYLHGVPFYFLILVRIISFLIGDMEDVLLNCTLLKR 60  
  
Qy 61 SSRFRFGALVCSMDSCRSFSAVYRFTILLNIPSPAVVMARNTIDQOVLRSRIKLEIKR 120  
Db 61 SSRFRFGALVCSMDSCRSFSAVYRFTILLNIPSPAVVMARNTIDQOVLRSRIKLEIKR 120  
  
Qy 121 CL 122  
Db 121 CL 122

## RESULT 8

US-10-920-313-1  
; Sequence 1, Application US/10920313  
; Publication No. US20050032704A1  
; GENERAL INFORMATION:  
; APPLICANT: AVERBACK, PAUL  
; APPLICANT: GEMMEL, JACK  
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER  
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF CELLS  
; FILE REFERENCE: 59003.000010  
; CURRENT APPLICATION NUMBER: US/10/920,313  
; CURRENT FILING DATE: 2004-08-18  
; PRIOR FILING DATE: 2004-08-18  
; PRIOR APPLICATION NUMBER: 60/331,447  
; PRIOR FILING DATE: 2001-11-16  
; NUMBER OF SEQ ID NOS: 49  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1  
; LENGTH: 122  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-920-313-1

Query Match 100.0%; Score 651; DB 17; Length 122;  
Best Local Similarity 100.0%; Pred. No. 9.6e-70;  
Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 MMVCNRFKGVYFISAIENFGPRYLHGVPFYFLILVRIISFLIGDMEDVLLNCTLLKR 60  
Db 1 MMVCNRFKGVYFISAIENFGPRYLHGVPFYFLILVRIISFLIGDMEDVLLNCTLLKR 60  
  
Qy 61 SSRFRFGALVCSMDSCRSFSAVYRFTILLNIPSPAVVMARNTIDQOVLRSRIKLEIKR 120  
Db 61 SSRFRFGALVCSMDSCRSFSAVYRFTILLNIPSPAVVMARNTIDQOVLRSRIKLEIKR 120  
  
Qy 121 CL 122  
Db 121 CL 122

## RESULT 9

US-10-294-891-9

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; Sequence 9, Application US/10294891
; Publication No. US20030166569A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; APPLICANT: GEMMEL, JACK
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF CELLS
; FILE REFERENCE: 59003.000010
; CURRENT APPLICATION NUMBER: US/10/294,891
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: 60/331,447
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-294-891-9

Query Match      14.4%; Score 94; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.00044;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MMVCNRFQKQWYFI 15
Db      1 MMVCNRFQKQWYFI 15
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RESULT 10
US-10-920-313-9
; Sequence 9, Application US/10920313
; Publication No. US20050032704A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; APPLICANT: GEMMEL, JACK
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF CELLS
; FILE REFERENCE: 59003.000010
; CURRENT APPLICATION NUMBER: US/10/920,313
; CURRENT FILING DATE: 2004-08-18
; PRIOR APPLICATION NUMBER: 60/331,447
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-920-313-9

Query Match      14.4%; Score 94; DB 17; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.00044;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MMVCNRFQKQWYFI 15
Db      1 MMVCNRFQKQWYFI 15
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RESULT 11
US-10-294-891-10
; Sequence 10, Application US/10294891
; Publication No. US20030166569A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; APPLICANT: GEMMEL, JACK
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF CELLS
; FILE REFERENCE: 59003.000010
; CURRENT APPLICATION NUMBER: US/10/294,891
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: 60/331,447
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-294-891-10

Query Match      12.9%; Score 84; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0007;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      16 SAIFNFGPRYLXGV 30
Db      1 SAIFNFGPRYLXGV 15
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RESULT 12
US-10-920-313-10
; Sequence 10, Application US/10920313
; Publication No. US20050032704A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; APPLICANT: GEMMEL, JACK
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF CELLS
; FILE REFERENCE: 59003.000010
; CURRENT APPLICATION NUMBER: US/10/920,313
; CURRENT FILING DATE: 2004-08-18
; PRIOR APPLICATION NUMBER: 60/331,447
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-920-313-10

Query Match      12.9%; Score 84; DB 17; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0007;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      16 SAIFNFGPRYLXGV 30
Db      1 SAIFNFGPRYLXGV 15
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RESULT 13
US-10-294-891-13
; Sequence 13, Application US/10294891
; Publication No. US20030166569A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; APPLICANT: GEMMEL, JACK
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF CELLS
; FILE REFERENCE: 59003.000010
; CURRENT APPLICATION NUMBER: US/10/294,891
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: 60/331,447
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 13
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-294-891-13

Query Match      12.7%; Score 83; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0092;
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Qy 61 SSRFRFWGALVCSMD 75
Db 1 SSRFRFWGALVCSMD 15
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1 IDQVLSRIKLEIKRCL 17

Search completed: October 11, 2005, 07:39:42
Job time : 205.529 secs

RESULT 14
US-10-920-313-13
; Sequence 13, Application US/10920313
; Publication No. US20050032704A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; APPLICANT: GENMEL, JACK
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF CELLS
; FILE REFERENCE: 59003.000010
; CURRENT APPLICATION NUMBER: US/10/920,313
; CURRENT FILING DATE: 2004-08-18
; PRIOR APPLICATION NUMBER: 60/331,447
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 13
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-920-313-13

Query Match 12.7%; Score 83; DB 17; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0092;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 61 SSRFRFWGALVCSMD 75
Db 1 SSRFRFWGALVCSMD 15
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RESULT 15
US-10-198-070-15
; Sequence 15, Application US/10198070
; Publication No. US20030109437A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; APPLICANT: GENMEL, JACK
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 59003.000008
; CURRENT APPLICATION NUMBER: US/10/198,070
; CURRENT FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/306,161
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/306,150
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/331,477
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-198-070-15

Query Match 12.6%; Score 82; DB 14; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 106 IDQVLSRIKLEIKRCL 122
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 11, 2005, 06:57:19 ; Search time 27.8904 Seconds  
(without alignments)  
326.535 Million cell updates/sec

Title: US-10-092-934-2

Perfect score: 651

Sequence: 1 MMVCNRFKGVVYFSAIFN.....RNTIDQVLSRIKLEIKRCL 122

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Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*
- 3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*
- 4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*
- 5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep.\*
- 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	651	100.0	122	2	US-08-454-557C-40
2	651	100.0	122	2	US-08-340-426D-40
3	651	100.0	122	2	US-08-450-673C-40
4	651	100.0	122	5	PCT-US93-17111A-40
5	76	11.7	515	4	US-09-489-039A-12306
6	68.5	10.5	178	4	US-09-673-395A-330
7	68	10.4	233	4	US-09-886-319A-11
8	68	10.4	452	4	US-09-540-236-3030
9	67.5	10.4	222	1	US-07-732-242C-7
10	67	10.3	461	4	US-09-489-039A-9623
11	67	10.3	515	4	US-09-170-496D-104
12	66	10.1	515	4	US-09-170-496D-220
13	65.5	10.1	120	4	US-09-583-110-5022
14	65.5	10.1	122	4	US-09-107-433-3697
15	65.5	10.1	590	4	US-09-489-039A-8178
16	65	10.0	606	4	US-09-107-532A-4683
17	65	10.0	2596	4	US-09-949-016-9970
18	64.5	9.9	170	4	US-09-358-383C-27
19	64.5	9.9	341	4	US-09-270-767-45876
20	64.5	9.9	451	3	US-09-412-102-8
21	64.5	9.9	451	3	US-09-217-787-8
22	64.5	9.9	522	4	US-09-902-540-12872
23	64.5	9.9	832	4	US-09-206-551-21
24	64	9.8	352	4	US-09-495-406-22
25	64	9.8	352	4	US-09-816-028A-36
26	64	9.8	352	4	US-10-303-162-36
27	64	9.8	352	4	US-10-303-134-36

28 63.5 9.8 541 4 US-09-543-681A-4323 Sequence 4323, Ap  
29 63 9.7 416 4 US-09-540-236-2393 Sequence 2393, Ap  
30 63 9.7 434 4 US-09-543-681A-7154 Sequence 7154, Ap  
31 63 9.7 623 4 US-09-252-991A-19867 Sequence 19867, A  
32 62.5 9.6 453 4 US-09-743-742B-9 Sequence 9, Appli  
33 62.5 9.6 453 4 US-09-825-294-209 Sequence 209, App  
34 62.5 9.6 453 4 US-09-970-966-209 Sequence 209, App  
35 62.5 9.6 1581 3 US-08-726-320-4 Sequence 4, Appli  
36 62.5 9.6 1581 3 US-09-208-716-4 Sequence 4, Appli  
37 62 9.5 160 4 US-09-107-532A-3836 Sequence 3836, Ap  
38 62 9.5 233 4 US-09-148-545-137 Sequence 137, App  
39 62 9.5 241 3 US-08-808-148-1 Sequence 1, Appli  
40 62 9.5 241 3 US-09-020-956-114 Sequence 114, App  
41 62 9.5 241 3 US-09-030-607-114 Sequence 114, App  
42 62 9.5 241 3 US-09-439-313-114 Sequence 114, App  
43 62 9.5 241 3 US-09-352-616A-114 Sequence 114, App  
44 62 9.5 241 4 US-09-232-149A-114 Sequence 114, App  
45 62 9.5 241 4 US-09-159-812-114 Sequence 114, App

#### ALIGNMENTS

RESULT 1

US-08-454-557C-40  
; Sequence 40, Application US/08454557C  
; Patent No. 5830670  
; GENERAL INFORMATION:  
; APPLICANT: de la Monte, Suzanne  
; APPLICANT: Wands, Jack R.  
; TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection  
; TITLE OF INVENTION: of Alzheimer's Disease  
; NUMBER OF SEQUENCES: 121  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.  
; STREET: 1100 New York Avenue, Suite 600  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/454.557C  
; FILING DATE: 30-MAY-1995  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ludwig, Steven R.  
; REGISTRATION NUMBER: 36,203  
; REFERENCE/DOCKET NUMBER: 0609.3840003  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 371-2600  
; TELEFAX: (202) 371-2540  
; INFORMATION FOR SEQ ID NO: 40:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 122 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
US-08-454-557C-40

Query Match 100.0%; Score 651; DB 2; Length 122;  
Best Local Similarity 100.0%; Pred. No. 6.3e-75;  
Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MMVCNRFKGVVYFSAIFNPGPRYLXGVFPFYFLILVRIISFLIGDMEDVLLNCTLKR 60  
Db 1 MMVCNRFKGVVYFSAIFNPGPRYLXGVFPFYFLILVRIISFLIGDMEDVLLNCTLKR 60  
Qy 61 SSRFRFVLCVSDSCFRSFRVAVTYFITLLNIPSPAVVMARNTIDQVLSRIKLETKR 120

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Db 61 SSRFRFGALVCSMDSCRSRVAVTYRFTLLNIPSPAVWMAARNTIDQOVLRSIKLEIKR 120
QY 121 CL 122
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Db 121 CL 122

RESULT 2
US-08-340-426D-40
; Sequence 40, Application US/08340426D
; Patent No. 5948634
; GENERAL INFORMATION:
; APPLICANT: de la Monte, Suzanne
; APPLICANT: Wands, Jack R.
; TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
; TITLE OF INVENTION: of Alzheimer's Disease
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/340,426D
; FILING DATE: 14-NOV-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ludwig, Steven R.
; REGISTRATION NUMBER: 36,203
; REFERENCE/DOCKET NUMBER: 0609.3840002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 122 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-340-426D-40

Query Match 100.0%; Score 651; DB 2; Length 122;
Best Local Similarity 100.0%; Pred. No. 6.3e-75;
Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVCWNRFGKWVYFISAIENFGPRYLYHGVPFFYLILVRIISFLIGDMEDVLLNCTLLKR 60
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 MMVCWNRFGKWVYFISAIENFGPRYLYHGVPFFYLILVRIISFLIGDMEDVLLNCTLLKR 60
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 61 SSRFRFGALVCSMDSCRSRVAVTYRFTLLNIPSPAVWMAARNTIDQOVLRSIKLEIKR 120
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 61 SSRFRFGALVCSMDSCRSRVAVTYRFTLLNIPSPAVWMAARNTIDQOVLRSIKLEIKR 120
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 121 CL 122
   ||
Db 121 CL 122

RESULT 3
US-08-450-673C-40
; Sequence 40, Application US/08450673C
; Patent No. 5948888
; GENERAL INFORMATION:
; APPLICANT: de la Monte, Suzanne
; APPLICANT: Wands, Jack R.
; TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
; TITLE OF INVENTION: of Alzheimer's Disease
```

```
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,673C
; FILING DATE: 30-MAY-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Ludwig, Steven R.
; REGISTRATION NUMBER: 36,203
; REFERENCE/DOCKET NUMBER: 0609.3840004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 122 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-450-673C-40

Query Match 100.0%; Score 651; DB 2; Length 122;
Best Local Similarity 100.0%; Pred. No. 6.3e-75;
Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMVCWNRFGKWVYFISAIENFGPRYLYHGVPFFYLILVRIISFLIGDMEDVLLNCTLLKR 60
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 MMVCWNRFGKWVYFISAIENFGPRYLYHGVPFFYLILVRIISFLIGDMEDVLLNCTLLKR 60
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 61 SSRFRFGALVCSMDSCRSRVAVTYRFTLLNIPSPAVWMAARNTIDQOVLRSIKLEIKR 120
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 61 SSRFRFGALVCSMDSCRSRVAVTYRFTLLNIPSPAVWMAARNTIDQOVLRSIKLEIKR 120
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 121 CL 122
   ||
Db 121 CL 122

RESULT 4
PCT-US95-17111A-40
; Sequence 40, Application PC/TUS9517111A
; GENERAL INFORMATION:
; APPLICANT: de la Monte, Suzanne
; APPLICANT: Wands, Jack R.
; TITLE OF INVENTION: Neural Thread Protein Gene Expression and
; TITLE OF INVENTION: Detection of Alzheimer's Disease
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/17111A
; FILING DATE:
; CLASSIFICATION:
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/340,426
; FILING DATE: 14-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ludwig, Steven R.
; REGISTRATION NUMBER: 36,203
; REFERENCE/DOCKET NUMBER: 0609.3840002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 122 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
PCT-US95-17111A-40

Query Match 100.0%; Score 651; DB 5; Length 122;
Best Local Similarity 100.0%; Pred. No. 6.3e-75;
Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MVVCNRFKQWVYFISAIFFGPRYLHGVPFFYLILVRIISFLIGMEDVLLNCTLLKR 60
Db 1 MVVCNRFKQWVYFISAIFFGPRYLHGVPFFYLILVRIISFLIGMEDVLLNCTLLKR 60

Qy 61 SSRFRFGALVCSMDSCRSRVAVTYRFTLLNIPSPAVVMARNTIDQVLSRIKLEIKR 120
Db 61 SSRFRFGALVCSMDSCRSRVAVTYRFTLLNIPSPAVVMARNTIDQVLSRIKLEIKR 120

Qy 121 CL 122
Db 121 CL 122

RESULT 5
US-09-489-039A-12306
; Sequence 12306, Application US/09489039A
; Patent No. 8610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 12306
; LENGTH: 515
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-12306

Query Match 11.7%; Score 76; DB 4; Length 515;
Best Local Similarity 23.4%; Pred. No. 0.43;
Matches 28; Conservative 21; Mismatches 44; Indels 32; Gaps 6;

Qy 10 KWV-YFISAIFFGPRYLHGVPFFYLILVRIISFLIGMEDVLLN 54
Db 277 QWVRIILLTLCNVCFGPIRMATWYTYTWNGQKHFPANLFTTLGVIGMIGSLAKVLT 336

Qy 55 ---CTLLKRSRRFRFGALVCSMDSCRF-----SRVAVTYRFTLLN-IPSPAVVMA 102
Db 337 DRWCKL-----QVFFWNIWLAVFSCAFYFPFNPHATTLLIMLYFLNLIHQIPSLHWSL 391

Qy 103 RNTID 107
Db 392 MSDVD 396

RESULT 6
US-09-673-395A-330
```

```
; Sequence 330, Application US/09673395A
; Patent No. 6620923
; GENERAL INFORMATION:
; APPLICANT: SPECHT, THOMAS
; APPLICANT: HINZMANN, BERND
; APPLICANT: SCHMITT, ARMIN
; APPLICANT: PILARSKY, CHRISTIAN
; APPLICANT: DAHL, EDGAR
; APPLICANT: ROSENTHAL, ANDRE
; TITLE OF INVENTION: HUMAN NUCLEIC ACID SEQUENCES FROM UTERUS TUMOR TISSUE
; FILE REFERENCE: ALBRE-12
; CURRENT APPLICATION NUMBER: US/09/673,395A
; CURRENT FILING DATE: 2000-10-17
; NUMBER OF SEQ ID NOS: 637
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 330
; LENGTH: 178
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-673-395A-330

Query Match 10.5%; Score 68.5; DB 4; Length 178;
Best Local Similarity 35.2%; Pred. No. 1;
Matches 25; Conservative 11; Mismatches 22; Indels 13; Gaps 4;

Qy 8 FGKVVYFISAIFFGPRYLHGVPFFYLILVRIISFLIGMEDVLLNCTLL 58
Db 110 FGLSVYFVN--DFSFFFLCH-EPFLFLPLPVPFSLFLPLFPLSPVLSUSLLCSCFSFL 165

Qy 59 KRSSRRFRFWGA 69
Db 166 RRSRIRLFCS 176

RESULT 7
US-09-886-319A-11
; Sequence 11, Application US/09886319A
; Patent No. 6586185
; GENERAL INFORMATION:
; APPLICANT: Wolf, Eckard
; APPLICANT: Werner, Sabine
; APPLICANT: Halle, Jorn-Peter
; APPLICANT: Regenbogen, Johannes
; APPLICANT: Goppelt, Andreas
; TITLE OF INVENTION: Use of Polypeptides or Nucleic Acids for
; TITLE OF INVENTION: the Diagnosis or Treatment of Skin Disorders and Wound
; TITLE OF INVENTION: Healing and for the Identification of Pharmacologically
; TITLE OF INVENTION: Active Substances
; FILE REFERENCE: 50125/014002
; CURRENT APPLICATION NUMBER: US/09/886,319A
; CURRENT FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: US 60/222,081
; PRIOR FILING DATE: 2000-08-01
; PRIOR APPLICATION NUMBER: DE 10030149.5
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-886-319A-11

Query Match 10.4%; Score 68; DB 4; Length 233;
Best Local Similarity 25.6%; Pred. No. 1.7;
Matches 22; Conservative 14; Mismatches 22; Indels 28; Gaps 4;

Qy ...34 FLILVRIISFLIGMEDVLLNCTLLKRSRRFRFGALVCSMDSCRF SRVAVTYRFTLLN 93
Db 163 FIVLVFFVWFII--FKAYLINCV-----N-----NC-----YKVINRN 194

Qy 94 IPSPAVVMARNTIDQVLSRIKLEIK 119
Db 94 IPSPAVVMARNTIDQVLSRIKLEIK 119
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Db 195 VPEIAVYPAFETPPQYVLPYEMAVK 220

RESULT 8

US-09-540-236-3030

; Sequence 3030, Application US/09540236

; Patent No. 6673910

; GENERAL INFORMATION:

; APPLICANT: Gary L. Breton et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATARRHALIS

; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 2709.2005-001

; CURRENT APPLICATION NUMBER: US/09/540,236

; CURRENT FILING DATE: 2000-04-04

; NUMBER OF SEQ ID NOS: 3840

; SEQ ID NO 3030

; LENGTH: 452

; TYPE: PRT

; ORGANISM: M.catarrhalis

US-09-540-236-3030

Query Match 10.4%; Score 68; DB 4; Length 452;

Best Local Similarity 26.5%; Pred. No. 3.8;

Matches 30; Conservative 14; Mismatches 43; Indels 26; Gaps 7;

QY 9 GKVVYFISAFN-----FGPR-----LYHG-VPFYFLVRIISFLIGDM 48

Db 265 GRWFAVAVLTVVGLIMGIPFPQVVAEYVYLIAGTIVLYP--LYRFISPSLKN 322

QY 49 EDV-LLNCTLLKSSRRFRFGALVCSMDSCFRSRAVAVTYRFTLLNIPSPAV 100

Db 323 EKVRLLICFLIIGSTL-FWSSF--EQPTSFNLFADRYTDLNMGMFNISLW 372

RESULT 9

US-07-732-242C-7

; Sequence 7, Application US/07732242C

; Patent No. 5298399

; GENERAL INFORMATION:

; APPLICANT: Uozumi, Takeshi; Masaki, Haruhiko;

; APPLICANT: Hidaka, Makoto; Nakamura, Akira;

; APPLICANT: Maeda, Michihisa; Yoneta, Yasuo

; TITLE OF INVENTION: Gene of Urease

; NUMBER OF SEQUENCES: 14

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Frishauf, Holtz, Goodman & Woodward, P.C.

; STREET: 600 Third Avenue

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10016-2088

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch, 0.72mb

; COMPUTER: IBM PC compatible (NEC PC-9801 RX)

; OPERATING SYSTEM: MS DOS

; SOFTWARE: ASCII Form

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/732,242C

; FILING DATE: 19910718

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: JPN 2-210178

; FILING DATE: 10-AUG-1990

; ATTORNEY/AGENT INFORMATION:

; NAME: Goodman, Herbert

; REGISTRATION NUMBER: 17081

; REFERENCE/DOCKET NUMBER: 910532/HG

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212)972-1400

; TELEFAX: (212)370-1622

; TELEX: 236268

; INFORMATION FOR SEQ ID NO: 7:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 222 amino acids

; TYPE: AMINO ACID

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-07-732-242C-7

Query Match 10.4%; Score 67.5; DB 1; Length 222;

Best Local Similarity 26.7%; Pred. No. 1.8;

Matches 28; Conservative 12; Mismatches 34; Indels 31; Gaps 4;

QY 12 VYF-ISAIFNF-----GPRYLHGVFPFYFLIIVRIISFLIGDMEDVLLN 54

Db 88 VYFGISAILSLKKTTHESHRLHLDHPITYYKGIPIYVKSFLGIHGLAGSAAMVLLT 147

QY 55 CTLKRRSR-----FRFGALVCSMDSCFRSRAVAVTYRFTLLNIP 95

Db 148 MSTVEKAWEGLLYLFFGA-----GTVLGMLSFYTLIGIP 182

RESULT 10

US-09-489-039A-9623

; Sequence 9623, Application US/09489039A

; Patent No. 6610836

; GENERAL INFORMATION:

; APPLICANT: Gary Breton et. al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 2709.2004001

; CURRENT APPLICATION NUMBER: US/09/489,039A

; CURRENT FILING DATE: 2000-01-27

; PRIOR APPLICATION NUMBER: US 60/117,747

; PRIOR FILING DATE: 1999-01-29

; NUMBER OF SEQ ID NOS: 14342

; SEQ ID NO 9623

; LENGTH: 461

; TYPE: PRT

; ORGANISM: Klebsiella pneumoniae

US-09-489-039A-9623

Query Match 10.3%; Score 67; DB 4; Length 461;

Best Local Similarity 20.9%; Pred. No. 5.2;

Matches 24; Conservative 29; Mismatches 32; Indels 30; Gaps 5;

QY 29 GVPFYFLIIVRIISFLIGDMEDVLLNCTLLKSSRRFPWG-----ALVCSM- 74

Db 43 GLPAYVYGLMFLVRLVDGVADVLMLGLVIDNTTTR---WGRCRPLLIGALPGLLCILA 99

QY 75 -----DSCFRSRAVAVTYRFI---TLNIPSPAV--WMARNTIDQQVLSRIKL 116

Db 100 FYVPDFGTTGKLLYAFVTVYLCISFLYTLVNIIPFCAMLPFLTSDSAERTLSAVRI 154

RESULT 11

US-09-170-496D-104

; Sequence 104, Application US/09170496D

; Patent No. 6555339

; GENERAL INFORMATION:

; APPLICANT: Behan, Dominic P.

; APPLICANT: Chalmers, Derek T.

; APPLICANT: Liaw, Chen W.

; TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-Coupled Receptors

; FILE REFERENCE: AREN-0040

; CURRENT APPLICATION NUMBER: US/09/170,496D

; CURRENT FILING DATE: 1998-10-13

; NUMBER OF SEQ ID NOS: 294

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 104

; LENGTH: 515

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-170-496D-104

Query Match 10.3%; Score 67; DB 4; Length 515;  
Best Local Similarity 22.1%; Pred. No. 6;  
Matches 33; Conservative 23; Mismatches 49; Indels 44; Gaps 8;

QY 5 W-NRFGKVVYFISAIENFGPRYLHGVFPYFLILVR-----IIS 42  
DB 196 WNSLGLHLVYVL--VYNITTVIVPVVVVFLILIRALSASOKKKVILIAALRTPONTIS 253  
QY 43 FLIGMEDVLNCTLLKSSRFHWGALVCSMDSCFRSVAVTYRFTLLNIPS-----96  
DB 254 IPYASQREAEHLATLLSMVVF-----ILCSVPYA---TLVVYQ--TVLNVPTSVFLL 302  
QY 97 -PAVMARNTI--DQOVLRSRIKLIKRL 122  
DB 303 LTAVWLPKVSLLANPVLFTVKNKSVRKCL 331

RESULT 12  
US-09-170-496D-220  
; Sequence 220, Application US/09170496D  
; Patent No. 655339  
; GENERAL INFORMATION:  
; APPLICANT: Behan, Dominic P.  
; APPLICANT: Chalmers, Derek T.  
; APPLICANT: Liaw, Chen W.  
; TITLE OF INVENTION: No. 655339--Endogenous, Constitutively Activated Human G Protein-  
; TITLE OF INVENTION: Receptors  
; FILE REFERENCE: AREN-0040  
; CURRENT APPLICATION NUMBER: US/09/170,496D  
; CURRENT FILING DATE: 1998-10-13  
; NUMBER OF SEQ ID NOS: 294  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 220  
; LENGTH: 515  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-170-496D-220

Query Match 10.1%; Score 66; DB 4; Length 515;  
Best Local Similarity 22.1%; Pred. No. 8;  
Matches 33; Conservative 22; Mismatches 50; Indels 44; Gaps 8;

QY 5 W-NRFGKVVYFISAIENFGPRYLHGVFPYFLILVR-----IIS 42  
DB 196 WNSLGLHLVYVL--VYNITTVIVPVVVVFLILIRALSASOKKKVILIAALRTPONTIS 253  
QY 43 FLIGMEDVLNCTLLKSSRFHWGALVCSMDSCFRSVAVTYRFTLLNIPS-----96  
DB 254 IPYASQREAEHLATLLSMVVF-----ILCSVPYA---TLVVYQ--TVLNVPTSVFLL 302  
QY 97 -PAVMARNTI--DQOVLRSRIKLIKRL 122  
DB 303 LTAVWLPKVSLLANPVLFTVKNKSVRKCL 331

RESULT 13  
US-09-583-110-5022  
; Sequence 5022, Application US/09583110  
; Patent No. 6699703  
; GENERAL INFORMATION:  
; APPLICANT: Lynn Doucette-Stamm et al.  
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus  
; TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics  
; FILE REFERENCE: PATH00-07A  
; CURRENT APPLICATION NUMBER: US/09/583,110  
; CURRENT FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/107,433  
; PRIOR FILING DATE: 1998-06-30  
; PRIOR APPLICATION NUMBER: US 60/085,131  
; PRIOR FILING DATE: 1998-05-12  
; PRIOR APPLICATION NUMBER: US 60/051,553  
; PRIOR FILING DATE: 1997-07-02

; NUMBER OF SEQ ID NOS: 5322  
; SEQ ID NO 5022  
; LENGTH: 120  
; TYPE: PRT  
; ORGANISM: Streptococcus pneumoniae  
US-09-583-110-5022

Query Match 10.1%; Score 65.5; DB 4; Length 120;  
Best Local Similarity 28.8%; Pred. No. 1.6;  
Matches 19; Conservative 9; Mismatches 17; Indels 21; Gaps 2;

QY 51 VLNCTLLKSSRFHWGALVCSMDSCFRSVAVTYRFTLLNIPSPAVVMARNTIDQOV 110  
DB 75 VLNCTPKVKQKSNFWSVHSTPDTRF-----FNFKDFL-----QLL 113  
QY 111 LSRIKL 116  
DB 114 LTHIKL 119

RESULT 14  
US-09-107-433-3697  
; Sequence 3697, Application US/09107433  
; Patent No. 6800744  
; GENERAL INFORMATION:  
; APPLICANT: Lynn A Doucette-Stamm and David Bush  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID  
; SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE  
; THERAPEUTICS  
; NUMBER OF SEQUENCES: 5206  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION  
; STREET: 100 Beaver Street  
; CITY: Waltham  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02354  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: CD-ROM ISO9660  
; COMPUTER: <Unknown>  
; OPERATING SYSTEM: <Unknown>  
; SOFTWARE: <Unknown>  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/107,433  
; FILING DATE: 30-Jun-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/ 085131  
; FILING DATE: May 12, 1998  
; APPLICATION NUMBER: 60/051553  
; FILING DATE: July 2, 1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ariniello, Pamela Deneke  
; REGISTRATION NUMBER: 40,489  
; REFERENCE/DOCKET NUMBER: GTC-011  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (781)893-5007  
; TELEFAX: (781)893-8277  
; INFORMATION FOR SEQ ID NO: 3697:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 122 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: YES  
; ORIGINAL SOURCE:  
; ORGANISM: Streptococcus pneumoniae  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (B) LOCATION 1...122  
; SEQUENCE DESCRIPTION: SEQ ID NO: 3697:  
US-09-107-433-3697

Query Match 10.1%; Score 65.5; DB 4; Length 122;

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Best Local Similarity 28.8%; Pred. No. 1.6;
Matches 19; Conservative 9; Mismatches 17; Indels 21; Gaps 2;

Qy 51 VLLNCTLLKSSRRFRFWGALVCSMDSCRSRVAVTYRFTLLNIPSPAVMMARNTIDQQV 110
Db 77 VLNCTPKVQKSNFWSVHSTPDTRF-----FNKDFL-----QLL 115

Qy 111 LSRKL 116
Db 116 LTHIKL 121

RESULT 15
US-09-489-039A-8178
; Sequence 8178, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 8178
; LENGTH: 590
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-8178

Query Match 10.1%; Score 65.5; DB 4; Length 590;
Best Local Similarity 27.7%; Pred. No. 11;
Matches 38; Conservative 11; Mismatches 45; Indels 43; Gaps 7;

Qy 2 MVCNRRFGKVVYFISAFN-----FGPRYLY-----HGVPFFYLILVRIISFLIGD 47
Db 19 MVSW---GHWF---ALFNMLLAMVLGSRYLFDVADWPTTLAQLRFSYVSLVGHFSFL--- 68

Qy 48 MEDVLLNCTLLKSSRRFRFWGALVCSMDSCRSRVAVTYRFTLLNIPS----- 96
Db 69 ---VFTSYVLILPFLTF-----IWSQRLMRFLSVILATAGMTLLLLIDSEVTRFHLN 120

Qy 97 PAVMMARNTIDQQVLSR 113
Db 121 PVWVELVINPDQEMAR 137
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Search completed: October 11, 2005, 07:42:46  
Job time : 29.8904 secs

A;Reference number:



C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004

R;Levedakou, E.N.; He, M.; Baptist, E.W.; Craven, R.J.; Cance, W.G.; Welcsh, P.L.; Simmo  
Oncogene 9, 1977-1988, 1994

A;Title: Two novel human serine/threonine kinases with homologies to the cell cycle regu  
A;Reference number: I58396; MUID:94268838; PMID:8208544

A;Accession: I78885

A;Status: preliminary; translated from GB/EMBL/DBDJ

A;Molecule type: mRNA

A;Residues: 1-841 <RES>

A;Cross-references: UNIPROT:P51957; GB:L20321; NID:G348244; PIDN:AAA36658.1; PID:G348245

C;Genetics:

A;Gene: GDB:STK2

A;Cross-references: GDB:374125

A;Map position: 3p21.1-3p21.1

C;Superfamily: human serine/threonine-specific protein kinase STK2; protein kinase homol

C;Keywords: phosphotransferase

F;4-261/Domain: protein kinase homology <KIN>

Query Match 16.3%; Score 93; DB 1; Length 841;  
Best Local Similarity 33.0%; Pred. No. 0.1;  
Matches 29; Conservative 10; Mismatches 33; Indels 16; Gaps 3;

QY 14 VQAILLQPQKQLGRAPANTPLIFVFSLEAGFHHCQAGLKLLTSGDPPASAFQSAGIT 73  
Db : :: ||| : | : | : | : | : | : | : | : | : | : | :  
444 LQLIKQSKPKQDSL--ALSP-----KLECSGTILAHNLRLLGSSDSPASASRVAGIT 495

QY 74 GVSHLTQPNLDKKICNSGGSCYVAQG 101  
Db 496 GVCHHAOD-----QVAGECIIEKQG 515

RESULT 10

D40201

artifact-warning sequence (translated ALU class D) - human

C;Species: Homo sapiens (man)

C;Date: 31-Mar-1992 #sequence\_revision 11-Aug-1995 #text\_change 19-May-2000

C;Accession: D40201

R;Claverie, J.M.

personal communication, 1992

A;Reference number: A40201

A;Accession: D40201

A;Molecule type: DNA

A;Residues: 1-579 <CLA>

R;Claverie, J.M.  
Genomics 12, 838-841, 1992

A;Title: Identifying coding exons by similarity search: Alu-derived and other potentiall

A;Reference number: A40200; MUID:92241891; PMID:1572861

A;Contents: annotation

C;Comment: This "warning" entry is a conceptual translation in all 6 reading frames of o  
in-frame stop codons are shown as 'X'.

C;Comment: Any significant similarity of a predicted protein sequence to a portion of th  
.

Query Match 15.8%; Score 90; DB 4; Length 579;  
Best Local Similarity 45.7%; Pred. No. 0.14;  
Matches 21; Conservative 9; Mismatches 14; Indels 2; Gaps 1;

QY 15 QAILLSQPQKQLGRAPANTP--LIFVFSLEAGFHHCQAGLKLLT 58  
Db ||||| :  
416 QVILLQPPEFXGLQAYATRSXFLYLFVEVGFRHVAQAVLELLS 461

RESULT 11

S65657

alpha-1C-adrenergic receptor splice form 2 - human

N;Alternate names: alpha-1C-adrenoceptor isoform 2

C;Species: Homo sapiens (man)

C;Date: 22-Nov-1996 #sequence\_revision 22-Nov-1996 #text\_change 09-Jul-2004

C;Accession: S65657; S65655

R;Tanaka, T.  
submitted to the EMBL Data Library, July 1994

A;Reference number: S65656





Qy 62 PPASAFOSAGITGVSHLTOPANLDKIKCSNGGSCVVAQ---AGIKLLASCNP 110  
Db 164 -NTSSSTSTTGTSHLVKCAEKEKTPCVNGGECFMVADLSNPSRYLCKCQP 214

Search completed: October 11, 2005, 07:01:34  
Job time : 19.369 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 11, 2005, 06:57:07 ; Search time 67.2299 Seconds  
(without alignments)  
853.085 Million cell updates/sec

Title: US-10-092-934-3

Perfect score: 570

Sequence: 1 MAQSRLTATSASRVQAILLS.....GSCVVAQAGLKLASCPNPSK 112

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query	Match	Length	ID	Description
1	232.5	40.8	133	2	Q6ZQZ5	Q6zqz5 homo sapien
2	223.5	39.2	184	2	Q6ZW29	Q6zw29 homo sapien
3	214.5	37.6	123	2	Q9HAD8	Q9had8 homo sapien
4	208	36.5	174	2	Q8N2A0	Q8n2a0 homo sapien
5	205	36.0	139	2	Q6ZVJ8	Q6zvj8 homo sapien
6	201.5	35.4	587	1	ALU3 HUMAN	P39190 homo sapien
7	201	35.3	239	2	Q6ZWA9	Q6zwa9 homo sapien
8	201	35.3	585	1	ALU5 HUMAN	P39192 homo sapien
9	200.5	35.2	587	1	ALU2 HUMAN	P39189 homo sapien
10	200	35.1	138	2	Q6ZR23	Q6zr23 homo sapien
11	200	35.1	138	2	Q6ZVB3	Q6zvb3 homo sapien
12	198	34.7	109	2	Q8NI81	Q8ni81 homo sapien
13	191.5	33.6	188	2	Q8ZQN4	Q6zqn4 homo sapien
14	187	32.8	593	1	ALU7 HUMAN	P39194 homo sapien
15	184	32.3	202	2	Q6ZUA4	Q6zua4 homo sapien
16	183	32.1	128	2	Q6ZPB2	Q6zpb2 homo sapien
17	181.5	31.8	603	1	ALU4 HUMAN	P39191 homo sapien
18	181	31.8	133	2	Q96JR5	Q96jr5 homo sapien
19	181	31.8	155	2	Q6ZSW8	Q6zsw8 homo sapien
20	181	31.8	222	2	Q6ZU09	Q6zu09 homo sapien
21	180	31.6	146	2	Q6ZTX8	Q6ztx8 homo sapien
22	179	31.4	174	2	Q9H926	Q9h926 homo sapien
23	178.5	31.3	164	2	Q6ZTS0	Q6zts0 homo sapien
24	177	31.1	124	2	Q6ZUN5	Q6zun5 homo sapien
25	176	30.9	118	2	Q9H387	Q9h387 homo sapien
26	175	30.7	115	2	Q9N083	Q9n083 macaca fasc
27	174	30.5	140	2	Q8N891	Q8n891 homo sapien
28	173.5	30.4	169	2	Q9H397	Q9h397 homo sapien
29	173	30.4	140	2	Q6ZP99	Q6zp99 homo sapien
30	173	30.4	164	2	Q6ZUK0	Q6zuk0 homo sapien
31	172.5	30.3	138	2	Q6ZUF3	Q6zuf3 homo sapien

32	172.5	30.3	179	2	Q8N1K7	Q8n1k7 homo sapien
33	172	30.2	123	2	Q6ZTE8	Q6zte8 homo sapien
34	172	30.2	125	2	Q6ZTE1	Q6zte1 homo sapien
35	172	30.2	593	1	ALU6 HUMAN	P39193 homo sapien
36	171.5	30.1	171	2	Q9H728	Q9h728 homo sapien
37	170.5	29.9	150	2	Q6ZPA0	Q6zpa0 homo sapien
38	170.5	29.9	156	2	Q6ZUA3	Q6zua3 homo sapien
39	170	29.8	101	2	Q6STG2	Q6stg2 homo sapien
40	170	29.8	125	2	Q6ZTC7	Q6ztc7 homo sapien
41	170	29.8	156	2	Q8NBH4	Q8nbh4 homo sapien
42	170	29.8	204	2	Q8N8P8	Q8n8p8 homo sapien
43	169.5	29.7	148	2	Q6ZUC5	Q6zuc5 homo sapien
44	169.5	29.7	170	2	Q8NAI3	Q8nai3 homo sapien
45	168.5	29.6	224	2	Q8N210	Q8n210 homo sapien

#### ALIGNMENTS

##### RESULT 1

ID Q6ZQZ5 PRELIMINARY; PRT; 133 AA.  
AC Q6ZQZ5;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein FLJ46775.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Trachea;  
RA Kanehori K., Ishibashi T., Chiba Y., Fujimori K., Hiraoka S.,  
RA Tanai H., Watanabe S., Ishida S., Ono Y., Hotuta T., Watanabe M.,  
RA Sugiyama T., Irie R., Otsuki T., Sato H., Ota T., Wakamatsu A.,  
RA Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T.,  
RA Kimura K., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,  
RA Wagatsuma M., Takahashi-Fujii A., Oshina A., Sugiyama A., Kawakami B.,  
RA Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;  
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AK128616; BAC87531.1;  
SQ SEQUENCE 133 AA; 14947 MW; 3A349D8E39D62D3C CRC64;

Query Match 40.8%; Score 232.5; DB 2; Length 133;

Best Local Similarity 68.5%; Pred. No. 6.3e-16;

Matches 50; Conservative 5; Mismatches 17; Indels 1; Gaps 1;

Qy 10 SASRVQAILLSOPPKQLGLRAPANTP-LIFVFSLEAGFHHCQAGLKLITSGDPPASAFQ 68  
Db 42 TASQVQAILTQPPKWLGLRAYATAPGYFFVLVEIGHVHVRPGLKLLTSGDPPALASQ 101

Qy 69 SAGITGVSHLTOP 81

Db 102 GAGIAGVSHRTWP 114

##### RESULT 2

ID Q6ZW29 PRELIMINARY; PRT; 184 AA.  
AC Q6ZW29;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein FLJ41703.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Heart;



```

QY 65 SAFOSAGITGVSHLTQANLDDKKICNSGGSCYVAQAG 101
DB 149 SASOSAGITGVSHSARPK-----SCFLQLLG 174

RESULT 5
Q6ZVJ8 PRELIMINARY; PRT; 139 AA.
AC Q6ZVJ8 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein FLJ42505.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Cerebellum;
RA Kawakami B., Sugiyama A., Takemoto M., Sugiyama T., Irie R.,
RA Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M.,
RA Murakawa K., Kanehori K., Takahashi-Puji A., Oshima A., Suzuki Y.,
RA Sugano S., Nagahari K., Maehou Y., Nagai K., Isogai T.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK12496; BAC85863.1; -
SQ SEQUENCE 139 AA; 15636 MW; 92C7CF6C06316811 CRC64;

Query Match 36.0%; Score 205; DB 2; Length 139;
Best Local Similarity 55.2%; Pred. No. 4.3e-13;
Matches 48; Conservative 11; Mismatches 22; Indels 6; Gaps 1;

QY 1 MAQSRLTATSASRVOAILLSQPPKQLGRAPANTP-----LIFVFSLEAGFHHCQAGL 54
DB 41 VARSRLTETSASRIQAILLSRPSRWLGLQACATWPGYLVVVVVLLVETMFLHFGQAGL 100

QY 55 KLLTSGDPPASAFOSAGITGVSHLTQ 81
DB 101 ELLTSGDPPASASQSTGITRMDRAQ 127

RESULT 6
ALU3 HUMAN STANDARD; PRT; 587 AA.
AC P39190;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Alu subfamily SBI sequence contamination warning entry.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=92241891; PubMed=1572661;
RA Claverie J.-M.; Makalowski W.;
RT "Alu alert.";
RL Nature 371:752-752(1994).
RN [2]
RP CONCEPT.
RX MEDLINE=92241891; PubMed=1572661;
RA Claverie J.-M.;
RT "Identifying coding exons by similarity search: alu-derived and other
potentially misleading protein sequences.";
RL Genomics 12:838-841(1992).
RN [3]
RP ALU FAMILIES CLASSIFICATION.
RX MEDLINE=88333009; PubMed=3138422;
RA Quentin Y.;
RT "The Alu family developed through successive waves of fixation closely

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connected with primate lineage history.";
J. Mol. Evol. 27:194-202(1988).
[4]
RP ALU FAMILIES CLASSIFICATION.
RX MEDLINE=91178815; PubMed=1706781;
RA Jurka J., Milosavljevic A.;
RT "Reconstruction and analysis of human Alu genes.";
J. Mol. Evol. 32:105-121(1991).
CC -!- MISCELLANEOUS: Various analyses indicate that Alu repeats fall
into 8 subfamilies (Ref.3 and Ref.4). Therefore, 8 Alu warning
consensus sequences have been constituted that contain all six
frames conceptual translations of each of these classes of Alu
repeats.
CC -!- MISCELLANEOUS: Isolated 'X' indicates the presence of a stop
codon, 'XXX' is used to separate the various translation phases.
CC -!- CAUTION: This Alu entry is provided in order to avoid the further
pollution of protein sequence databases with Alu-derived amino
acid sequences.
CC -!- CAUTION: Alu repetitive sequences are interspersed in human and
primate genomes with an average spacing of 4 kb. Some of them are
actively transcribed by pol III. Normal transcripts may contain
Alu-derived sequences in 5' or 3' untranslated regions. However,
cDNA libraries also contain partial and/or rearranged cDNAs
ligated with Alu-derived sequence in any orientation. Although Alu
elements (especially situated on the complementary strand) have a
great potential to create additional/alternative exons,
consideration should be given to the possibility that the presence
of an Alu in an open reading frame may have resulted from a
cloning artifact or may be due to misinterpretation of sequencing
data. This point has been overlooked on several occasions, with
the consequence of erroneous Alu-derived amino acid sequences
being reported.
CC -!- CAUTION: Any significant similarity of a putative protein sequence
with an Alu-translated entry must be taken as a warning that a
part of Alu repeat may have been artifactually included in the
coding nucleotide sequence.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
-----
DR EMBL; U14569; -; NOT_ANNOTATED_CDS.
KW Hypothetical protein.
FT DOMAIN 1 96 Frame-1.
FT DOMAIN 100 194 Frame-2.
FT DOMAIN 198 292 Frame-3.
FT DOMAIN 296 391 Frame-4.
FT DOMAIN 395 489 Frame-5.
FT DOMAIN 493 587 Frame-6.
SQ SEQUENCE 587 AA; 63573 MW; 85C4155726DEF235 CRC64;

Query Match 35.4%; Score 201.5; DB 1; Length 587;
Best Local Similarity 52.4%; Pred. No. 4.7e-12;
Matches 55; Conservative 11; Mismatches 30; Indels 9; Gaps 4;

QY 1 MAQSRLTATSASRVOAILLSQPPKQLGRAPANTPLIFV-PSLEAGFHHCQAGL-KLLT 58
DB 410 VAGSRLTASSASRVHAILLPQPKLGLQADPATTPGFLFYXRRRGFTVL--AGNVSISX 467

QY 59 SGDPFPASAFOSAGITGVSHLTQANLDDKKICNSGGSCYVAQAGLK 103
DB 468 PRDPPASASQAGITGVSHRAXXXFFET-----ESRSVAQAGVQ 507

RESULT 7
Q6ZWA9 PRELIMINARY; PRT; 239 AA.
ID Q6ZWA9
AC Q6ZWA9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)

```









ligated with Alu-derived sequence in any orientation. Although Alu elements (especially situated on the complementary strand) have a great potential to create additional/alternative exons, consideration should be given to the possibility that the presence of an Alu in an open reading frame may have resulted from a cloning artifact or may be due to misinterpretation of sequencing data. This point has been overlooked on several occasions, with the consequence of erroneous Alu-derived amino acid sequences being reported.

-!- CAUTION: Any significant similarity of a putative protein sequence with an Alu-translated entry must be taken as a warning that a part of Alu repeat may have been artifactually included in the coding nucleotide sequence.

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EMBL; U14573; -; NOT ANNOTATED CDS.  
ProDom; PD003738; GIDA; 1.  
KW Hypothetical protein.  
FT DOMAIN 1 97 Frame-1.  
FT DOMAIN 101 196 Frame-2.  
FT DOMAIN 200 295 Frame-3.  
FT DOMAIN 299 395 Frame-4.  
FT DOMAIN 399 494 Frame-5.  
FT DOMAIN 498 593 Frame-6.  
SQ SEQUENCE 593 AA; 64417 MW; 54A4F50F33A6089F CRC64;

Query Match 32.8%; Score 187; DB 1; Length 593;  
Best Local Similarity 64.7%; Pred. No. 1.5e-10;  
Matches 44; Conservative 3; Mismatches 11; Indels 10; Gaps 2;  
  
Qy 10 SASRVQAILLSQPPKQLGLRAPANTPLIFVFSLEAGFHHCQAGLKLLTSGDPPASAFQS 69  
Db 434 SASRVAGI-----TGARHAR--LIFVFLVETGFHHVQAGLELLTSGDPPASQS 483  
  
Qy 70 AGITGVSH 77  
Db 484 AGITGVSH 491

RESULT 15  
Q6ZUA4  
ID Q6ZUA4 PRELIMINARY; PRT; 202 AA.  
AC Q6ZUA4;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein FLJ43866.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUES=restis;  
RA Tashiro H., Yamazaki M., Watanabe K., Kumagai A., Itakura S.,  
RA Fukuzumi Y., Fujimori Y., Komiyama M., Sugiyama T., Irie R.,  
RA Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,  
RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,  
RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M.,  
RA Murakawa K., Kaneshiro K., Takahashi-Fujii A., Oshima A., Sugiyama A.,  
RA Kawakami B., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K.,  
RA Isogai T.,  
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AK125854; BAC86322.1; - 7C402B7E86DD01FA CRC64;  
SQ SEQUENCE 202 AA; 22509 MW; 7C402B7E86DD01FA CRC64;

Query Match 32.3%; Score 184; DB 2; Length 202;  
Best Local Similarity 59.2%; Pred. No. 9.2e-11;  
Matches 42; Conservative 6; Mismatches 13; Indels 10; Gaps 1;  
  
Qy 10 SASRVQAILLSQPPKQLGLRAPANTPLIFVFSLEAGFHHCQAGLKLLTSGDPPASAFQS 69  
Db 77 SASRVAGITV-----ARHAWLIFVFLVETGFHHVQAGLELLTSGDPPASQS 126  
  
Qy 70 AGITGVSHLTQ 80  
Db 127 AGITGVSHHTTR 137

Search completed: October 11, 2005, 07:18:42  
Job time : 69.2299 secs

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OM protein - protein search, using sw model

Run on: October 11, 2005, 06:57:07 ; Search time 82.9519 Seconds  
(without alignments)  
522.196 Million cell updates/sec

Title: US-10-092-934-3

Perfect score: 570

Sequence: 1 MAQSRLTATSASRVQAILLS.....GSCVYAQGLKLLASCNPSK 112

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq16Dec04.\*

- 1: Geneseq1980s.\*
- 2: Geneseq1990s.\*
- 3: Geneseq2000s.\*
- 4: Geneseq2001s.\*
- 5: Geneseq2002s.\*
- 6: Geneseq2003as.\*
- 7: Geneseq2003bs.\*
- 8: Geneseq2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	570	100.0	112	5	AAB29144 Neural th
2	570	100.0	112	6	ABP59925 Human 112
3	570	100.0	112	6	AAB33191 Neural th
4	570	100.0	112	7	ADL96023 Human neu
5	565	99.1	112	6	ABR63242 112 amino
6	565	99.1	112	6	ABU02974 Human neu
7	565	99.1	112	6	ABJ19447 112-mer n
8	565	99.1	112	7	ADB37521 Neural th
9	282.5	49.6	170	7	ADC86487 Human GPC
10	251.5	44.1	151	7	ADC86543 Human GPC
11	240	42.1	160	7	ADC86547 Human GPC
12	232.5	40.8	133	8	ADR10295 Human pro
13	230.5	40.4	109	7	ADM03914 Human pro
14	227.5	39.9	80	5	AAB20824 Human gen
15	227.5	39.9	80	5	AAB20801 Human gen
16	227.5	39.9	80	5	ABG64654 Human alb
17	227.5	39.9	80	5	ABG64656 Human alb
18	227.5	39.9	80	8	ADL77923 Albumin f
19	227.5	39.9	80	8	ADL77921 Albumin f
20	226.5	39.7	104	6	ABP60670 Steroid t
21	226.5	39.7	200	7	ADC86585 Human GPC
22	223.5	39.2	184	8	ADQ65893 Novel hum
23	219	38.4	397	2	AA95913 Neural th
24	216	37.9	276	4	ABG07919 Novel hum
25	215.5	37.8	138	4	AAM24396 Human EST

26	214.5	37.6	123	4	AAB94974	Aab94974 Human pro
27	214.5	37.6	123	7	ADB37562	Neural th
28	212.5	37.3	164	4	AAE07113	Human gen
29	208	36.5	174	7	ADB64029	Human pro
30	207.5	36.4	87	4	AAAM23681	Human EST
31	205	36.0	139	8	ADQ65120	Novel hum
32	204.5	35.9	116	6	ABJ18397	Breast sp
33	201	35.3	239	8	ADQ65417	Novel hum
34	200	35.1	103	4	AAAM82366	Human imm
35	200	35.1	138	7	ADM04871	Human pro
36	200	35.1	138	8	ADQ65405	Novel hum
37	200	35.1	138	8	ADR10238	Human pro
38	199	34.9	161	7	ADC86933	Human GPC
39	198.5	34.8	156	7	ADC87053	Human GPC
40	198	34.7	109	7	ADD22434	HLA-B*46 T
41	198	34.7	109	7	ADL15930	Human PP
42	195.5	34.3	122	7	ADB64336	Human pro
43	195	34.2	113	7	ADB64756	Human pro
44	195	34.2	130	4	AAO07175	Human pol
45	194	34.0	115	8	ADR09436	Human pro

#### ALIGNMENTS

##### RESULT 1

AAE29144  
ID AAE29144 standard; protein; 112 AA.

XX  
AC AAE29144;

XX  
DT 27-JAN-2003 (first entry)

XX  
DE Neural thread protein (NTP) #2.

XX  
KW Neural thread protein; NTP; hyperplasia; hypertrophy; arteriosclerosis;  
KW haemorrhoid; gene therapy; tumour; vascular disease; atherosclerosis;  
KW inflammatory disease; nutritional deficiency disease; genetic disease;  
KW autoimmune disease; metabolic disease; traumatic disease; intoxication;  
KW infectious disease; congenital malformation; enzyme deficiency disease;  
KW amyloid disease; fibrosis disease; storage disease; radiation disease;  
KW poisoning; environmental disease; endocrine disease; protein therapy;  
KW degenerative disease; mechanical disease.

XX  
OS Unidentified.

XX  
PN WO200274323-A2.

XX  
PD 26-SEP-2002.

XX  
PF 08-MAR-2002; 2002WO-IB001959.

XX  
PR 08-MAR-2001; 2001US-0273957P.

XX  
PA (AVER/) AVERBACK P.

XX  
PI Averbach P;

XX  
DR WPI; 2002-759864/82.

XX  
PT Treating a condition in a patient requiring removal or destruction of  
PT cells, such as a benign or malignant tumor of a tissue or an inflammatory  
PT disease, comprises administering a neural thread protein (NTP) or a NTP  
PT gene to a mammal.

XX  
PS Claim 23; Fig 3; 70pp; English.

XX  
CC The invention relates to a method for treating a condition in a patient  
CC requiring removal or destruction of cells. The method involves  
CC administering to a mammal a neural thread protein (NTP), or administering  
CC to a tumour or other target cell a NTP gene, where the expression of the  
CC NTP gene is induced resulting in expression of the NTP protein. The  
CC method and NTP are useful for treating a condition in a patient requiring

CC removal or destruction of cells, such as a benign or malignant tumour of  
CC a tissue, a hyperplasia, hypertrophy, or overgrowth of a tissue,  
CC preferably tonsillar hypertrophy or prostatic hyperplasia, a virally,  
CC bacterially, or parasitically altered tissue, or a malformation of a  
CC tissue. Other conditions include a cosmetic modification to a tissue,  
CC such as removal of unwanted facial hair, warts or unwanted fatty tissue,  
CC a vascular disease, particularly atherosclerosis or arteriosclerosis,  
CC haemorrhoids, or varicose veins, an inflammatory disease, autoimmune  
CC or physical injury, nutritional deficiency disease, infectious disease,  
CC congenital malformation, amyloid disease, fibrosis disease, storage  
CC disease, enzyme deficiency disease, poisoning, intoxication, degenerative  
CC disease, radiation disease, environmental disease, endocrine disease or  
CC mechanical disease. The invention is useful in protein therapy and gene  
CC therapy. The present sequence is NTP protein  
XX  
SQ Sequence 112 AA;

Query Match 100.0%; Score 570; DB 5; Length 112;  
Best Local Similarity 100.0%; Pred. No. 2e-57;  
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAOSRLTATSASRVQAILLSQPPKQLGLRAPANTPLIFVFSLEAGFHHCQAGLKLTSG 60  
Db 1 MAOSRLTATSASRVQAILLSQPPKQLGLRAPANTPLIFVFSLEAGFHHCQAGLKLTSG 60  
QY 61 DPASAFQSAGITGVSHLTQPANLDKKKICSGGSCYVAQAAGLKLLASCNPSK 112  
Db 61 DPASAFQSAGITGVSHLTQPANLDKKKICSGGSCYVAQAAGLKLLASCNPSK 112

RESULT 2  
ABP59925

ID ABP59925 standard; protein; 112 AA.

AC ABP59925;

XX 08-SEP-2003 (first entry)

XX Human 112 amino acid neural thread protein.

XX Human; tumour; cancer; neural thread protein; NTP; cell removal;  
KW cell destruction; antipsoriatic; antimicrobial; immunosuppressive;  
KW antiinflammatory; dermatological; antiarteriosclerotic; vasotropic;  
KW gene therapy.

XX Homo sapiens.

XX WO2003044053-A2.

XX 30-MAY-2003.

XX 18-NOV-2002; 2002WO-CA001757.

XX 16-NOV-2001; 2001US-0331477P.

XX (NYMO-) NYMOX CORP.

XX Averbach P, Gemmell J;

XX WPI; 2003-457592/43.

XX New neural thread protein (NTP), useful for preparing a composition for  
PT treating or preventing a condition in a mammal requiring removal or  
PT destruction of cells, e.g. psoriasis, eczema, atherosclerosis or  
PT inflammatory disease.

XX Disclosure; Fig 2; 98pp; English.

XX The present invention relates to peptides derived from the human neural  
CC thread protein (NTP). The peptides are useful for preparing a composition  
CC for treating or preventing a condition in a mammal requiring removal or  
CC destruction of cells, comprising tonsillar hypertrophy, prostatic

CC hyperplasia, psoriasis, eczema, dermatosis, cosmetic modification to a  
CC breast, connective, skin, eye, ear, nose, throat, mouth or muscle tissue,  
CC varicose veins, atherosclerosis, inflammatory, metabolic, infectious,  
CC fibrosis, endocrine or autoimmune disease, or stenosis, restenosis, in  
CC occlusion or blockage of an artery or of a stent placed or implanted in  
CC an artery. The present sequence is an NTP protein used to produce  
CC peptides of the invention  
XX

SQ Sequence 112 AA;

Query Match 100.0%; Score 570; DB 6; Length 112;  
Best Local Similarity 100.0%; Pred. No. 2e-57;  
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAOSRLTATSASRVQAILLSQPPKQLGLRAPANTPLIFVFSLEAGFHHCQAGLKLTSG 60

Db 1 MAOSRLTATSASRVQAILLSQPPKQLGLRAPANTPLIFVFSLEAGFHHCQAGLKLTSG 60

QY 61 DPASAFQSAGITGVSHLTQPANLDKKKICSGGSCYVAQAAGLKLLASCNPSK 112

Db 61 DPASAFQSAGITGVSHLTQPANLDKKKICSGGSCYVAQAAGLKLLASCNPSK 112

## RESULT 3

AAE33191

ID AAE33191 standard; protein; 112 AA.

XX AAE33191;

XX 16-APR-2003 (first entry)

XX Neural thread protein (NTP) #2.

XX Cell death; tissue necrosis; neural thread protein; NTP; amyloidosis;

KW stroke; brain tumour; Pick's disease; Parkinson's disease; glaucoma;

KW Alzheimer's disease; gene therapy.

XX Unidentified.

XX WO200289841-A2.

XX 14-NOV-2002.

XX 06-MAY-2002; 2002WO-CA000681.

XX 04-MAY-2001; 2001US-0288463P.

XX (NYMO-) NYMOX CORP.

XX Averbach PA;

XX WPI; 2003-120506/11.

XX Preventing, controlling, modulating, ameliorating and/or treating cell  
PT death or tissue necrosis using antibodies to neural thread proteins,  
PT useful in disorders such as stroke, brain tumor, glaucoma and Alzheimer's  
PT disease.

XX Disclosure; Fig 6; 60pp; English.

XX The invention relates to a method of preventing, and/or inhibiting cell  
CC death and/or tissue necrosis in live tissue containing neural thread  
CC proteins (NTP). The method involves contacting the live tissue with at  
CC least one antibody, fragment or derivative that recognises NTP, where the  
CC antibody, fragment or derivative is present to prevent, control,  
CC ameliorate and/or inhibit cell death and/or tissue necrosis caused by the  
CC presence of NTP. Methods and compositions of the invention are useful for  
CC preventing, modulating, controlling and/or treating disorders associated  
CC with cell death and/or tissue necrosis such as stroke, brain tumour,  
CC Pick's disease, Parkinson's disease, amyloidosis, glaucoma and  
CC Alzheimer's disease. The invention is useful in gene therapy. The present  
CC sequence is NTP protein  
XX

SQ Sequence 112 AA;

Query Match 100.0%; Score 570; DB 6; Length 112;  
Best Local Similarity 100.0%; Pred. NO. 2e-57;  
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAQSRLTATSASRVOAILLSQPPKQLGLRAPANTPLIFVFSLEAGFHHICOAGLKLITSG 60  
Db 1 MAQSRLTATSASRVOAILLSQPPKQLGLRAPANTPLIFVFSLEAGFHHICOAGLKLITSG 60

Qy 61 DPPASAFQSAGITGVSHLTQPNALDKKICNSGGSCYVAQAGLKLASCNPSK 112  
Db 61 DPPASAFQSAGITGVSHLTQPNALDKKICNSGGSCYVAQAGLKLASCNPSK 112

RESULT 4  
ADL96023  
ID ADL96023 standard; protein; 112 AA.  
XX ADL96023;  
XX  
DT 20-MAY-2004 (first entry)  
XX  
DE Human neural thread protein, NTP112.  
XX  
KW Human; neural thread protein; NTP112; NTP106; NTP98; NTP75;  
KW NTP68; NTP61; stenosis; stent; tumour; prostatic hyperplasia; psoriasis;  
KW eczema; haemorrhoid; atherosclerosis; inflammatory disease;  
KW autoimmune disease; metabolic disease; hereditary disease;  
KW genetic disease; traumatic disease; physical injury;  
KW nutritional deficiency disease; infectious disease; amyloid disease;  
KW Alzheimer's disease; storage disease; congenital malformation;  
KW enzyme deficiency disease; poisoning; intoxication;  
KW environmental disease; radiation disease; endocrine disease;  
KW degenerative disease; mechanical disease.  
XX  
OS Homo sapiens.  
XX  
XX US2003166569-A1.  
XX  
XX 04-SEP-2003.  
XX  
XX 15-NOV-2002; 2002US-00294891.  
XX  
XX 16-NOV-2001; 2001US-0331477P.  
XX  
XX (AVER/) AVERBACK P.  
XX (GEMM/) GEMMELL J.  
XX  
XX Averbach P, Gemmell J;  
XX  
XX WPI; 2003-898099/82.  
XX  
XX New neural thread protein or its variants, useful for treating tumors and  
XX other conditions requiring the removal or destruction of cells (e.g.  
XX prostatic hyperplasia, psoriasis, eczema, hemorrhoids or  
XX atherosclerosis).  
XX  
XX Disclosure; SEQ ID NO 2; 32pp; English.  
XX  
XX The invention relates to a peptide, or its homologue, derivative,  
XX fragment, variant or mimetic, comprising at least one neural thread  
XX protein (NTP) peptide appearing as ADL96029-ADL96069, derived from  
XX NTP122, 112, 106, 98, 75, 68 or 61. Also included are a nucleic acid  
XX encoding an amino acid sequence corresponding to the above peptide, a  
XX composition comprising one or more peptides or nucleic acids cited above  
XX and a carrier, a method of treating a condition in a mammal requiring  
XX removal or destruction of cells (comprising administering to the mammal  
XX an amount of the peptide cited above) and a method of preventing or  
XX inhibiting the stenosis, occlusion or blockage of a stent, comprising  
XX coating the stent with an amount of the above peptide. The peptide  
XX further comprises an amino acid in a reverse-D order based on the above  
XX amino acid sequences. The composition and methods are useful in treating

CC tumours and other conditions requiring the removal or destruction of  
CC cells (e.g. prostatic hyperplasia, psoriasis, eczema, haemorrhoids or  
CC atherosclerosis). These may also be used in treating inflammatory  
CC diseases, autoimmune diseases, metabolic diseases, hereditary/genetic  
CC diseases, traumatic diseases or physical injuries, nutritional deficiency  
CC diseases, infectious diseases, amyloid diseases e.g. Alzheimer's disease,  
CC storage diseases, congenital malformation, enzyme deficiency diseases,  
CC poisoning, intoxication, environmental diseases, radiation diseases,  
CC endocrine diseases, degenerative diseases or mechanical diseases. The  
CC present sequence is a human NTP protein from which the peptides of the  
CC invention are derived.  
XX  
SQ Sequence 112 AA;

Query Match 100.0%; Score 570; DB 7; Length 112;  
Best Local Similarity 100.0%; Pred. NO. 2e-57;  
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAQSRLTATSASRVOAILLSQPPKQLGLRAPANTPLIFVFSLEAGFHHICOAGLKLITSG 60  
Db 1 MAQSRLTATSASRVOAILLSQPPKQLGLRAPANTPLIFVFSLEAGFHHICOAGLKLITSG 60

Qy 61 DPPASAFQSAGITGVSHLTQPNALDKKICNSGGSCYVAQAGLKLASCNPSK 112  
Db 61 DPPASAFQSAGITGVSHLTQPNALDKKICNSGGSCYVAQAGLKLASCNPSK 112

RESULT 5  
ABR63242  
ID ABR63242 standard; protein; 112 AA.  
XX ABR63242;  
XX  
DT 28-AUG-2003 (first entry)  
XX  
DE 112 amino acid neural thread protein.  
XX  
KW Cytostatic; Antibacterial; Immunosuppressive; Antiinflammatory;  
KW neural thread protein; NTP; tumour.  
XX  
XX Unidentified.  
XX  
XX WO2003008443-A2.  
XX  
XX 30-JAN-2003.  
XX  
XX 19-JUL-2002; 2002WO-CA001105.  
XX  
XX 19-JUL-2001; 2001US-0306150P.  
XX 19-JUL-2001; 2001US-0306161P.  
XX 16-NOV-2001; 2001US-0331477P.  
XX  
XX (NYMO-) NYMOX CORP.  
XX  
XX Averbach PA;  
XX  
XX WPI; 2003-247999/24.  
XX  
XX Novel neural thread protein peptide, referred as cell death peptide,  
XX useful for treating prostatic hyperplasia, psoriasis, eczema, dermatosis,  
XX atherosclerosis, cosmetic modification to skin, throat, mouth, muscle.  
XX  
XX Disclosure; Fig 3; 77pp; English.  
XX  
XX The present invention relates to a neural thread protein (NTP) peptide  
XX referred to as cell death peptide. Thought to be cytostatic,  
XX antibacterial, immunosuppressive and antiinflammatory. It is useful for  
XX treating a condition in a patient requiring removal or destruction of  
XX cells, for treating a condition such as benign or malignant tumor,  
XX inflammatory disease, autoimmune disease and infectious disease. The  
XX peptide useful for treatment is derived from the amino acid sequence for  
XX a pancreatic thread protein. The peptide is conjugated, linked or bound  
XX to a molecule chosen from antibody or its fragment, antibody-like binding

CC molecule, where the molecule has a higher affinity for binding to a tumor  
CC or other target than binding to other cells. Treatment using NTP peptides  
CC can remove benign tumors with less risk and fewer of the undesirable side  
CC effects of surgery. The present sequence is an NTP amino acid sequence  
XX  
SQ Sequence 112 AA;

Query Match 99.1%; Score 565; DB 6; Length 112;  
Best Local Similarity 99.1%; Pred. No. 7.6e-57;  
Matches 111; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAQSRLTATSASRVAQAILLSQPPKQLGLRAPANTPLIFVFSLEAGFHHCQAGLKLLTSG 60  
|||||

Db 1 MAQSRLTATSASRVAQAILLSQPPKQLGLRAPANTPLIFVFSLEAGFHHCQAGLKLLTSG 60  
|||||

QY 61 DPASAFQSGAGITGVSHLTQPNALDKKICSNNGSCYVAQAGLKLLASCNPSK 112  
|||||

Db 61 DPASAFQSGAGITGVSHLTQPNALDKKICSNNGSCYVAQAGLKLLASCNPSK 112  
|||||

RESULT 6  
ABU02974  
ID ABU02974 standard; protein; 112 AA.  
XX  
AC ABU02974;  
XX  
XX  
DT 20-JAN-2003 (first entry)  
XX  
DE Human neural thread protein AD7C-NTP, protein fragment #2.

XX Neural thread protein; NTP-peptide; AD7C-NTP; surgical excision;  
XX transplantation; grafting; chemotherapy; immunotherapy; vaccination;  
KW ablation; cryotherapy; laser therapy; phototherapy; gene therapy;  
KW radiation; tumor; hyperplasia; hypertrophy; overgrowth of tissue;  
KW malformation of tissue; tonsillary hypertrophy; prostatic hyperplasia;  
KW cosmetic modification; vascular disease; atherosclerosis;  
KW arteriosclerosis; haemorrhoid; varicose vein; inflammatory disease;  
KW autoimmune disease; metabolic disease; traumatic disease;  
KW physical injury; nutritional deficiency disease; infectious disease;  
KW amyloid disease; fibrosis disease; storage disease;  
KW congenital malformation; enzyme deficiency disease; poisoning;  
KW intoxication; environmental disease; radiation disease;  
KW endocrine disease; degenerative disease; mechanical disease.

XX Homo sapiens.

OS  
XX WO200297030-A2.

XX  
XX  
PD 05-DEC-2002.

XX  
XX 24-MAY-2002; 2002WO-CA000759.

XX  
XX 25-MAY-2001; 2001US-0293156P.

XX (NYMO-) NYMOX CORP.

XX  
XX Averbach PA;

XX WPI; 2003-041406/03.

XX Novel peptides similar in amino acid sequence to neural thread proteins  
PT (NTP), useful for treating unwanted cellular proliferations such as  
PT malignant tumors and prostatic hyperplasia.

XX Disclosure; Fig 3; 78pp; English.

XX The invention describes an NTP-peptide (I) comprising at least one amino  
CC acid sequence corresponding to part of the amino acid sequence of a  
CC neural thread protein, AD7C-NTP. The invention provides a method of  
CC treating a condition requiring removal or destruction of cells of a  
CC mammal comprising administering to a mammal, a therapeutic amount of (I).  
CC The treatment is administered to the mammal before, during or after  
CC surgical excision, transplantation, grafting, chemotherapy.

CC immunotherapy, vaccination, thermal or electrical ablation, cryotherapy,  
CC laser therapy, phototherapy, gene therapy and/or radiation. The method is  
CC useful for treatment of benign or malignant tumour; hyperplasia,  
CC hypertrophy or overgrowth of tissue; virally, bacterially or  
CC parasitically altered tissue; malformation of tissue selected from lung,  
CC breast, stomach, pancreas, prostate, bladder, bone, ovary, skin, kidney,  
CC sinus, colon, intestine, rectum, esophagus, heart, spleen, salivary  
CC gland, blood, brain and its coverings, spinal cord, muscle, connective  
CC tissue, adrenal, parathyroid, thyroid, uterus, testis, pituitary,  
CC reproductive organs, liver, hair, gall bladder, eye, ear, nose, throat,  
CC tonsils, mouth and lymph nodes and lymphoid system; tonsillary  
CC hypertrophy; prostatic hyperplasia; cosmetic modification to a tissue;  
CC vascular disease (atherosclerosis or arteriosclerosis); haemorrhoids;  
CC varicose veins; inflammatory disease; autoimmune disease; metabolic  
CC disease; hereditary/genetic disease; traumatic disease; physical injury;  
CC nutritional deficiency disease; infectious disease; amyloid disease;  
CC fibrosis disease; storage disease; congenital malformation; enzyme  
CC deficiency disease; poisoning; intoxication; environmental disease;  
CC radiation disease; endocrine disease; degenerative disease and mechanical  
CC disease. This is the amino acid sequence of a human neural thread protein  
CC AD7C-NTP protein fragment  
XX  
SQ Sequence 112 AA;

Query Match 99.1%; Score 565; DB 6; Length 112;  
Best Local Similarity 99.1%; Pred. No. 7.6e-57;  
Matches 111; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAQSRLTATSASRVAQAILLSQPPKQLGLRAPANTPLIFVFSLEAGFHHCQAGLKLLTSG 60  
|||||

Db 1 MAQSRLTATSASRVAQAILLSQPPKQLGLRAPANTPLIFVFSLEAGFHHCQAGLKLLTSG 60  
|||||

QY 61 DPASAFQSGAGITGVSHLTQPNALDKKICSNNGSCYVAQAGLKLLASCNPSK 112  
|||||

Db 61 DPASAFQSGAGITGVSHLTQPNALDKKICSNNGSCYVAQAGLKLLASCNPSK 112  
|||||

RESULT 7  
ABJ19447

ID ABJ19447 standard; protein; 112 AA.

XX  
AC ABJ19447;

XX 27-MAR-2003 (first entry)

XX 112-mer neural thread protein.

XX Nootropic; neuroprotective; cell death; tissue necrosis; NTP;

KW neural thread protein; neurodegenerative disorder; Alzheimer's disease.

XX Unidentified.

XX WO200292115-A2.

XX 21-NOV-2002.

XX 16-MAY-2002; 2002WO-CA000712.

XX 16-MAY-2001; 2001US-0290971P.

XX (NYMO-) NYMOX CORP.

XX Averbach PA;

XX WPI; 2003-129234/12.

XX Preventing and/or inhibiting cell death and/or tissue necrosis in a  
PT tissue for treating a neurodegenerative disorder, e.g. Alzheimer's  
PT disease, by contacting the live tissue with at least one segment of  
PT neural thread proteins (NTP).

XX Disclosure; Fig 3; 60pp; English.

XX

CC The invention relates to a novel method for preventing and/or inhibiting  
CC cell death and/or tissue necrosis in a tissue comprising contacting the  
CC live tissue with at least one segment of neural thread proteins (NTP).  
CC The methods are composition are useful for treating a neurodegenerative  
CC disorder, such as Alzheimer's disease. This sequence represents an NTP  
CC protein of the invention  
XX  
SQ Sequence 112 AA;

Query Match 99.1%; Score 565; DB 6; Length 112;  
Best Local Similarity 99.1%; Pred. No. 7.6e-57;  
Matches 111; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MAQSRLTATSASRVQAILLSQPPKQLGLRAPANTPLIFVFSLEAGFHHICQAGLKLTSG 60  
Db 1 MAQSRLTATSASRVQAILLSQPPKQLGLRAPANTPLIFVFSLEAGFHHICQAGLKLTSG 60

Qy 61 DPPASAFQSAGITGVSHLTQPNLDKKICSNNGSGCYVAQAGLKLLASCNPSK 112

Db 61 DPPASAFQSAGITGVSHLTQPNLDKKICSNNGSGCYVAQAGLKLLASCNPSK 112

## RESULT 8

ADB37521  
ID ADB37521 standard; protein; 112 AA.

XX ADB37521;

XX 04-DEC-2003 (first entry)

XX Neural thread protein #2.

XX Cytostatic; Antitumour; Antipsoriatic; Dermatological;

KW Antiatherosclerotic; Antiarteriosclerotic; Vasotropic; Antiinflammatory;

KW Immunosuppressive; Tranquillizer; Antiemetic; Virucide; AD7c-NTP;

KW neural thread protein; neuritic sprouting.

XX Unidentified.

XX WO2003008444-A2.

XX 30-JAN-2003.

XX 19-JUL-2002; 2002WO-CA001106.

XX 19-JUL-2001; 2001US-0306150P.

XX 19-JUL-2001; 2001US-0306161P.

XX 16-NOV-2001; 2001US-0331477P.

XX (NYMO-) NYMOX CORP.

XX Averbach PA, Gemmell J;

XX WPI; 2003-248000/24.

XX Novel Related peptide or AD7c-neural thread peptide, useful for treating  
PT unwanted cellular proliferations, glandular hyperplasia, unwanted facial  
PT hair, warts and unwanted fatty tissue.

XX Disclosure; Fig 3; 109pp; English.

XX The present invention relates to AD7c-neural thread protein (NTP) and  
CC related proteins and peptides (I; ADB37528-ADB37641). The sequences are  
CC useful for treating a condition in a patient requiring removal or  
CC destruction of cells. The condition can be selected from benign or  
CC malignant tumour of a tissue, hyperplasia, hypertrophy or overgrowth of a  
CC tissue, virally, bacterially or parasitically altered tissue, or  
CC malformation of a tissue, where the tissue is selected from lung, breast,  
CC stomach, pancreas, prostate, bladder, bone, ovary, skin, kidney, sinus,  
CC colon, intestine, stomach, rectum, oesophagus, heart, spleen, salivary  
CC gland, blood, brain and its coverings, spinal cord and its coverings,  
CC muscle, connective tissue, adrenal, parathyroid, thyroid, uterus, testis,  
CC pituitary, reproductive organs, liver, gall bladder, eye, ear, nose,

CC throat, tonsils, mouth, lymph nodes and lymphoid tissue. The condition is  
CC preferably tonsillar hypertrophy, prostatic hyperplasia, psoriasis,  
CC eczema, dermatosis, cosmetic modification to a tissue (skin, eye, ear,  
CC nose, throat, mouth, muscle, connective, hair or breast tissue), vascular  
CC disease (atherosclerosis or arteriosclerosis), haemorrhoids, varicose  
CC veins, inflammatory disease, autoimmune disease, metabolic injury,  
CC hereditary/genetic disease, traumatic disease or physical injury,  
CC nutritional deficiency disease, infectious disease, amyloid disease,  
CC fibrosis disease, storage disease, congenital malformation, enzyme  
CC deficiency disease, poisoning, intoxication, environmental disease,  
CC radiation disease, endocrine disease, degenerative disease and mechanical  
CC disease. The peptides are useful for treating unwanted cellular  
CC proliferations, glandular (e.g. prostate) hyperplasia, unwanted facial  
CC hair, warts and unwanted fatty tissue, or for preparing antibodies that  
CC recognize and/or bind to Related proteins, Related peptides or NTP  
CC peptides. The present sequence was used to illustrate the invention.

XX SQ Sequence 112 AA;

Query Match 99.1%; Score 565; DB 7; Length 112;  
Best Local Similarity 99.1%; Pred. No. 7.6e-57;  
Matches 111; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MAQSRLTATSASRVQAILLSQPPKQLGLRAPANTPLIFVFSLEAGFHHICQAGLKLTSG 60

Db 1 MAQSRLTATSASRVQAILLSQPPKQLGLRAPANTPLIFVFSLEAGFHHICQAGLKLTSG 60

Qy 61 DPPASAFQSAGITGVSHLTQPNLDKKICSNNGSGCYVAQAGLKLLASCNPSK 112

Db 61 DPPASAFQSAGITGVSHLTQPNLDKKICSNNGSGCYVAQAGLKLLASCNPSK 112

## RESULT 9

ADC86487

ID ADC86487 standard; protein; 170 AA.

XX ADC86487;

XX 01-JAN-2004 (first entry)

XX Human GPCR protein SEQ ID NO:940.

XX human; GPCR; guanosine triphosphate-binding protein coupled receptor;  
KW gene therapy.

XX Homo sapiens.

XX EPI270724-A2.

XX 02-JAN-2003.

XX 18-JUN-2002; 2002EP-00013517.

XX 18-JUN-2001; 2001JP-00246789.

XX (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.

XX (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.

XX Suwa M, Asai K, Akiyama Y, Aburatani H;

XX WPI; 2003-315783/31.

XX N-PSDB; ADC86486.

XX New polynucleotide, useful for preparing a composition for treating a  
PT patient in need of increased or suppressed activity or expression of the  
PT guanosine triphosphate-binding protein coupled receptor.

XX Claim 2; SEQ ID NO 940; 28pp; English.

XX The invention relates to a novel polynucleotide encoding a guanosine  
CC triphosphate-binding protein coupled receptor (GPCR). A polynucleotide of  
CC the invention may have a use in gene therapy. The polynucleotide and  
CC polypeptide are useful for preparing a composition for treating a patient

```
CC in need of increased or suppressed activity or expression of the
CC guanosine triphosphate-binding protein coupled receptor. The protein
CC sequences shown in ADC85549-ADC87617 represent GPCR's of the invention.
XX
XX
SQ Sequence 170 AA;

Query Match          49.6%; Score 282.5; DB 7; Length 170;
Best Local Similarity 70.2%; Pred. No. 4.3e-24;
Matches 59; Conservative 8; Mismatches 16; Indels 1; Gaps 1;

QY 1 MAQSLRTATSASRVQAILLSQPPKQLGLRAPANTP-LIFVFSLEAGFHHICQAGLKLLTS 59
Db 79 MVQSLRTATSASRVQAILLPQPESLGLQVPATTPSYFFIFLVETGFHCVGQAVLELLTS 138

QY 60 GDPPASAFQSGAGITGVSHLTQPAN 83
Db 139 GDPPASASQSGAGISGVSHCARPLN 162

RESULT 10
ADC86543
ID ADC86543 standard; protein; 151 AA.
XX
AC ADC86543;
XX
XX 01-JAN-2004 (first entry)
XX Human GPCR protein SEQ ID NO:996.
XX human; GPCR; guanosine triphosphate-binding protein coupled receptor;
XX gene therapy.
XX Homo sapiens.
XX
XX EP1270724-A2.
XX
XX 02-JAN-2003.
XX
XX 18-JUN-2002; 2002EP-00013517.
XX
XX 18-JUN-2001; 2001JP-00246789.
XX (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
XX (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
XX Suwa M, Asai K, Akiyama Y, Aburatani H;
XX WPI; 2003-315783/31.
XX N-PSDB; ADC86542.
XX
XX New polynucleotide, useful for preparing a composition for treating a
XX patient in need of increased or suppressed activity or expression of the
XX guanosine triphosphate-binding protein coupled receptor.
XX Claim 2; SEQ ID NO 996; 28pp; English.
XX
XX The invention relates to a novel polynucleotide encoding a guanosine
XX triphosphate-binding protein coupled receptor (GPCR). A polynucleotide of
XX the invention may have a use in gene therapy. The polynucleotide and
XX polypeptide are useful for preparing a composition for treating a patient
XX in need of increased or suppressed activity or expression of the
XX guanosine triphosphate-binding protein coupled receptor. The protein
XX sequences shown in ADC85549-ADC87617 represent GPCR's of the invention.
XX
XX Sequence 151 AA;

Query Match          44.1%; Score 251.5; DB 7; Length 151;
Best Local Similarity 67.9%; Pred. No. 1.4e-20;
Matches 55; Conservative 9; Mismatches 16; Indels 1; Gaps 1;

QY 1 MAQSLRTATSASRVQAILLSQPPKQLGLRAPANTPLIFVFSLEAGFHHICQAGLKLLTSG 60
Db 57 VAQSLRTATSASRVQAILLPQPEQLG-DMHHHTWLIFVFLVERGFHVGKAGLELLTSS 115
```

```
QY 61 DPPASAFQSGAGITGVSHLTQP 81
Db 116 DPPTSASQSGAGITGISHCARP 136

RESULT 11
ADC86547
ID ADC86547 standard; protein; 160 AA.
XX
AC ADC86547;
XX
XX 01-JAN-2004 (first entry)
XX Human GPCR protein SEQ ID NO:1000.
XX human; GPCR; guanosine triphosphate-binding protein coupled receptor;
XX gene therapy.
XX Homo sapiens.
XX
XX EP1270724-A2.
XX
XX 02-JAN-2003.
XX
XX 18-JUN-2002; 2002EP-00013517.
XX
XX 18-JUN-2001; 2001JP-00246789.
XX (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
XX (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
XX Suwa M, Asai K, Akiyama Y, Aburatani H;
XX WPI; 2003-315783/31.
XX N-PSDB; ADC86546.
XX
XX New polynucleotide, useful for preparing a composition for treating a
XX patient in need of increased or suppressed activity or expression of the
XX guanosine triphosphate-binding protein coupled receptor.
XX Claim 2; SEQ ID NO 1000; 28pp; English.
XX
XX The invention relates to a novel polynucleotide encoding a guanosine
XX triphosphate-binding protein coupled receptor (GPCR). A polynucleotide of
XX the invention may have a use in gene therapy. The polynucleotide and
XX polypeptide are useful for preparing a composition for treating a patient
XX in need of increased or suppressed activity or expression of the
XX guanosine triphosphate-binding protein coupled receptor. The protein
XX sequences shown in ADC85549-ADC87617 represent GPCR's of the invention.
XX
XX Sequence 160 AA;

Query Match          42.1%; Score 240; DB 7; Length 160;
Best Local Similarity 63.9%; Pred. No. 3.1e-19;
Matches 53; Conservative 8; Mismatches 20; Indels 2; Gaps 1;

QY 1 MAQSLRTATSASRVQAILLSQPPKQLGLRAPA--NTPLIFVFSLEAGFHHICQAGLKLLT 58
Db 23 MVQSLRTATSASRVQAILLSQPEELGLCTGACRHAQLIFCILMETGFHCVQAGLELLS 82

QY 59 SGDPASAFQSGAGITGVSHLTQP 81
Db 83 SGSPFVSASRSARITGVSHHWP 105

RESULT 12
ADRL0295
ID ADRL0295 standard; protein; 133 AA.
XX
AC ADRL0295;
XX
XX 04-NOV-2004 (first entry)
```



```

XX Human protein useful for treating neurological disease Seq 3801.
DE
XX human; oligo-capping method; diagnostic marker; gene therapy;
KW osteoporosis; neurological disease; Alzheimer's disease;
KW Parkinson's disease; dementia; short memory; cancer;
KW sense or motor function; emotional reaction; fear response; panic;
KW osteopathic; neuroprotective; nootropic; antiparkinsonian; cytostatic;
KW tranquilliser.
XX
XX Homo sapiens.
XX
XX EPI447413-A2.
XX
XX 18-AUG-2004.
XX
XX 12-FEB-2004; 2004EP-00003145.
XX
XX 14-FEB-2003; 2003JP-00102207.
XX
XX 09-MAY-2003; 2003JP-00131452.
XX
XX (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
XX Isogai T, Yamamoto J, Nishikawa T, Isono Y, Sugiyama T, Otsuki T;
XX Wakamatsu A, Ishii S, Nagai K, Irie R;
XX WPI; 2004-583265/57.
XX
XX N-PSDB; ADR08339.
XX
XX New 1995 cDNA, useful for treating osteoporosis, neurological disease,
XX Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.
XX
XX Claim 1; SEQ ID NO 3801; 2686pp; English.
XX
XX This invention relates to novel, isolated full length human cDNA
XX molecules and the encoded proteins thereof. Specifically, it refers to
XX cDNA clones obtained by an oligo-capping method, where none of these
XX clones are identical to any known human mRNAs. The present invention
XX describes an immunoassay to identify agonists and antagonists, as well as
XX antibodies, antisense molecules and siRNAs that can all be used to bind
XX to and modulate expression of the cDNA molecules. As such, these
XX molecules are useful for diagnostic markers or therapeutic targets for
XX the various diseases or morbid states. In particular, they are useful in
XX gene therapy for treating osteoporosis, neurological disease, Alzheimer's
XX disease, Parkinson's disease, dementia, short memory and various cancers,
XX as well as for maintaining equilibrium of sense or motor function, and
XX for treating emotional reaction, fear response and panic. Accordingly,
XX they exhibit osteopathic, neuroprotective, nootropic, antiparkinsonian,
XX cytostatic and tranquilliser activities. This polypeptide is a protein
XX encoded by a full length human cDNA sequence of the invention. NOTE: This
XX sequence is not given in the sequence listing of the specification but
XX can be obtained on CD-ROM from the European Patent Office, Vienna Sub-
XX office.
XX
XX Sequence 133 AA;
Qy Query Match 40.8%; Score 232.5; DB 8; Length 133;
Dd Best Local Similarity 68.5%; Pred. No. 1.8e-18;
Matches 50; Conservative 5; Mismatches 17; Indels 1; Gaps 1;
Qy 10 SASRVQAILLSQPPKQLGLRAPANTP-LIFVFSLEAGFHHCQAGLKLLTSGDPPASAFQ 68
Dd :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
42 TASQVQAILLTQPPKQLGLRAYATAPGVFFVFLVIGFHHVGRPGKLLTSGDPPALASQ 101
Qy 69 SAGITGVSHLTOP 81
Dd |||||:|||:|||
102 GAGIAGVSHRTWP 114
RESULT 13
ADM03914
ID ADM03914 standard; protein; 109 AA.
XX

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AC ADM03914;
XX
XX 20-MAY-2004 (first entry)
XX
XX Human protein of the invention SEQ ID NO:2599.
XX
XX human; gene therapy; diagnostic marker; pharmaceutical.
XX
XX Homo sapiens.
XX
XX EPI347046-A1.
XX
XX 24-SEP-2003.
XX
XX 12-APR-2002; 2002EP-00008400.
XX
XX 22-MAR-2002; 2002JP-00137785.
XX
XX (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
XX Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
XX Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
XX Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;
XX WPI; 2003-723558/69.
XX
XX N-PSDB; ADM01471.
XX
XX New polynucleotides and polypeptides are useful in gene therapy, for
XX developing a diagnostic marker or medicines for regulating their
XX expression and activity, or as a target of gene therapy.
XX
XX Claim 1; SEQ ID NO 2599; 305pp; English.
XX
XX The invention relates to a novel human polynucleotide and the encoded
XX polypeptide. A polynucleotide of the invention may have a use in gene
XX therapy. An oligonucleotide of the invention ADM06202-ADM06773 is useful
XX as a primer for synthesizing the polynucleotide or as a probe for
XX detecting the polynucleotide. The polynucleotides ADM01316-ADM03758 are
XX useful in gene therapy, for developing a diagnostic marker or medicines
XX for regulating their expression and activity, or as a target of gene
XX therapy. The proteins ADM03759-ADM06201 encoded by the polynucleotides
XX are useful as pharmaceutical agents. The present sequence represents a
XX protein sequence of the invention.
XX
XX Sequence 109 AA;
Qy Query Match 40.4%; Score 230.5; DB 7; Length 109;
Dd Best Local Similarity 66.7%; Pred. No. 2.4e-18;
Matches 54; Conservative 4; Mismatches 20; Indels 3; Gaps 1;
Qy 1 MAQSRLTATSASRVQAILLSQPPKQLGLRAPANTPLIFVFSLEAGFHHCQAGLKLLTSG 60
Dd |||||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
1 MAQSRLTATSASRVQVILL--PKSGITGMHHHTLIFVFLVEMGFHHIGQAGLELLTSG 57
Qy 61 DPPASAFQSAGITGVSHLTOP 81
Dd |||||:|||:|||:|||
58 DPPASAFQSAGIAGVKHHAQP 78
RESULT 14
AAE20824
ID AAE20824 standard; protein; 80 AA.
XX
XX AAE20824;
XX
XX 01-JUL-2002 (first entry)
XX
XX Human gene 9 encoded secreted protein HDABU01, SEQ ID NO:86.
XX
XX Human; secreted protein; gene therapy; human immunodeficiency virus; HIV;
XX immune disease; autoimmune disease; anaemia; multiple sclerosis; cancer;
XX rheumatoid arthritis; hyperproliferative disorder; melanoma; neoplasm;
XX seary syndrome; Gaucher's disease; neurological disease; cardiac arrest;

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 11, 2005, 06:57:16 ; Search time 187.765 Seconds  
(without alignments)  
248.149 Million cell updates/sec

Title: US-10-092-934-3

Perfect score: 570

Sequence: 1 MAQSLTATSASRVQAILLS.....GSCVQAQGLKLLASCNPSK 112

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1854112 seqs, 416015017 residues

Total number of hits satisfying chosen parameters: 1854112

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*
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- 11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*
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- 14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/2/pubpaa/US10D\_PUBCOMB.pep.\*
- 17: /cgn2\_6/ptodata/2/pubpaa/US10E\_PUBCOMB.pep.\*
- 18: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*
- 19: /cgn2\_6/ptodata/2/pubpaa/US11A\_PUBCOMB.pep.\*
- 20: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep.\*
- 21: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*
- 22: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	570	100.0	112	14	US-10-138-516-2
2	570	100.0	112	14	US-10-146-130-4
3	570	100.0	112	14	US-10-092-934-3
4	570	100.0	112	14	US-10-153-334-3
5	570	100.0	112	14	US-10-198-069-3
6	570	100.0	112	14	US-10-198-070-3
7	570	100.0	112	14	US-10-294-891-2
8	570	100.0	112	17	US-10-920-313-2
9	282.5	49.6	170	14	US-10-017-161-1108
10	282.5	49.6	170	15	US-10-292-798-940
11	251.5	44.1	151	14	US-10-017-161-1178

12	251.5	44.1	151	15	US-10-292-798-996	Sequence 996, App
13	240	42.1	160	14	US-10-017-161-1184	Sequence 1184, App
14	240	42.1	160	15	US-10-292-798-1000	Sequence 1000, App
15	230.5	40.4	109	15	US-10-108-260A-2599	Sequence 2599, App
16	227.5	39.9	80	11	US-09-833-245-1403	Sequence 1403, App
17	227.5	39.9	80	11	US-09-833-245-1405	Sequence 1405, App
18	226.5	39.7	200	14	US-10-017-161-1242	Sequence 1242, App
19	226.5	39.7	200	15	US-10-292-798-1038	Sequence 1038, App
20	216	37.9	276	18	US-10-450-763-38278	Sequence 38278, App
21	214.5	37.6	123	14	US-10-198-070-44	Sequence 44, Appl
22	208	36.5	174	15	US-10-104-047-2183	Sequence 2183, App
23	204.5	35.9	116	11	US-09-989-890-206	Sequence 206, App
24	200	35.1	138	15	US-10-108-260A-3556	Sequence 3556, App
25	199	34.9	161	14	US-10-017-161-1730	Sequence 1730, App
26	199	34.9	161	15	US-10-292-798-1386	Sequence 1386, App
27	198.5	34.8	156	14	US-10-017-161-1850	Sequence 1850, App
28	198.5	34.8	156	15	US-10-292-798-1506	Sequence 1506, App
29	198	34.7	109	17	US-10-734-049A-274	Sequence 274, App
30	195.5	34.3	122	15	US-10-104-047-2490	Sequence 2490, App
31	195	34.2	113	15	US-10-104-047-2910	Sequence 2910, App
32	191	33.5	190	14	US-10-017-161-1734	Sequence 1734, App
33	191	33.5	190	15	US-10-292-798-1390	Sequence 1390, App
34	189	33.2	341	18	US-10-220-335-586	Sequence 586, App
35	188	33.0	127	14	US-10-074-475-215	Sequence 215, App
36	187	32.8	109	15	US-10-121-016-48	Sequence 48, Appl
37	182	31.9	143	10	US-09-974-879-533	Sequence 533, App
38	182	31.9	143	10	US-09-305-736-535	Sequence 535, App
39	182	31.9	143	10	US-09-818-683-535	Sequence 535, App
40	182	31.9	143	11	US-09-818-683-535	Sequence 535, App
41	182	31.9	143	15	US-10-621-401-533	Sequence 533, App
42	181.5	31.8	129	10	US-09-764-891-2977	Sequence 2977, App
43	181.5	31.8	163	15	US-10-104-047-3081	Sequence 3081, App
44	181.5	31.8	603	16	US-10-408-765A-140	Sequence 140, App
45	180	31.6	155	14	US-10-017-161-1958	Sequence 1958, App

#### ALIGNMENTS

RESULT 1  
US-10-138-516-2  
; Sequence 2, Application US/10138516  
; Publication No. US20030003445A1  
; GENERAL INFORMATION:  
; APPLICANT: AVERBACK, PAUL  
; TITLE OF INVENTION: METHOD OF PREVENTING CELL DEATH USING ANTIBODIES TO  
; TITLE OF INVENTION: NEURAL THREAD PROTEINS  
; FILE REFERENCE: 59003.000004  
; CURRENT APPLICATION NUMBER: US/10/138.516  
; CURRENT FILING DATE: 2002-07-23  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 112  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-138-516-2

Query Match 100.0%; Score 570; DB 14; Length 112;  
Best Local Similarity 100.0%; Pred. No. 5e-57;  
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAQSLTATSASRVQAILLSQPKQLGLRAPANTPLIFVFSLEAGFHHICQAGLKLTSG 60  
Db 1 MAQSLTATSASRVQAILLSQPKQLGLRAPANTPLIFVFSLEAGFHHICQAGLKLTSG 60

Qy 61 DPPASAFQSAGITGVSHLTQPNLDKKICNSGGSCYVAQGLKLLASCNPSK 112  
Db 61 DPPASAFQSAGITGVSHLTQPNLDKKICNSGGSCYVAQGLKLLASCNPSK 112

RESULT 2  
US-10-146-130-4

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; Sequence 4, Application US/10146130
; Publication No. US20030004107A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; TITLE OF INVENTION: METHOD OF PREVENTING CELL DEATH USING SEGMENTS OF
; TITLE OF INVENTION: NEURAL THREAD PROTEINS
; FILE REFERENCE: 59003.000007
; CURRENT APPLICATION NUMBER: US/10/146.130
; CURRENT FILING DATE: 2002-08-06
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-146-130-4

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Best Local Similarity 100.0%; Pred. No. 5e-57;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 DPPASAFQSAGITGVSHLTQPANLDKKICNSGGSCYVAQAGLKLLASCNP 112
Db 61 DPPASAFQSAGITGVSHLTQPANLDKKICNSGGSCYVAQAGLKLLASCNP 112

RESULT 3
US-10-092-934-3
; Sequence 3, Application US/10092934
; Publication No. US20030054990A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; TITLE OF INVENTION: METHODS OF USING NEURAL THREAD PROTEINS TO TREAT TUMORS
; TITLE OF INVENTION: AND CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 018792-0199
; CURRENT APPLICATION NUMBER: US/10/092.934
; CURRENT FILING DATE: 2002-06-05
; PRIOR APPLICATION NUMBER: 60/273,957
; PRIOR FILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-092-934-3

Query Match      100.0%; Score 570; DB 14; Length 112;
Best Local Similarity 100.0%; Pred. No. 5e-57;
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QY 61 DPPASAFQSAGITGVSHLTQPANLDKKICNSGGSCYVAQAGLKLLASCNP 112
Db 61 DPPASAFQSAGITGVSHLTQPANLDKKICNSGGSCYVAQAGLKLLASCNP 112

RESULT 4
US-10-153-334-3
; Sequence 3, Application US/10153334
; Publication No. US20030096350A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF
```

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; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 59003-000006
; CURRENT APPLICATION NUMBER: US/10/153.334
; CURRENT FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: 60/293,156
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-153-334-3

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QY 61 DPPASAFQSAGITGVSHLTQPANLDKKICNSGGSCYVAQAGLKLLASCNP 112
Db 61 DPPASAFQSAGITGVSHLTQPANLDKKICNSGGSCYVAQAGLKLLASCNP 112

RESULT 5
US-10-198-069-3
; Sequence 3, Application US/10198069
; Publication No. US20030096756A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 59003.000009
; CURRENT APPLICATION NUMBER: US/10/198.069
; CURRENT FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/306,161
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/306,150
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/331,477
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-198-069-3

Query Match      100.0%; Score 570; DB 14; Length 112;
Best Local Similarity 100.0%; Pred. No. 5e-57;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MAQSRLTATSASRVQAILLSQPPKQLGLRAPANTPLIFVFSLEAGFHHICQAGLKLLTSG 60

QY 61 DPPASAFQSAGITGVSHLTQPANLDKKICNSGGSCYVAQAGLKLLASCNP 112
Db 61 DPPASAFQSAGITGVSHLTQPANLDKKICNSGGSCYVAQAGLKLLASCNP 112

RESULT 6
US-10-198-070-3
; Sequence 3, Application US/10198070
; Publication No. US20030109437A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; APPLICANT: GEMMELL, JACK
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; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 59003.000008
; CURRENT APPLICATION NUMBER: US/10/198,070
; CURRENT FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/306,161
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/306,150
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/331,477
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-198-070-3

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Qy      61 DPPASAFQSAGITGVSHLTQPANLDKKICNSGGSCYVAQAGLKLLASCNPSK 112
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RESULT 7
US-10-294-891-2
; Sequence 2, Application US/10294891
; Publication No. US20030166569A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; APPLICANT: GENMEL, JACK
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; FILE REFERENCE: 59003.000010
; CURRENT APPLICATION NUMBER: US/10/294,891
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: 60/331,447
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-294-891-2

Query Match      100.0%; Score 570; DB 14; Length 112;
Best Local Similarity 100.0%; Pred. No. 5e-57;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MAQSLRTATSASRVQAILLSQPPKQLGLRAPANTPLIFVFSLEAGFHHCQAGLKLLTSG 60
Db      1 MAQSLRTATSASRVQAILLSQPPKQLGLRAPANTPLIFVFSLEAGFHHCQAGLKLLTSG 60

Qy      61 DPPASAFQSAGITGVSHLTQPANLDKKICNSGGSCYVAQAGLKLLASCNPSK 112
Db      61 DPPASAFQSAGITGVSHLTQPANLDKKICNSGGSCYVAQAGLKLLASCNPSK 112

RESULT 8
US-10-920-313-2
; Sequence 2, Application US/10920313
; Publication No. US20050032704A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; APPLICANT: GENMEL, JACK
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; FILE REFERENCE: 59003.000010
; CURRENT APPLICATION NUMBER: US/10/920,313
; CURRENT FILING DATE: 2004-08-18
; PRIOR APPLICATION NUMBER: 60/331,447
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-920-313-2

Query Match      100.0%; Score 570; DB 17; Length 112;
Best Local Similarity 100.0%; Pred. No. 5e-57;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MAQSLRTATSASRVQAILLSQPPKQLGLRAPANTPLIFVFSLEAGFHHCQAGLKLLTSG 60
Db      1 MAQSLRTATSASRVQAILLSQPPKQLGLRAPANTPLIFVFSLEAGFHHCQAGLKLLTSG 60

Qy      61 DPPASAFQSAGITGVSHLTQPANLDKKICNSGGSCYVAQAGLKLLASCNPSK 112
Db      61 DPPASAFQSAGITGVSHLTQPANLDKKICNSGGSCYVAQAGLKLLASCNPSK 112

RESULT 9
US-10-017-161-1108
; Sequence 1108, Application US/10017161
; Publication No. US20030143668A1
; GENERAL INFORMATION:
; APPLICANT: SUWA, MAKIKO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ABURATANI, HIROYUKI
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 084335/0152
; CURRENT APPLICATION NUMBER: US/10/017,161
; CURRENT FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: JP 2001/246789
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 2430
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1108
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-017-161-1108

Query Match      49.6%; Score 282.5; DB 14; Length 170;
Best Local Similarity 70.2%; Pred. No. 6.1e-24;
Matches 59; Conservative 8; Mismatches 16; Indels 1; Gaps 1;

Qy      1 MAQSLRTATSASRVQAILLSQPPKQLGLRAPANTPLIFVFSLEAGFHHCQAGLKLLTSG 59
Db      79 MVQSLRTATSASRVQAILLSQPPKQLGLRAPANTPLIFVFSLEAGFHHCQAGLKLLTSG 138

Qy      60 GDPASAFQSAGITGVSHLTQPAN 83
Db      139 GDPASAFQSAGISGVSHCARPLN 162

RESULT 10
US-10-292-798-940
; Sequence 940, Application US/10292798
; Publication No. US20030235833A1
; GENERAL INFORMATION:
; APPLICANT: SUWA, MAKIKO
; APPLICANT: ASAI, KIYOSHI
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; APPLICANT: AVERBACK, PAUL
; APPLICANT: GENMEL, JACK
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF CELLS
; FILE REFERENCE: 59003.000010
; CURRENT APPLICATION NUMBER: US/10/920,313
; CURRENT FILING DATE: 2004-08-18
; PRIOR APPLICATION NUMBER: 60/331,447
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-920-313-2

Query Match      100.0%; Score 570; DB 17; Length 112;
Best Local Similarity 100.0%; Pred. No. 5e-57;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MAQSLRTATSASRVQAILLSQPPKQLGLRAPANTPLIFVFSLEAGFHHCQAGLKLLTSG 60
Db      1 MAQSLRTATSASRVQAILLSQPPKQLGLRAPANTPLIFVFSLEAGFHHCQAGLKLLTSG 60

Qy      61 DPPASAFQSAGITGVSHLTQPANLDKKICNSGGSCYVAQAGLKLLASCNPSK 112
Db      61 DPPASAFQSAGITGVSHLTQPANLDKKICNSGGSCYVAQAGLKLLASCNPSK 112

RESULT 9
US-10-017-161-1108
; Sequence 1108, Application US/10017161
; Publication No. US20030143668A1
; GENERAL INFORMATION:
; APPLICANT: SUWA, MAKIKO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ABURATANI, HIROYUKI
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 084335/0152
; CURRENT APPLICATION NUMBER: US/10/017,161
; CURRENT FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: JP 2001/246789
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 2430
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1108
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-017-161-1108

Query Match      49.6%; Score 282.5; DB 14; Length 170;
Best Local Similarity 70.2%; Pred. No. 6.1e-24;
Matches 59; Conservative 8; Mismatches 16; Indels 1; Gaps 1;

Qy      1 MAQSLRTATSASRVQAILLSQPPKQLGLRAPANTPLIFVFSLEAGFHHCQAGLKLLTSG 59
Db      79 MVQSLRTATSASRVQAILLSQPPKQLGLRAPANTPLIFVFSLEAGFHHCQAGLKLLTSG 138

Qy      60 GDPASAFQSAGITGVSHLTQPAN 83
Db      139 GDPASAFQSAGISGVSHCARPLN 162

RESULT 10
US-10-292-798-940
; Sequence 940, Application US/10292798
; Publication No. US20030235833A1
; GENERAL INFORMATION:
; APPLICANT: SUWA, MAKIKO
; APPLICANT: ASAI, KIYOSHI
```

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; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ABURATANI, HIROYUKI
; TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: 084335/166
; CURRENT APPLICATION NUMBER: US/10/292,798
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: 10/017,161
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: JP 2001-246789
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 2070
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 940
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-292-798-940
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Query Match 49.6%; Score 282.5; DB 15; Length 170;
Best Local Similarity 70.2%; Pred. No. 6.1e-24;
Matches 59; Conservative 8; Mismatches 16; Indels 1; Gaps 1;

QY 1 MAQSRLTATSASRVQAILLSQPPKQLGLRAPANTP-LIFVFSLEAGFHHICQAGLKLTSS 59
Db 79 MVQSRLTATSASRVQAILLPQPPEQLG-DMHHHTLWLFVFLVERGFHCVQAGLELLTS 138

QY 60 DPPASAFQSAGITGVSHLTQPN 83
Db 139 GDPPASASQSAGISGVSHCARPLN 162
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RESULT 11
US-10-017-161-1178
; Sequence 1178, Application US/10017161
; Publication No. US20030143668A1
; GENERAL INFORMATION:
; APPLICANT: SUWA, MAKIKO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ABURATANI, HIROYUKI
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 084335/0152
; CURRENT APPLICATION NUMBER: US/10/017,161
; CURRENT FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: JP 2001/246789
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 2430
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1178
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-017-161-1178
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Query Match 44.1%; Score 251.5; DB 14; Length 151;
Best Local Similarity 67.9%; Pred. No. 1.8e-20;
Matches 55; Conservative 9; Mismatches 16; Indels 1; Gaps 1;

QY 1 MAQSRLTATSASRVQAILLSQPPKQLGLRAPANTPLIFVFSLEAGFHHICQAGLKLTSG 60
Db 57 VAQSRLTATSASRVQAILLPQPPEQLG-DMHHHTLWLFVFLVERGFHCVQAGLELLTS 115

QY 61 DPPASAFQSAGITGVSHLTQPN 81
Db 116 DPPTSASQSAGITGVSHCARP 136
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RESULT 12
US-10-292-798-996
; Sequence 996, Application US/10292798
; Publication No. US20030235833A1
; GENERAL INFORMATION:
; APPLICANT: SUWA, MAKIKO
```

```
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ABURATANI, HIROYUKI
; TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: 084335/166
; CURRENT APPLICATION NUMBER: US/10/292,798
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: 10/017,161
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: JP 2001-246789
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 2070
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 996
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-292-798-996
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Query Match 44.1%; Score 251.5; DB 15; Length 151;
Best Local Similarity 67.9%; Pred. No. 1.8e-20;
Matches 55; Conservative 9; Mismatches 16; Indels 1; Gaps 1;

QY 1 MAQSRLTATSASRVQAILLSQPPKQLGLRAPANTPLIFVFSLEAGFHHICQAGLKLTSG 60
Db 57 VAQSRLTATSASRVQAILLPQPPEQLG-DMHHHTLWLFVFLVERGFHCVQAGLELLTS 115

QY 61 DPPASAFQSAGITGVSHLTQPN 81
Db 116 DPPTSASQSAGITGVSHCARP 136
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RESULT 13
US-10-017-161-1184
; Sequence 1184, Application US/10017161
; Publication No. US20030143668A1
; GENERAL INFORMATION:
; APPLICANT: SUWA, MAKIKO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ABURATANI, HIROYUKI
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 084335/0152
; CURRENT APPLICATION NUMBER: US/10/017,161
; CURRENT FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: JP 2001/246789
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 2430
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1184
; LENGTH: 160
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-017-161-1184
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Query Match 42.1%; Score 240; DB 14; Length 160;
Best Local Similarity 63.9%; Pred. No. 4.1e-19;
Matches 53; Conservative 8; Mismatches 20; Indels 2; Gaps 1;

QY 1 MAQSRLTATSASRVQAILLSQPPKQLGLRAPA--NTPLIFVFSLEAGFHHICQAGLKLT 58
Db 23 MVQSRLTATSASRVQAILLSQPPPELGLCTACRHAQLIFCILMETGTGFHCVQAGLELLS 82

QY 59 SGDPASAFQSAGITGVSHLTQPN 81
Db 83 SGSPPVASASRSARITGVSHHAMP 105
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RESULT 14
US-10-292-798-1000
; Sequence 1000, Application US/10292798
; Publication No. US20030235833A1
; GENERAL INFORMATION:
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; APPLICANT: SUWA, MAKIKO  
; APPLICANT: ASAI, KIYOSHI  
; APPLICANT: AKIYAMA, YUTAKA  
; APPLICANT: ABURATANI, HIROYUKI  
; TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS  
; FILE REFERENCE: 084335/166  
; CURRENT APPLICATION NUMBER: US/10/292,798  
; CURRENT FILING DATE: 2002-11-13  
; PRIOR APPLICATION NUMBER: 10/017,161  
; PRIOR FILING DATE: 2001-12-18  
; PRIOR APPLICATION NUMBER: JP 2001-246789  
; PRIOR FILING DATE: 2001-06-18  
; NUMBER OF SEQ ID NOS: 2070  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1000  
; LENGTH: 160  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-292-798-1000

Query Match 42.1%; Score 240; DB 15; Length 160;  
Best Local Similarity 63.9%; Pred. No. 4.1e-19;  
Matches 53; Conservative 8; Mismatches 20; Indels 2; Gaps 1;  
  
Qy 1 MAQSRLTATSASRYQAILLSPKQLGLRAPA--NTPLIFVFSLEAGFHHCQAGLKLLT 58  
Db 23 MVQSRLTATSTRVQAILLSPPEELGLCTGACRHAQLIFCILMETGFHCVAQAQGLELLS 82  
  
Qy 59 SGDPFASAFQSAGITGVSHLTQP 81  
Db 83 SGSPFVSASRSARITGVSHHAWP 105

RESULT 15  
US-10-108-260A-2599  
; Sequence 2599, Application US/10108260A  
; Publication No. US20040005560A1  
; GENERAL INFORMATION:  
; APPLICANT: HELIX RESEARCH INSTITUTE  
; TITLE OF INVENTION: NO. US20040005560A1e1 full length cDNA  
; FILE REFERENCE: H1-A0106  
; CURRENT APPLICATION NUMBER: US/10/108,260A  
; CURRENT FILING DATE: 2002-03-27  
; NUMBER OF SEQ ID NOS: 5458  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2599  
; LENGTH: 109  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-108-260A-2599

Query Match 40.4%; Score 230.5; DB 15; Length 109;  
Best Local Similarity 66.7%; Pred. No. 3.1e-18;  
Matches 54; Conservative 4; Mismatches 20; Indels 3; Gaps 1;  
  
Qy 1 MAQSRLTATSASRYQAILLSPKQLGLRAPANTPLIFVFSLEAGFHHCQAGLKLLTSG 60  
Db 1 MAQSWLTATSVSQVQVILL---PKSGITGMHHHTRLIFVFLVEMGFHHIGQAGLELLTSG 57  
  
Qy 61 DPPASAFQSAGITGVSHLTQP 81  
Db 58 DPPASQSAGIAGVKHHAQP 78

Search completed: October 11, 2005, 07:39:43  
Job time : 188.765 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 11, 2005, 06:57:19 ; Search time 25.6043 Seconds  
(without alignments)  
326.535 Million cell updates/sec

Title: US-10-092-934-3

Perfect score: 570

Sequence: 1 MAQSRLTATASRVQAILLS.....GSCVVAQAGLKLLASCNPSK 112

Scoring table: BLOSUM62

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Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.\*

- 1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep.\*
- 2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*
- 3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*
- 4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*
- 5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep.\*
- 6: /cgn2\_6/ptodata/1/iaa/backfiles.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	219	38.4	397	5	PCT-US95-17111A-121
2	215	37.7	92	4	US-09-621-976-5895
3	215	37.7	92	4	US-09-621-976-5901
4	215	37.7	92	4	US-09-621-976-5909
5	215	37.7	92	4	US-09-621-976-5914
6	182	31.9	74	4	US-09-513-999C-4478
7	176	30.9	74	4	US-09-513-999C-4488
8	174.5	30.6	99	4	US-09-288-143-168
9	167	29.3	144	4	US-09-513-999C-6953
10	165	28.9	90	3	US-09-227-357-171
11	164	28.8	90	4	US-09-513-999C-6012
12	163.5	28.7	108	4	US-09-513-999C-4433
13	161.5	28.3	239	4	US-09-800-729-193
14	161.5	28.3	310	4	US-09-800-729-190
15	161	28.2	112	4	US-09-513-999C-7870
16	160.5	28.2	95	4	US-09-621-976-5602
17	158	27.7	84	4	US-09-513-999C-4457
18	158	27.7	87	4	US-09-621-976-5672
19	157.5	27.6	85	4	US-09-513-999C-6550
20	156	27.4	88	4	US-09-621-976-5850
21	154	27.0	776	4	US-10-020-079-24
22	154	27.0	789	4	US-10-020-079-22
23	154	27.0	863	4	US-10-020-079-32
24	154	27.0	876	4	US-10-020-079-30
25	154	27.0	889	4	US-10-020-079-20
26	154	27.0	895	4	US-10-020-079-18
27	154	27.0	976	4	US-10-020-079-28

28	154	27.0	982	4	US-10-020-079-26	Sequence 26, Appl
29	152	26.7	72	4	US-09-513-999C-4419	Sequence 4119, Ap
30	150.5	26.4	118	4	US-09-663-600A-114	Sequence 114, App
31	149.5	26.2	169	4	US-09-663-600A-208	Sequence 208, App
32	149	26.1	85	4	US-09-621-976-6679	Sequence 6679, Ap
33	149	26.1	94	4	US-09-621-976-4078	Sequence 4078, Ap
34	149	26.1	94	4	US-09-621-976-4079	Sequence 4079, Ap
35	148	26.0	71	4	US-09-621-976-5550	Sequence 5550, Ap
36	146	25.6	53	4	US-09-621-976-6507	Sequence 6507, Ap
37	143.5	25.2	70	4	US-09-621-976-4189	Sequence 4189, Ap
38	141	24.7	396	4	US-09-949-016-6783	Sequence 6783, Ap
39	141	24.7	442	4	US-09-949-016-9762	Sequence 9762, Ap
40	140	24.6	53	4	US-09-513-999C-7092	Sequence 7092, Ap
41	138	24.2	52	4	US-09-513-999C-4441	Sequence 4441, Ap
42	137	24.0	52	4	US-09-513-999C-4444	Sequence 4444, Ap
43	137	24.0	96	4	US-09-513-999C-6065	Sequence 6065, Ap
44	136.5	23.9	638	4	US-09-949-016-11391	Sequence 11391, A
45	136	23.9	69	4	US-09-621-976-7243	Sequence 7243, Ap

ALIGNMENTS

RESULT 1  
PCT-US95-17111A-121  
; Sequence 121, Application PC/TUS9517111A  
; GENERAL INFORMATION:  
; APPLICANT: de la Monte, Suzanne  
; TITLE OF INVENTION: Neural Thread Protein Gene Expression and  
; TITLE OF INVENTION: Detection of Alzheimer's Disease  
; NUMBER OF SEQUENCES: 121  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.  
; STREET: 1100 New York Avenue, Suite 600  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/17111A  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/340,426  
; FILING DATE: 14-NOV-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ludwig, Steven R.  
; REGISTRATION NUMBER: 36,203  
; REFERENCE/DOCKET NUMBER: 0609.3840002  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 371-2600  
; TELEFAX: (202) 371-2540  
; INFORMATION FOR SEQ ID NO: 121:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 397 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
PCT-US95-17111A-121

Query Match 38.4%; Score 219; DB 5; Length 397;  
Best Local Similarity 95.5%; Pred. No. 1.9e-18;  
Matches 42; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
Qy 33 NTPLIFVFSLEAGPHHICQAGLKLLTSGDPPASAFQSGAGITGV 76  
Db 349 HTPLIFVFSLEAGPHHICQAGLKLLTSGDPPASAFQSGAGITGV 392

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RESULT 2
US-09-621-976-5895
; Sequence 5895, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 5895
; LENGTH: 92
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -46..-1
US-09-621-976-5895

Query Match 37.7%; Score 215; DB 4; Length 92;
Best Local Similarity 61.8%; Pred. No. 8.5e-19;
Matches 47; Conservative 4; Mismatches 25; Indels 0; Gaps 0;

Qy 8 ATASRVQAILLSQPPKQLGLRAPANTPLIFVFSLEAGFHHCQAGLKLTSGDPPASAF 67
Db 2 ATFTSQVQVILLPQPLSSWDYRHAPTCPANFVFLVETGFLHVQAGLKLTSGDPPAS 61

Qy 68 QSAGITGVSHLTOPAN 83
Db 62 QSAGITGVSHRAOPTS 77

RESULT 3
US-09-621-976-5901
; Sequence 5901, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 5901
; LENGTH: 92
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -46..-1
US-09-621-976-5901

Query Match 37.7%; Score 215; DB 4; Length 92;
Best Local Similarity 61.8%; Pred. No. 8.5e-19;
Matches 47; Conservative 4; Mismatches 25; Indels 0; Gaps 0;

Qy 8 ATASRVQAILLSQPPKQLGLRAPANTPLIFVFSLEAGFHHCQAGLKLTSGDPPASAF 67
Db 2 ATFTSQVQVILLPQPLSSWDYRHAPTCPANFVFLVETGFLHVQAGLKLTSGDPPAS 61

Qy 68 QSAGITGVSHLTOPAN 83
Db 62 QSAGITGVSHRAOPTS 77

RESULT 4
US-09-621-976-5909
; Sequence 5909, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 5909
; LENGTH: 92
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -46..-1
US-09-621-976-5909

Query Match 37.7%; Score 215; DB 4; Length 92;
Best Local Similarity 61.8%; Pred. No. 8.5e-19;
Matches 47; Conservative 4; Mismatches 25; Indels 0; Gaps 0;

Qy 8 ATASRVQAILLSQPPKQLGLRAPANTPLIFVFSLEAGFHHCQAGLKLTSGDPPASAF 67
Db 2 ATFTSQVQVILLPQPLSSWDYRHAPTCPANFVFLVETGFLHVQAGLKLTSGDPPAS 61

Qy 68 QSAGITGVSHLTOPAN 83
Db 62 QSAGITGVSHRAOPTS 77

RESULT 5
US-09-621-976-5914
; Sequence 5914, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 5914
; LENGTH: 92
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -46..-1
US-09-621-976-5914

Query Match 37.7%; Score 215; DB 4; Length 92;
Best Local Similarity 61.8%; Pred. No. 8.5e-19;
Matches 47; Conservative 4; Mismatches 25; Indels 0; Gaps 0;

Qy 8 ATASRVQAILLSQPPKQLGLRAPANTPLIFVFSLEAGFHHCQAGLKLTSGDPPASAF 67
Db 2 ATFTSQVQVILLPQPLSSWDYRHAPTCPANFVFLVETGFLHVQAGLKLTSGDPPAS 61

Qy 68 QSAGITGVSHLTOPAN 83
Db 62 QSAGITGVSHRAOPTS 77
```

	Matches	34;	Conservative	4;	Mismatches	4;	Indels	0;	Gaps	0;
QY	36	LIFVFSLEAGFHHIC	AGLKL	TSG	PPSA	FA	SAGITGV	SH	77	
			:		:					
Db	9	LIFVFLVETGFHNVG	AGLELL	TSG	PPSA	FA	SAGITGL	SH	50	
			:		:					

```

RESULT 8
US-09-288-143-168
; Sequence 168, Application US/09288143
; Patent NO. 6433139
; GENERAL INFORMATION:
; APPLICANT: Brewer et al.
; TITLE OF INVENTION: 53 Human Secreted Proteins
; FILE REFERENCE: P2018P1
; CURRENT APPLICATION NUMBER: US/09/288,143
; CURRENT FILING DATE: 1999-04-08
; EARLIER APPLICATION NUMBER: PCT/US98/21142
; EARLIER FILING DATE: 1998-10-08
; EARLIER APPLICATION NUMBER: 60/061,463
; EARLIER FILING DATE: 1997-10-09
; EARLIER APPLICATION NUMBER: 60/061,529
; EARLIER FILING DATE: 1997-10-09
; EARLIER APPLICATION NUMBER: 60/071,498
; EARLIER FILING DATE: 1997-10-09
; EARLIER APPLICATION NUMBER: 60/061,527
; EARLIER FILING DATE: 1997-10-09
; EARLIER APPLICATION NUMBER: 60/061,536
; EARLIER FILING DATE: 1997-10-09
; EARLIER APPLICATION NUMBER: 60/061,532
; EARLIER FILING DATE: 1997-10-09
; NUMBER OF SEQ ID NOS: 219
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 168
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-288-143-168

```

```

Query Match      30.6%; Score 174.5; DB 4; Length 99;
Best Local Similarity 52.4%; Pred. No. 8.8e-14;
Matches 43; Conservative 11; Mismatches 27; Indels 1; Gaps 1
Qy 1 MAQRLTATSASRVQAILLSQPPKQLGIRAPAN-TPLIFVPSLQAGFHHCQAGKLLTS 59
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 9 VVRSWLTATLASWYQAILMDSASQVAGITSVHHQALSFVFLVEMGLCHVQAGKLLAS 68
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 60 GDPPASAFQAGITGVSHLTQP 81
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 69 SDLPASASQAGITGMSHHSWP 90
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

```

RESULT 9
US-09-513-999C-6953
; Sequence 6953, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513.999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 6953
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Homo sapiens

```

```

Qy      68  QSAGITGVSHLTQPAN  83
        |||||||||
Db      62  QSAGITGVSHRAQPTS  77

RESULT 6
US-09-513-999C-4478
; Sequence 4478, Application US/09513999C
; Patent NO. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins
; Patent NO. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 4478
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -37..-1
; OTHER INFORMATION: score 4.4
; OTHER INFORMATION: seq LELLTSGDPPASA/SQ
US-09-513-999C-4478

```

	Query Match	31.9%;	Score 182;	DB 4;	Length 74;
	Best Local Similarity	75.5%;	Pred. No. 7.2e-15;		
	Matches	37;	Conservative	3;	Mismatches 9; Indels 0; Gaps
Qy	33	NTPLIFVFSLEAGPHHICQAGLKLTGSDPPASAFQSGAGITGVSHLTQP	81		
Db	4	HTRLIFVFLVEMGPHHICQASLELTGSDPPASASQSGAGITGVKHAQP	52		

```

RESULT 7
US-09-513-999C-4488
; Sequence 4488, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A. Y.
; APPLICANT: Giordano, J. Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins
; Patent No. 6783961
; FILE REFERENCE: 59 US2 REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 4488
; LENGTH: 53
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -39...-1
; OTHER INFORMATION: score 4.4
; OTHER INFORMATION: seq LELLTSGDPPASA/SQ
US-09-513-999C-4488

Query Match          30.9%; Score 176; DB 4; Length 53;
Best Local Similarity 81.0%; Pred. No. 2.5e-14;

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```
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-513-999C-6012

Query Match      28.8%; Score 164; DB 4; Length 90;
Best Local Similarity 64.6%; Pred. No. 1.5e-12;
Matches 31; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

Qy 33 NTPLIIFVFSLEAGFHHCQAGLKLLTSGDPPASAFQSGAGITGVSHLTQ 80
   :|||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 42 HTQLIFIFLVKTFPHVQGSHELLTSGDPPASASQASGAGITGMNHCQ 89

RESULT 12
US-09-513-999C-4433
; Sequence 4433, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.Y.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59 US2 REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 4433
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -20...-1
; OTHER INFORMATION: score 8.4
; OTHER INFORMATION: seq FSLTVLFLRQSF/HV
US-09-513-999C-4433

Query Match      28.7%; Score 163.5; DB 4; Length 108;
Best Local Similarity 50.7%; Pred. No. 2.2e-12;
Matches 37; Conservative 7; Mismatches 16; Indels 13; Gaps 2;

Qy 21 QPP-----KQLGLRAPA-----NTPLIFVFSLEAGFHHCQAGLKLLTSGDPPASAF 67
   |||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 36 QPPPRFKLLSCLSPQVGGITGTCHHAQLIFVFLIENGFFHVHGQAGLELLTSGDPPTSAS 65

Qy 68 QSAGITGVSHLTQ 80
   |||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 96 QPAGIIGWNHHAQ 108

RESULT 13
US-09-800-729-193
; Sequence 193, Application US/09800729
; Patent No. 6605592
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: 32 Human secreted proteins
; FILE REFERENCE: P2044P1
; CURRENT APPLICATION NUMBER: US/09/800,729
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: PCT/US00/26013
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 60/155,709
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 193
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens

Query Match      28.3%; Score 161.5; DB 4; Length 310;
Best Local Similarity 54.7%; Pred. No. 1.6e-11;
Matches 35; Conservative 8; Mismatches 10; Indels 11; Gaps 1;

Qy 37 IFVFSLEAGFHHCQAGLKLLTSGDPPASAFQSGAGITGVSHLTOPANLDKKICNSGSCY 96
   |||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 241 IFVFLVETGFGVQAGLELLISGDSPPASAFQSGAGITGVSHRARP-----GSVF 289

Qy 97 VAQA 100
   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 290 LARS 293

RESULT 14
US-09-800-729-190
; Sequence 190, Application US/09800729
; Patent No. 6605592
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: 32 Human secreted proteins
; FILE REFERENCE: P2044P1
; CURRENT APPLICATION NUMBER: US/09/800,729
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: PCT/US00/26013
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 60/155,709
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 190
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-800-729-190

Query Match      28.3%; Score 161.5; DB 4; Length 310;
Best Local Similarity 54.7%; Pred. No. 1.6e-11;
Matches 35; Conservative 8; Mismatches 10; Indels 11; Gaps 1;

Qy 37 IFVFSLEAGFHHCQAGLKLLTSGDPPASAFQSGAGITGVSHLTOPANLDKKICNSGSCY 96
   |||||:|:|:~|:|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|
Db 241 IFVFLVETGFGVQAGLELLISGDSPPASAFQSGAGITGVSHRARP-----GSVF 289

Qy 97 VAQA 100
   :|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|:~|
Db 290 LARS 293

RESULT 15
US-09-513-999C-7870
; Sequence 7870, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59 US2 REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 7870
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
```

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; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -49...-1
; OTHER INFORMATION: score 7.7
; OTHER INFORMATION: seq LCLLGSSDSPASA/SQ
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 55
; OTHER INFORMATION: Xaa=Ser or Thr
US-09-513-999C-7870

Query Match      28.2%; Score 161; DB 4; Length 112;
Best Local Similarity 69.2%; Pred. No. 4.7e-12;
Matches 36; Conservative 3; Mismatches 11; Indels 2; Gaps 1;

Qy      33  NTPLIIVFVSLFAGFHHICQAGLKLTSGDPPASAFOSAGITGYSHLTQPNL 84
Db      61  HTQLIFVFLIETGFLHIGQAALLETSGDPPASASQSAGITGVX--TTPGRL 110

```

Search completed: October 11, 2005, 07:42:47  
Job time : 26.6043 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 11, 2005, 06:57:07 ; Search time 16.4385 Seconds  
(without alignments)  
620.432 Million cell updates/sec

Title: US-10-092-934-4  
Perfect score: 573  
Sequence: 1 MWTLKSLVLLCLTCSYAF.....APFLHHIDSIGVSGKRMF 106

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: Pir1.\*

2: Pir2.\*

3: Pir3.\*

4: Pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	DB ID	Description
1	81	14.1	435	2 S00833	finger protein (cl
2	79.5	13.9	196	2 S06581	finger protein (cl
3	77.5	13.5	636	2 I48689	gene NK10 protein
4	73.5	12.8	224	2 C31201	GLI-related finger
5	73.5	12.8	485	2 S75655	anthranilate synth
6	71.5	12.5	569	2 T21225	hypothetical prote
7	70.5	12.3	200	2 S47067	finger protein HZF
8	70.5	12.3	2185	1 GNNYSV	genome polypotein
9	70.5	12.3	2185	1 GNNYSV	genome polypotein
10	69.5	12.1	651	2 B32891	finger protein 2,
11	69.5	12.1	674	2 T21217	hypothetical prote
12	69	12.0	296	2 A45447	zinc finger (alter
13	69	12.0	332	2 S31848	heat shock protein
14	68.5	12.0	223	2 S06576	finger protein (cl
15	68.5	12.0	351	2 T19223	hypothetical prote
16	68.5	12.0	548	2 S42077	zinc finger protei
17	68	11.9	282	2 T19393	hypothetical prote
18	68	11.9	464	2 S75362	hypothetical prote
19	68	11.9	1043	2 A56037	DNA-binding protei
20	68	11.9	1114	2 I50222	deltaE1 - chicken
21	68	11.9	1117	2 JC4934	delta-crystallin/E
22	68	11.9	1124	2 J02093	zinc finger protei
23	68	11.9	1154	2 A36242	E-box-binding repr
24	67.5	11.8	185	2 T36480	probable transmem
25	67.5	11.8	252	2 S06567	finger protein (cl
26	67.5	11.8	349	2 T40990	hypothetical wtf p
27	67.5	11.8	614	2 JH0500	zinc finger protei
28	67	11.7	336	2 S06578	finger protein (cl
29	67	11.7	485	2 A40751	finger protein MZF

30	67	11.7	496	2 T08674	probable finger pr
31	66.5	11.6	951	2 G82965	conserved hypothet
32	66.5	11.6	1374	1 GNNYEC	genome polypotein
33	66.5	11.6	2182	1 GNNYB1	genome polypotein
34	66	11.5	149	2 A29942	developmental cont
35	66	11.5	688	2 A56360	zinc finger protei
36	65.5	11.4	457	2 A54604	regulatory protei
37	65.5	11.4	835	2 C86444	hypothetical prote
38	65.5	11.4	962	2 C43274	N-methyl D-asparta
39	65.5	11.4	1250	1 B45219	N-methyl D-asparta
40	65.5	11.4	2193	2 S52919	polypotein (1A, 1
41	64.5	11.3	560	2 T14616	hypothetical prote
42	64.5	11.3	613	2 JC7992	negatively regulat
43	64.5	11.3	2185	1 J02021	genome polypotein
44	64	11.2	134	1 F64361	hypothetical prote
45	64	11.2	318	2 H89632	protein F13B6.5 [1

ALIGNMENTS

RESULT 1

S00833  
finger protein (clone XlCOF22) - African clawed frog  
C:Species: Xenopus laevis (African clawed frog)  
C>Date: 31-Dec-1988 #sequence\_revision 31-Dec-1988 #text\_change 09-Jul-2004  
C:Accession: S00833  
R:Koester, M.; Pieler, T.; Poeting, A.; Knoechel, W.  
EMBO J. 7, 1735-1741, 1988  
A:Title: The finger motif defines a multigene family represented in the maternal mRNA of  
A:Reference number: S00832; MUID:89005062; PMID:3139407  
A:Accession: S00833  
A>Status: not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-435 <KOE>  
A:Cross-references: UNIPROT:P18745  
C:Keywords: DNA binding; embryo; oocyte; zinc finger  
F:99-430/Region: zinc fingers

Query Match 14.1%; Score 81; DB 2; Length 435;  
Best Local Similarity 26.1%; Pred. No. 0.26;  
Matches 24; Conservative 12; Mismatches 32; Indels 24; Gaps 4;

Oy	13	CLTCSYAFMFSSL---RQKT---SEPOGKVPDGHFRIRQNLPEHTQGLGSKWLWLLFA	66
Db	184	CLECGKCFLFRSRLLEHQRTHTGKCFSCLCGKCFSVRSRLKDKHQTHTGKEK-----	236
Oy	67	VVPFVILKCOR-----DSEKNKVRMAPF	89
Db	237	--PFSLECGKFSFRPCLIDHQRTHTGKRPF	266

RESULT 2

S06581  
finger protein (clone XlCGF64-1) - African clawed frog (fragment)  
C:Species: Xenopus laevis (African clawed frog)  
C>Date: 28-Feb-1990 #sequence\_revision 28-Feb-1990 #text\_change 09-Jul-2004  
C:Accession: S06581  
R:Nietfeld, W.; El-Baradi, T.; Mentzel, H.; Pieler, T.; Koester, M.; Poeting, A.; Knoechel, A.;  
J. Mol. Biol. 208, 639-659, 1989  
A:Title: Second-order repeats in Xenopus laevis finger proteins.  
A:Reference number: S05632; MUID:90040698; PMID:2509712  
A:Accession: S06581  
A>Status: not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-196 <NIE>  
A:Cross-references: UNIPROT:P18732  
C:Keywords: DNA binding; zinc finger

Query Match 13.9%; Score 79.5; DB 2; Length 196;  
Best Local Similarity 24.0%; Pred. No. 0.17;  
Matches 25; Conservative 14; Mismatches 40; Indels 25; Gaps 4;

```
QY 5 KSSLVL-----LLCLTCSYAFMFSSLRQK-----TSE-PQGVKPCGEHFRIRQNL 48
Db 74 KSQLIQRHGHTGKPTCTECGSGFRHKQVLMRHFQIHTGCKEYECTQCGEGFLLSKL 133
QY 49 PEHTQGLGSKWLWLLFAVVPFVILKCORDSEKKNKVRMAPFFLH 92
Db 134 IHORGHGTGK-----PFMTECGKGRQKQVLIHQFIH 168

RESULT 3
I48689
gene NK10 protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I48689; S49078
R;Lange, R.; Christoph, A.; Thiesen, H.J.; Vopper, G.; Johnson, K.R.; Lemaire, L.; Plomaz
DNA Cell Biol. 14, 971-981, 1995
A;Title: Developmentally regulated mouse gene NK10 encodes a x2Inc Finger Repressor Pro
A;Reference number: I48689; MUID:9609544; PMID:7576184
A;Accession: I48689
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-636 <RES>
A;Cross-references: UNIPROT:Q61967; EMBL:X79828; NID:G506501; PIDN:CAA56225.1; PID:G5065
C;Superfamily: zinc finger protein ZFP-36; LIM metal-binding repeat homology

Query Match 13.5%; Score 77.5; DB 2; Length 636;
Best Local Similarity 29.9%; Pred. No. 0.95;
Matches 26; Conservative 8; Mismatches 34; Indels 19; Gaps 4;

QY 13 CLTCSYAF-MFSSLRQKTS-PQGVK-----CGEHFRIRQNLPEHTQGLGSKWLWLLFA 66
Db 552 CIDCGKAFSSSLIQHRTHTGKPYECNECGRAFRKTNLDHQRTHTGK----- 604

QY 67 VVPFVILKCORDSEKKNKVRMAPFFLH 93
Db 605 --PYACEGCR---NFSRSSALTKHH 625

RESULT 4
C31201
GLI-related finger protein HKR1 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004
C;Accession: C31201
R;Ruppert, J.M.; Kinzler, K.W.; Wong, A.J.; Bigner, S.H.; Kao, F.T.; Law, M.L.; Seunaez,
Mol. Cell. Biol. 8, 3104-3113, 1988
A;Title: The GLI-Kruppel family of human genes.
A;Reference number: A93103; MUID:89096896; PMID:2850480
A;Accession: C31201
A;Molecule type: DNA
A;Residues: 1-224 <RUP>
A;Cross-references: UNIPROT:P10072
C;Keywords: DNA binding; zinc finger

Query Match 12.8%; Score 73.5; DB 2; Length 224;
Best Local Similarity 30.0%; Pred. No. 0.94;
Matches 21; Conservative 6; Mismatches 28; Indels 15; Gaps 3;

QY 12 LCLTCSYAF-----MFSSLRQKTS-PQGVKPCGEHFRIRQNLPEHTQGLGSKWLWLLF 65
Db 139 ICRECEQGSQKGLIRHLRHTHTGKPYVTECGRHFWSKSNLKTQRTSHSGVK----- 192

QY 66 AVVPFVILKC 75
Db 193 ---PYVCLEC 199

RESULT 5
S75655
anthranilate synthase (EC 4.1.3.27) component I - Synecchocystis sp. (strain PCC 6803)
N;Alternate names: protein slr1979
C;Species: Synecchocystis sp.

QY 5 KSSLVL-----LLCLTCSYAFMFSSLRQK-----TSE-PQGVKPCGEHFRIRQNL 48
Db 74 KSQLIQRHGHTGKPTCTECGSGFRHKQVLMRHFQIHTGCKEYECTQCGEGFLLSKL 133
QY 49 PEHTQGLGSKWLWLLFAVVPFVILKCORDSEKKNKVRMAPFFLH 92
Db 134 IHORGHGTGK-----PFMTECGKGRQKQVLIHQFIH 168

RESULT 3
I48689
gene NK10 protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I48689; S49078
R;Lange, R.; Christoph, A.; Thiesen, H.J.; Vopper, G.; Johnson, K.R.; Lemaire, L.; Plomaz
DNA Cell Biol. 14, 971-981, 1995
A;Title: Developmentally regulated mouse gene NK10 encodes a x2Inc Finger Repressor Pro
A;Reference number: I48689; MUID:9609544; PMID:7576184
A;Accession: I48689
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-636 <RES>
A;Cross-references: UNIPROT:Q61967; EMBL:X79828; NID:G506501; PIDN:CAA56225.1; PID:G5065
C;Superfamily: zinc finger protein ZFP-36; LIM metal-binding repeat homology

Query Match 13.5%; Score 77.5; DB 2; Length 636;
Best Local Similarity 29.9%; Pred. No. 0.95;
Matches 26; Conservative 8; Mismatches 34; Indels 19; Gaps 4;

QY 13 CLTCSYAF-MFSSLRQKTS-PQGVK-----CGEHFRIRQNLPEHTQGLGSKWLWLLFA 66
Db 552 CIDCGKAFSSSLIQHRTHTGKPYECNECGRAFRKTNLDHQRTHTGK----- 604

QY 67 VVPFVILKCORDSEKKNKVRMAPFFLH 93
Db 605 --PYACEGCR---NFSRSSALTKHH 625

RESULT 4
C31201
GLI-related finger protein HKR1 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004
C;Accession: C31201
R;Ruppert, J.M.; Kinzler, K.W.; Wong, A.J.; Bigner, S.H.; Kao, F.T.; Law, M.L.; Seunaez,
Mol. Cell. Biol. 8, 3104-3113, 1988
A;Title: The GLI-Kruppel family of human genes.
A;Reference number: A93103; MUID:89096896; PMID:2850480
A;Accession: C31201
A;Molecule type: DNA
A;Residues: 1-224 <RUP>
A;Cross-references: UNIPROT:P10072
C;Keywords: DNA binding; zinc finger

Query Match 12.8%; Score 73.5; DB 2; Length 224;
Best Local Similarity 30.0%; Pred. No. 0.94;
Matches 21; Conservative 6; Mismatches 28; Indels 15; Gaps 3;

QY 12 LCLTCSYAF-----MFSSLRQKTS-PQGVKPCGEHFRIRQNLPEHTQGLGSKWLWLLF 65
Db 139 ICRECEQGSQKGLIRHLRHTHTGKPYVTECGRHFWSKSNLKTQRTSHSGVK----- 192

QY 66 AVVPFVILKC 75
Db 193 ---PYVCLEC 199

RESULT 5
S75655
anthranilate synthase (EC 4.1.3.27) component I - Synecchocystis sp. (strain PCC 6803)
N;Alternate names: protein slr1979
C;Species: Synecchocystis sp.
```

```
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: S75655
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
O, K.; Okumura, S.; Shampo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synecchocystis
s.
A;Reference number: S74322; MUID:97061201; PMID:8905231
A;Accession: S75655
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-485 <KAN>
A;Cross-references: UNIPROT:P74130; EMBL:D90912; GB:AB001339; NID:G1653228; PIDN:BAAL8211
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C;Genetics:
A;Gene: trpE
A;Start codon: GTG
C;Superfamily: anthranilate synthase component I
C;Keywords: carbon-carbon lyase; oxo-acid-lyase

Query Match 12.8%; Score 73.5; DB 2; Length 485;
Best Local Similarity 26.1%; Pred. No. 2;
Matches 36; Conservative 9; Mismatches 36; Indels 57; Gaps 8;

QY 1 MWTLKSSLVLLCLTCSYAFMFSSLRQKTS-PQGVKPCGEHFRIRQNLPEHTQ-----G 54
Db 95 LWTPKPEEI-----FSFLNQ-----LCPCNHDVNLTKNIPHLPHGCGWL 135

QY 55 WLGSKWLW-----LFPVV-----PFVILKQCR-----DSEKNKVRMAP 88
Db 136 WLGYDTAWAIEKLUPYSKADLDLPPVAYVYEPENFVILDHQQLWLATTQDEKIK----- 190

QY 89 FELHHI-DSISGVSGKRM 105
Db 191 FFOTQLADKINSVSPQV 208

RESULT 6
T21225
hypothetical protein F21H7.7 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T21225
R;Gardner, A.
submitted to the EMBL Data Library, March 1997
A;Reference number: Z19393
A;Accession: T21225
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-569 <WIL>
A;Cross-references: UNIPROT:O9XTV8; EMBL:Z93379; PIDN:CAB07593.1; GSPDB:GN00023; CESP:F21
C;Genetics:
A;Experimental source: clone F21H7
A;Gene: CESP:F21H7.7
A;Map position: 5
A;Introns: 122/1, 344/2; 455/1; 539/1

Query Match 12.5%; Score 71.5; DB 2; Length 569;
Best Local Similarity 28.6%; Pred. No. 4;
Matches 18; Conservative 14; Mismatches 12; Indels 19; Gaps 4;

QY 12 LCLTCSYAFMFSSLRQKTS-PQGVKPCGEHFRIRQNLPEHTQGLGSKWLWLLFAVVPF 70
Db 121 ICAIGSYTYLFES--RSSLPQNR-----FRISRRKI-----KFLYFFVFLPF 162

QY 71 VIL 73
Db 163 ILI 165

RESULT 7
S47067
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Search completed: October 11, 2005, 07:01:35  
Job time : 17.4385 secs

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OM protein - protein search, using sw model

Run on: October 11, 2005, 06:57:07 ; Search time 63.6283 seconds  
(without alignments)  
853.085 Million cell updates/sec

Title: US-10-092-934-4  
Perfect score: 573  
Sequence: 1 MWTLKSLVLLCLTCSYAF.....APFLHHDISGVSGKRMF 106

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_03.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Match	Query Length	ID	Description
1	426	74.3	94	2 Q9HCV7	Q9hc77 homo sapien
2	283	49.4	138	2 Q9HCV6	Q9hc66 homo sapien
3	258.5	45.1	170	2 Q9D9T2	Q9d9t2 mus musculus
4	84.5	14.7	653	2 Q64RH7	Q64rh7 bacteroides
5	81	14.1	380	2 Q8R3C2	Q8r3c2 mus musculus
6	81	14.1	435	1 Z022.XENLA	P18745 xenopus lae
7	81	14.1	463	2 Q8ZPG0	Q8zpg0 mus musculus
8	81	14.1	530	2 Q6P9Y7	Q6p9y7 mus musculus
9	80	14.0	276	2 Q9NPP0	Q9np00 homo sapien
10	80	14.0	545	2 Q86XJ3	Q86xj3 homo sapien
11	79.5	13.9	196	1 ZG64.XENLA	P18732 xenopus lae
12	77.5	13.5	636	1 ZF90.MOUSE	Q61967 mus musculus
13	77	13.4	140	2 Q8C194	Q8c194 mus musculus
14	77	13.4	330	2 Q95L04	Q95l04 macaca fasc
15	77	13.4	487	2 Q8TF53	Q8tf53 homo sapien
16	77	13.4	532	2 Q8N141	Q8n141 homo sapien
17	77	13.4	532	2 Q8NC63	Q8nc63 homo sapien
18	76	13.3	300	2 Q9CRL6	Q9crl6 mus musculus
19	76	13.3	813	2 Q6P1M5	Q6piw5 mus musculus
20	76	13.3	832	2 Q8BUQ3	Q8buq3 mus musculus
21	74.5	13.0	310	2 Q6DJZ0	Q6djz0 homo sapien
22	74.5	13.0	366	2 Q6ZML3	Q6zml3 homo sapien
23	74.5	13.0	382	2 Q6DD87	Q6dd87 homo sapien
24	74.5	13.0	385	2 Q00455	Q00455 homo sapien
25	74.5	13.0	478	2 Q6R2H7	Q6r2h7 human echov
26	74.5	13.0	537	2 Q6NSZ9	Q6nsz9 homo sapien
27	74.5	13.0	683	1 Z263.HUMAN	O14978 homo sapien
28	74	12.9	305	2 Q7SEU8	O7seu8 neurospora
29	74	12.9	317	2 Q8TAQ7	Q8taq7 homo sapien
30	73.5	12.8	485	1 TRE2.SYNY3	P74130 synechocyst
31	73.5	12.8	598	2 Q7Z6E1	Q7z6e1 homo sapien

## ALIGNMENTS

## RESULT 1

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Q9HCV7 ID Q9HCV7 PRELIMINARY; PRT; 94 AA.
AC Q9HCV7;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE DJ1153D9.3 (Novel protein).
GN Name=dj1153D9.3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Clark G.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL109806; CAC03742.1;
SQ SEQUENCE 94 AA; 11060 MW; E0AB7D817888A06C CRC64;
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Query Match 74.3%; Score 426; DB 2; Length 94;  
Best Local Similarity 95.2%; Pred. No. 1.9e-39;  
Matches 79; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

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Qy 1 MWTLKSLVLLCLTCSYAFMFSSLRKTSPOQKVPCEGHEFRIRQLPEHTQGLGSKW 60
Db 1 MWTLKSLVLLCLTCSYAFMFSSLRKTSPOQKVPCEGHEFRIRQLPEHTQGLGSKW 60
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Qy 61 LWLLFAVVVPFVILKCORDSEKNK 83
Db 61 LWLLFAVVVPFVILKCORDSEKNK 83
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## RESULT 2

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Q9HCV6 ID Q9HCV6 PRELIMINARY; PRT; 138 AA.
AC Q9HCV6;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE DJ1153D9.4 (Novel protein) (Fragment).
GN Name=dj1153D9.4;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Clark G.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL109806; CAC03743.1;
DR Genew; HGNC:16101; C20orf107.
FT NON TER
SQ SEQUENCE 138 AA; 15703 MW; E2D80F4A92B464BF CRC64;
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Query Match          49.4%; Score 283; DB 2; Length 138;
Best Local Similarity 90.9%; Pred. No. 2.2e-23;
Matches 50; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 34 GKVP CGHFRIRQNLPHPTQGLGSKWLWLLFAVVPVILKQCRDSEKNKVRMAP 88
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 GKVP CGHFRIRQNLPHPTQGLGSKWLWLLFAVVPVILKQCRDSEKNKREQSP 55
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 3
Q9D9T2 ID Q9D9T2 PRELIMINARY; PRT; 170 AA.
AC Q9D9T2;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Mus musculus adult male testis cDNA, RIKEN full-length enriched
DE library, clone:1700029J11Rik; product:hypothetical protein, full insert
DE sequence.
GN Name:1700029J11Rik;
OS Mus musculus (Mouse);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=92279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44 (1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690 (2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=20493774; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630 (2000).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kita A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771 (2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;

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RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Atakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Inotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK006503; BAB24622.1; -
DR MGD; MGI:1923676; 1700029J11Rik.
KW Hypothetical protein.
SQ SEQUENCE 170 AA; 19603 MW; 11DC56D4C0CFB5B5 CRC64;

Query Match          45.1%; Score 258.5; DB 2; Length 170;
Best Local Similarity 60.0%; Pred. No. 1.4e-20;
Matches 51; Conservative 11; Mismatches 22; Indels 1; Gaps 1;

QY 4 LKSSLVLLCLTCSYAFMFSSLRQKTSPEQKVPCEGHEFRIRQNLPHPTQGLGSKWLWL 63
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 5 LKWLFLSLGKLCACAFMFSSMRKTSKSGKVPCEGHEFRIRQNLPHPTQGLGSKWLWL 64
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 64 LFAVVPVILKQCRDSEKNKVRMAP 88
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 65 FVAIMYVWLKFRGDGE-NKEQHP 88
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 4
Q64RH7 ID Q64RH7 PRELIMINARY; PRT; 653 AA.
AC Q64RH7;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE Hypothetical protein.
GN CRFNames=BF3159;
OS Bacteroides fragilis.
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC Bacteroidaceae; Bacteroides.
OX NCBI_TaxID=817;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=YCH46;
RA Kuwahara T., Yamaehita A., Hirakawa H., Nakayama H., Toh H., Okada N.,
RA Kuhara S., Hattori M., Hayashi T., Ohnishi Y.;
RT "Genomic analysis of Bacteroides fragilis reveals extensive DNA
RT inversions regulating cell surface adaptation.";
RL Proc. Natl. Acad. Sci. U.S.A. 0:0-0 (2004).
DR EMBL; AP006841; BAD49904.1; -
KW Hypothetical protein.
SQ SEQUENCE 653 AA; 75745 MW; 1AB0B41CFB07838E CRC64;

Query Match          14.7%; Score 84.5; DB 2; Length 653;
Best Local Similarity 27.1%; Pred. No. 1.2;
Matches 39; Conservative 15; Mismatches 35; Indels 55; Gaps 9;

QY 1 MWTLKSSLVLLCLTCSYAFMFSSLRQKTSPEQKVPCEGHEFRIRQNLPHPTQGLGSK-- 43
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 17 LWLVL---LVGSLCCSTGKNRLEYALEFA-----GENRGELEKLVLEHYNDGLKQDAAR 67
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 44 -TRQNLP-----EHTQGLGSK--WLWLLFAVVPVILKQCRDSE 80
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 68 FLIENPRFYSYEGWQDLTKATHAATHTDGVNKKDKRKKWEHFS---FRTLKVVYDA- 123
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 81 KNKVRMAPFLLHHIDSISGVSGKR 104
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 124 --KVIAEFLIHHIDQAFVFEK 145
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 5

```



```
O8R3C2
ID Q8R3C2 PRELIMINARY; PRT; 380 AA.
AC Q8R3C2;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein (Fragment).
GN Name=Zfp82;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
RA MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426038999;
RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J.J., Helton E., Kettman M., Madan A.C., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A.C., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Stalska U., Smalls D.E., Schmerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC025629; AAH25629.1; -.
DR HSPB; P03001; IUN6
DR MGD; MGI:1890753; Zfp82.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR InterPro; IPR007087; Znf_C2H2.
DR Pfam; PF00096; zf-C2H2_13.
DR ProDom; PD000003; Znf_C2H2; 13.
DR SMART; SM00355; Znf_C2H2; 12.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 12.
DR PROSITE; PS00157; ZINC_FINGER_C2H2_2; 13.
KW Hypothetical protein.
FT NON_TER
SQ SEQUENCE 380 AA; 44484 MW; E2625817FF33184A CRC64;

Query Match 14.1%; Score 81; DB 2; Length 380;
Best Local Similarity 29.0%; Pred. No. 1.7;
Matches 27; Conservative 10; Mismatches 36; Indels 20; Gaps 4;

Qy 13 CLTCSYAF-MFSSLRQKTSFPGKVP-----CGBHFRIRQNLPEHTQGLGSKWLLFLFA 66
Db 272 CKDCGKAPLLSQTQHQSVHAGEPKPSCKGKGRFLRQKALHQSHHTGK----- 324

Qy 67 VVPFVILKQDSEKKNVMAFFLHHIDTSIG 99
Db 325 --PPECKECCR-----AFRLNSSLIQHLRIHSG 350

RESULT 6
2022_XENLA
ID _2022_XENLA STANDARD; PRT; 435 AA.

Query Match 14.1%; Score 81; DB 1; Length 435;
Best Local Similarity 26.1%; Pred. No. 1.9;
Matches 24; Conservative 12; Mismatches 32; Indels 24; Gaps 4;

Qy 13 CLTCSYAFMFSSL---RQKT---SEPGKVPCEGHEFRIRQNLPEHTQGLGSKWLLFLFA 66
Db 184 CLECGKFLFRSLLEHQHRTHTGKPFSCCLKGKCFVSRLKQHQHRTHTGK----- 236

Qy 67 VVPFVILKQDSEKKNVMAFF 89
Db 237 --PFSCLCGKGSFSPCLIDHQHRTHTGKPF 266

RESULT 7
Q6ZPGO
ID Q6ZPGO PRELIMINARY; PRT; 463 AA.
AC Q6ZPGO;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE MKTAA1948 protein (Fragment).
GN Name=MKIAA1948;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryonic tail;
PUBMED=14621295;
```

Okazaki N., Kikuno R., Ohara R., Inamoto S., Koseki H., Hiraoka S.,  
 Saga Y., Nagase T., Ohara O., Koga H.;  
 "Prediction of the coding sequences of mouse homologues of KIAA gene:  
 III. the complete nucleotide sequences of 500 mouse KIAA-homologous  
 cDNAs identified by screening of terminal sequences of cDNA clones  
 randomly sampled from size-fractionated libraries.";  
 DNA Res. 10:167-180(2003).  
 DR EMBL; AK129467; BAC98277.1; --  
 DR HSSP; P03001; 1UN6.  
 DR GO; GO:0005634; C:nucleus; IEA.  
 DR GO; GO:0003676; F:nucleic acid binding; IEA.  
 DR GO; GO:0008270; F:zinc ion binding; IEA.  
 DR InterPro; IPR007087; Znf\_C2H2.  
 DR Pfam; PF00096; zf-C2H2; 13.  
 DR ProDom; PD000003; Znf\_C2H2; 13.  
 DR SMART; SM00355; Znf\_C2H2; 13.  
 DR PROSITE; PS00028; ZINC\_FINGER\_C2H2\_1; 12.  
 DR PROSITE; PS00157; ZINC\_FINGER\_C2H2\_2; 13.  
 FT NON\_TER 1  
 SQ SEQUENCE 463 AA; 54252 MW; 2043BD957A8F277CE CRC64;  
 Query Match 14.1%; Score 81; DB 2; Length 463;  
 Best Local Similarity 29.0%; Pred. No. 2;  
 Matches 27; Conservative 10; Mismatches 36; Indels 20; Gaps 4;  
 QY 13 CLTCSYAF-MFSSLRQKTSBPQKVP-----CGEHFRIRQLPEHTQGWLGSKWMLLFA 66  
 DB 355 CKDCGAFRLLSQLTQHSVHAGEKPYSCKECKSFRLQKLAHQSIHTGK----- 407  
 QY 67 VVPFVLKCORDSEKNKVRMAPFLHHIDSIG 99  
 DB 408 --PFECKECKR-----AFRLNSSLIQHLRIHSG 433  
 RESULT 8  
 Q6P9Y7 PRELIMINARY; PRT; 530 AA.  
 AC Q6P9Y7;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Hypothetical protein.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6; TISSUE=Brain;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L.H., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan B., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettaman M., Madan A.C., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerk A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6; TISSUE=Brain;

Strausberg R.;  
 Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC060530; AAH60530.1; --  
 DR HSSP; P03001; 1UN6.  
 DR GO; GO:0005634; C:nucleus; IEA.  
 DR GO; GO:0003676; F:nucleic acid binding; IEA.  
 DR GO; GO:0008270; F:zinc ion binding; IEA.  
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
 DR InterPro; IPR001909; KRAB.  
 DR InterPro; IPR007087; Znf\_C2H2.  
 DR Pfam; PF01352; KRAB; 1.  
 DR ProDom; PD000096; zf-C2H2; 13.  
 DR SMART; SM00349; KRAB; 1.  
 DR SMART; SM00355; Znf\_C2H2; 13.  
 DR PROSITE; PS00028; ZINC\_FINGER\_C2H2\_1; 12.  
 DR PROSITE; PS00157; ZINC\_FINGER\_C2H2\_2; 13.  
 KW Hypothetical protein.  
 SQ SEQUENCE 530 AA; 62122 MW; 87CFAFB2A3CF1BD6 CRC64;  
 Query Match 14.1%; Score 81; DB 2; Length 530;  
 Best Local Similarity 29.0%; Pred. No. 2.3;  
 Matches 27; Conservative 10; Mismatches 36; Indels 20; Gaps 4;  
 QY 13 CLTCSYAF-MFSSLRQKTSBPQKVP-----CGEHFRIRQLPEHTQGWLGSKWMLLFA 66  
 DB 422 CKDCGAFRLLSQLTQHSVHAGEKPYSCKECKSFRLQKLAHQSIHTGK----- 474  
 QY 67 VVPFVLKCORDSEKNKVRMAPFLHHIDSIG 99  
 DB 475 --PFECKECKR-----AFRLNSSLIQHLRIHSG 500  
 RESULT 9  
 Q9NPP0 PRELIMINARY; PRT; 276 AA.  
 ID Q9NPP0;  
 AC Q9NPP0;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Hypothetical protein (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Auffray C., Ansorge W., Ballabio A., Estivill X., Gibson K.,  
 RA Lehrach H., Poustka A., Lundeberg J.;  
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Carim L., Estivill X., Escarceller M., Sumoy L.;  
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AL365370; CAB96946.1; --  
 DR HSSP; P25490; 1UBD  
 DR GO; GO:0005634; C:nucleus; IEA.  
 DR GO; GO:0003676; F:nucleic acid binding; IEA.  
 DR GO; GO:0008270; F:zinc ion binding; IEA.  
 DR InterPro; IPR007087; Znf\_C2H2.  
 DR InterPro; IPR007086; Znf\_C2H2\_sub.  
 DR Pfam; PF00096; zf-C2H2; 9.  
 DR PRINTS; PR00048; ZINC\_FINGER.  
 DR ProDom; PD000003; Znf\_C2H2; 10.  
 DR SMART; SM00355; Znf\_C2H2; 10.  
 DR PROSITE; PS00028; ZINC\_FINGER\_C2H2\_1; 10.  
 DR PROSITE; PS00157; ZINC\_FINGER\_C2H2\_2; 10.  
 KW Hypothetical protein.  
 FT NON\_TER 1  
 SQ SEQUENCE 276 AA; 31538 MW; 8EB93052A59B8E4E CRC64;  
 Query Match 14.0%; Score 80; DB 2; Length 276;

[illegible]

```

RESULT 12
ZF90 MOUSE
ID_ZF90_MOUSE STANDARD; PRT; 636 AA.
AC Q61967;
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Zinc finger protein 90 (Zfp-90) (Zinc finger protein NK10).
GN Name=zf90; Synonyms=NK10;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=96069544; PubMed=7576184;
RA Lange R., Christoph A., Thiesen H.-J., Vopper G., Johnson K.R.,
RA Lemaire L., Plomann M., Cremer H., Barthele D., Heinlein U.A.O.;
RT "Developmentally regulated mouse gene NK10 encodes a zinc finger
RT repressor protein with differential DNA-binding domains.";
RL DNA Cell Biol. 14:971-981(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N-3; TISSUE=Mammary gland;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -I- FUNCTION: May function as a repressor or silencer protein, and
CC most likely exerts its repressing activity upon zinc-dependent
CC binding to DNA. May be involved in proper spermatogenesis by
CC repressing the expression of genes unnecessary or incompatible
CC with the maintenance of a haploid cell state.
CC -I- SUBCELLULAR LOCATION: Nuclear.
CC -I- TISSUE SPECIFICITY: Brain, heart, spleen, thymus, and testis.
CC -I- DEVELOPMENTAL STAGE: There is a marked increase after postnatal
CC stages 18-20 (simultaneously to the appearance of haploid cell
CC stages). Maximal expression is observed around 2 weeks
CC postnatally, with the exception of brain and testis, where the
CC expression is highest in earlier developmental stages.
CC -I- SIMILARITY: Belongs to the krueppel C2H2-type zinc-finger protein
CC family.
CC -I- SIMILARITY: Contains 13 C2H2-type zinc fingers.
CC -I- SIMILARITY: Contains 1 KRAB domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X79828; CAA56225.1; -.
CC EMBL; BC046298; AAH46298.1; -.

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PIR; I48689; I48689.
DR HSSP; P08047; ISP2.
DR MGI; MGI:104786; Zfp90.
DR InterPro; IPR001909; KRAB.
DR InterPro; IPR007087; Znf_C2H2.
DR InterPro; IPR007086; Znf_C2H2_sub.
DR Pfam; PF01352; KRAB; 1.
DR Pfam; PF00096; zf-C2H2; 13.
DR PRINTS; PR00048; ZINCFINGER.
DR PRODOM; PD000003; Znf_C2H2; 10.
DR PROSITE; PS00805; KRAB; 1.
DR PROSITE; PS00285; ZINC_FINGER_C2H2_1; 13.
DR PROSITE; PS00157; ZINC_FINGER_C2H2_2; 13.
KW DNA-binding; Metal-binding; Nuclear protein; Repeat; Repressor;
KW Transcription regulation; Zinc-finger.
FT DOMAIN 14 85
FT ZN_FING 208 230 C2H2-type 1.
FT ZN_FING 250 272 C2H2-type 2.
FT ZN_FING 278 300 C2H2-type 3.
FT ZN_FING 306 328 C2H2-type 4.
FT ZN_FING 334 356 C2H2-type 5.
FT ZN_FING 362 384 C2H2-type 6.
FT ZN_FING 390 412 C2H2-type 7.
FT ZN_FING 446 468 C2H2-type 8.
FT ZN_FING 494 516 C2H2-type 9.
FT ZN_FING 522 544 C2H2-type 10.
FT ZN_FING 550 572 C2H2-type 11.
FT ZN_FING 578 600 C2H2-type 12.
FT ZN_FING 606 628 C2H2-type 13.
SQ SEQUENCE 636 AA; 72423 MW; 1269BEC7729E369F CRC64;

Query Match 13.5%; Score 77.5; DB 1; Length 636;
Best Local Similarity 29.9%; Pred. No. 6.9;
Matches 26; Conservative 8; Mismatches 34; Indels 19; Gaps 4;

QY 13 CUTCSVAP-MFSSLROKTSPOQKVP-----CGEHFRIRQLPEHTQGWLGSKWLWLLFA 66
Db 552 CIDCGKAFSSQSSSLIGHERTHTGKPYECNCGRAFRKTKNLHDHQRTHGTGK----- 604
QY 67 VVPFVLKQDSEKKNKVRMAPFFLHH 93
Db 605 --PYACEKCGR---NFSRSALTQKH 625

RESULT 13
R8CL194 PRELIMINARY; PRT; 140 AA.
AC Q8C194;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Mus musculus 10 days neonate skin cDNA, RIKEN full-length enriched
DE library, clone:4732438E01 product:MOB1 PROTEIN (HYPOTHETICAL 25.1 kDa
DE PROTEIN) homolog.
GN Name=Mobk1b;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Skin;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Skin;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).

```



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DR InterPro; IPR007087; Znf_C2H2.
DR Pfam; PF00096; zf-C2H2; 13.
DR ProDom; PD000003; Znf_C2H2; 13.
DR SMART; SM00355; Znf_C2H2; 13.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 12.
DR PROSITE; PS00157; ZINC_FINGER_C2H2_2; 13.
FT NON_TER 1
SQ SEQUENCE 487 AA; 57086 MW; F529A5495FC9E136 CRC64;

Query Match      13.4%; Score 77; DB 2; Length 487;
Best Local Similarity 29.0%; Pred. No. 6;
Matches 27; Conservative 10; Mismatches 36; Indels 20; Gaps 4;

Qy      13 CLTCSYAF-MFSSLRQKTSBPQKVP-----CGEHFRIRQNLPEHTQGLGSKWLILFA 66
Db      379 CKECGAFRLLSQLTQHSIHIGKPYKCKEKGAFRLRQKLTILHQSIIHTGEK-----431

Qy      67 VVPFVILKQDSEKKNVRMAPFLHHIDSIG 99
Db      432 --PFECKECHK-----AFRLNSSLIOHLRIHSG 457

```

Search completed: October 11, 2005, 07:18:45  
 Job time : 66.6283 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 11, 2005, 06:57:07 ; Search time 78.508 Seconds  
(without alignments)  
522.196 Million cell updates/sec

Title: US-10-092-934-4  
Perfect score: 573  
Sequence: 1 MWTLKSLVLLCLTCSYAF.....APFLHHIDISGVSGKRMF 106

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A Geneseq\_16Dec04:.\*  
1: Geneseqp1980s:.\*  
2: Geneseqp1990s:.\*  
3: Geneseqp2000s:.\*  
4: Geneseqp2001s:.\*  
5: Geneseqp2002s:.\*  
6: Geneseqp2003as:.\*  
7: Geneseqp2003bs:.\*  
8: Geneseqp2004s:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	573	100.0	106	5 AAE29145	Aae29145 Neural th
2	573	100.0	106	6 ABR63243	Abf63243 106 amino
3	573	100.0	106	6 ABU02975	Abu02975 Human neu
4	573	100.0	106	6 ABP59926	Abp59926 Human 106
5	573	100.0	106	6 AAE33192	Aae33192 Neural th
6	573	100.0	106	6 ABJ19448	Abj19448 106-mer n
7	573	100.0	106	7 ADB37522	Adb37522 Neural th
8	573	100.0	106	7 ADL96024	Adl96024 Human neu
9	453	79.1	171	6 ABU12055	Abu12055 Human NOV
10	430	75.0	171	3 AAY53032	Aay53032 Human sec
11	430	75.0	239	4 AAU68550	Aau68550 Human nov
12	430	75.0	239	6 ABR58389	Abf58389 Human NOV
13	430	75.0	292	8 ADS10718	Adsi10718 Human the
14	423	73.8	101	2 AAY12683	Aay12683 Human 5'
15	423	73.8	101	3 AAG00463	Aag00463 Human sec
16	358	62.5	156	6 ABU12061	Abu12061 Human NOV
17	358	62.5	156	6 ABU12060	Abu12060 Human NOV
18	358	62.5	156	6 ABU12058	Abu12058 Human NOV
19	354	61.8	156	6 ABU12059	Abu12059 Human NOV
20	339	59.2	156	6 ABU12062	Abu12062 Human NOV
21	252	44.0	47	6 ABU12056	Abu12056 Human NOV
22	233	40.7	47	6 ABU12057	Abu12057 Human NOV
23	92	16.1	15	6 ABP59901	Abp59901 Human neu
24	92	16.1	15	7 ADL96047	Adl96047 Human neu
25	87	15.2	15	6 ABP59900	Abp59900 Human neu

26	87	15.2	15	7 ADL96046	Adl96046 Human neu
27	83	14.5	16	6 ABP59904	Abp59904 Human neu
28	83	14.5	16	7 ADL96050	Adl96050 Human neu
29	80	14.0	15	6 ABP59902	Abp59902 Human neu
30	80	14.0	15	7 ADL96048	Adl96048 Human neu
31	80	14.0	513	4 AAB73600	Aab73600 Zinc fing
32	80	14.0	545	8 ADM87387	Adm87387 Human pro
33	78.5	13.7	111	8 ADP70944	Adp70944 Novel zin
34	78.5	13.7	111	8 ADP70943	Adp70943 Novel zin
35	78	13.6	15	6 ABP59903	Abp59903 Human neu
36	78	13.6	15	7 ADL96049	Adl96049 Human neu
37	77	13.4	15	6 ABP59899	Abp59899 Human neu
38	77	13.4	15	7 ADL96045	Adl96045 Human neu
39	77	13.4	194	7 ADL22738	Adl22738 Human dis
40	77	13.4	424	6 ABU11725	Abu11725 Human MDD
41	77	13.4	429	5 ABB98780	Abb98780 Human mac
42	77	13.4	475	8 ABM82090	Abm82090 Tumour-as
43	77	13.4	532	4 AAM93834	Aam93834 Human pol
44	77	13.4	532	8 ADL31870	Adl31870 Human pro
45	76	13.3	15	6 ABP59898	Abp59898 Human neu

## ALIGNMENTS

## RESULT 1

AAE29145  
ID AAE29145 standard; protein; 106 AA.

XX	AC	AAE29145;			
XX	AC	AAE29145;			
XX	DT	27-JAN-2003 (first entry)			
XX	XX	Neural thread protein (NTP) #3.			
DE	DE	Neural thread protein (NTP) #3.			
XX	KW	Neural thread protein; NTP; hyperplasia; hypertrophy; arteriosclerosis;			
KW	KW	haemorrhoid; gene therapy; tumour; vascular disease; atherosclerosis;			
KW	KW	inflammatory disease; nutritional deficiency disease; genetic disease;			
KW	KW	autoimmune disease; metabolic disease; traumatic disease; intoxication;			
KW	KW	infectious disease; congenital malformation; enzyme deficiency disease;			
KW	KW	amyloid disease; fibrosis disease; storage disease; radiation disease;			
KW	KW	poisoning; environmental disease; endocrine disease; protein therapy;			
KW	KW	degenerative disease; mechanical disease.			
XX	OS	Unidentified.			
XX	XX	WO200274323-A2.			
XX	PN	26-SEP-2002.			
PD	XX	08-MAR-2002; 2002WO-IB001959.			
XX	XX	08-MAR-2001; 2001US-0273957P.			
XX	XX	(AVER/) AVERAGE P.			
XX	XX	Average P;			
XX	XX	WPI; 2002-759864/82.			
XX	XX	Treating a condition in a patient requiring removal or destruction of			
PT	PT	cells, such as a benign or malignant tumor of a tissue or an inflammatory			
PT	PT	disease, comprises administering a neural thread protein (NTP) or a NTP			
PT	PT	gene to a mammal.			
XX	XX	Claim 23; Fig 4; 70pp; English.			
XX	XX	The invention relates to a method for treating a condition in a patient			
CC	CC	requiring removal or destruction of cells. The method involves			
CC	CC	administering to a mammal a neural thread protein (NTP), or administering			
CC	CC	to a tumour or other target cell a NTP gene, where the expression of the			
CC	CC	NTP gene is induced resulting in expression of the NTP protein. The			
CC	CC	method and NTP are useful for treating a condition in a patient requiring			

CC removal or destruction of cells, such as a benign or malignant tumour of  
CC a tissue, a hyperplasia, hypertrophy, or overgrowth of a tissue,  
CC preferably tonsillar hypertrophy or prostatic hyperplasia, a virally,  
CC bacterially, or parasitically altered tissue, or a malformation of a  
CC tissue. Other conditions include a cosmetic modification to a tissue,  
CC such as removal of unwanted facial hair, warts or unwanted fatty tissue,  
CC a vascular disease, particularly atherosclerosis or arteriosclerosis,  
CC haemorrhoids, or varicose veins, an inflammatory disease, autoimmune  
CC disease, metabolic disease, hereditary/genetic disease, traumatic disease  
CC or physical injury, nutritional deficiency disease, infectious disease,  
CC congenital malformation, amyloid disease, fibrosis disease, storage  
CC disease, enzyme deficiency disease, poisoning, intoxication, degenerative  
CC disease, radiation disease, environmental disease, endocrine disease or  
CC mechanical disease. The invention is useful in protein therapy and gene  
CC therapy. The present sequence is NTP protein  
XX  
SQ Sequence 106 AA;

Query Match 100.0%; Score 573; DB 5; Length 106;  
Best Local Similarity 100.0%; Pred. No. 1.1e-64;  
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MWTLKSSLVLLCLCTCSYAFMFSSLRQKTSEPOGKVPCEGHEFRIRQNLPEHTQGLGSKW 60  
Db 1 MWTLKSSLVLLCLCTCSYAFMFSSLRQKTSEPOGKVPCEGHEFRIRQNLPEHTQGLGSKW 60  
Qy 61 LWLLFAVVPFVILKQDSEKNKVRMAPFFLHHIDSISGVSGKRMF 106  
Db 61 LWLLFAVVPFVILKQDSEKNKVRMAPFFLHHIDSISGVSGKRMF 106

## RESULT 2

ABR63243  
ID ABR63243 standard; protein; 106 AA.

AC ABR63243;

XX 28-AUG-2003 (first entry)

DE 106 amino acid neural thread protein.

XX Cytostatic; Antibacterial; Immunosuppressive; Antiinflammatory;  
KW neural thread protein; NTP; tumour.

XX Unidentified.

XX WO2003008443-A2.

XX 30-JAN-2003.

XX 19-JUL-2002; 2002WO-CA001105.

XX 19-JUL-2001; 2001US-0306150P.

XX 19-JUL-2001; 2001US-0306161P.

XX 16-NOV-2001; 2001US-0331477P.

XX (NYMO-) NYMOX CORP.

XX Averbach PA;

XX WPI; 2003-247999/24.

XX Novel neural thread protein peptide, referred as cell death peptide,  
PT useful for treating prostatic hyperplasia, psoriasis, eczema, dermatosis,  
PT atherosclerosis, cosmetic modification to skin, throat, mouth, muscle.

XX Disclosure; Fig 4; 77pp; English.

XX The present invention relates to a neural thread protein (NTP) peptide  
CC referred to as cell death peptide. Thought to be cytostatic,  
CC antibacterial, immunosuppressive and antiinflammatory. It is useful for  
CC treating a condition in a patient requiring removal or destruction of  
CC cells, for treating a condition such as benign or malignant tumor,

CC inflammatory disease, autoimmune disease and infectious disease. The  
CC peptide useful for treatment is derived from the amino acid sequence for  
CC a pancreatic thread protein. The peptide is conjugated, linked or bound  
CC to a molecule chosen from antibody or its fragment, antibody-like binding  
CC molecule, where the molecule has a higher affinity for binding to a tumor  
CC or other target than binding to other cells. Treatment using NTP peptides  
CC can remove benign tumors with less risk and fewer of the undesirable side  
CC effects of surgery. The present sequence is an NTP amino acid sequence  
XX  
SQ Sequence 106 AA;

Query Match 100.0%; Score 573; DB 6; Length 106;  
Best Local Similarity 100.0%; Pred. No. 1.1e-64;  
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MWTLKSSLVLLCLCTCSYAFMFSSLRQKTSEPOGKVPCEGHEFRIRQNLPEHTQGLGSKW 60  
Db 1 MWTLKSSLVLLCLCTCSYAFMFSSLRQKTSEPOGKVPCEGHEFRIRQNLPEHTQGLGSKW 60  
Qy 61 LWLLFAVVPFVILKQDSEKNKVRMAPFFLHHIDSISGVSGKRMF 106  
Db 61 LWLLFAVVPFVILKQDSEKNKVRMAPFFLHHIDSISGVSGKRMF 106

## RESULT 3

ABU02975

ID ABU02975 standard; protein; 106 AA.

AC ABU02975;

XX 20-JAN-2003 (first entry)

DE Human neural thread protein AD7C-NTP, protein fragment #3.

XX Neural thread protein; NTP-peptide; AD7C-NTP; surgical excision;  
KW transplantation; grafting; chemotherapy; immunotherapy; vaccination;  
KW ablation; cryotherapy; laser therapy; phototherapy; gene therapy;  
KW radiation; tumour; hyperplasia; hypertrophy; overgrowth of tissue;  
KW malformation of tissue; tonsillary hypertrophy; prostatic hyperplasia;  
KW cosmetic modification; vascular disease; atherosclerosis;  
KW arteriosclerosis; haemorrhoid; varicose vein; inflammatory disease;  
KW autoimmune disease; metabolic disease; traumatic disease;  
KW physical injury; nutritional deficiency disease; infectious disease;  
KW amyloid disease; fibrosis disease; storage disease;  
KW congenital malformation; enzyme deficiency disease; poisoning;  
KW intoxication; environmental disease; radiation disease;  
KW endocrine disease; degenerative disease; mechanical disease.

XX Homo sapiens.

XX WO200297030-A2.

XX 05-DEC-2002.

XX 24-MAY-2002; 2002WO-CA0000759.

XX 25-MAY-2001; 2001US-0293156P.

XX (NYMO-) NYMOX CORP.

XX Averbach PA;

XX WPI; 2003-041406/03.

XX Novel peptides similar in amino acid sequence to neural thread proteins  
PT (NTP), useful for treating unwanted cellular proliferations such as  
PT malignant tumors and prostatic hyperplasia.

XX Disclosure; Fig 4; 78pp; English.

XX The invention describes an NTP-peptide (I) comprising at least one amino  
CC acid sequence corresponding to part of the amino acid sequence of a  
CC neural thread protein, AD7C-NTP. The invention provides a method of



CC treating a condition requiring removal or destruction of cells of a  
 CC mammal comprising administering to a mammal, a therapeutic amount of (I).  
 CC The treatment is administered to the mammal before, during or after  
 CC surgical excision, transplantation, grafting, chemotherapy,  
 CC immunotherapy, vaccination, thermal or electrical ablation,  
 CC laser therapy, phototherapy, gene therapy and/or radiation. The method is  
 CC useful for treatment of benign or malignant tumour; hyperplasia,  
 CC hyperthyroidism or overgrowth of tissue; virally, bacterially or  
 CC parasitically altered tissue; malformation of tissue selected from lung,  
 CC breast, stomach, pancreas, prostate, bladder, bone, ovary, skin, kidney,  
 CC sinus, colon, intestine, rectum, esophagus, heart, spleen, salivary  
 CC gland, blood, brain and its coverings, spinal cord, muscle, connective  
 CC tissue, adrenal, parathyroid, thyroid, uterus, testis, pituitary,  
 CC reproductive organs, liver, hair, gall bladder, eye, ear, nose, throat,  
 CC tonsils, mouth and lymph nodes and lymphoid system; tonsillary  
 CC hyperthyroidism; prostatic hyperplasia; cosmetic modification to a tissue;  
 CC vascular disease (atherosclerosis or arteriosclerosis); haemorrhoids;  
 CC varicose veins; inflammatory disease; autoimmune disease; metabolic  
 CC disease; hereditary/genetic disease; traumatic disease; physical injury;  
 CC nutritional deficiency disease; infectious disease; amyloid disease;  
 CC fibrosis disease; storage disease; congenital malformation; enzyme  
 CC deficiency disease; poisoning; intoxication; environmental disease;  
 CC radiation disease; endocrine disease; degenerative disease and mechanical  
 CC disease. This is the amino acid sequence of a human neural thread protein  
 CC AD7C-NTP protein fragment  
 CC  
 CC SQ Sequence 106 AA;

Query Match 100.0%; Score 573; DB 6; Length 106;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-64;  
 Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MWTLKSSLVLLCLTCSYAFMFSSLRQKTSPEQKVPCEGHEFRIRQLPEHTQGLGSKW 60  
 Db 1 MWTLKSSLVLLCLTCSYAFMFSSLRQKTSPEQKVPCEGHEFRIRQLPEHTQGLGSKW 60  
 Qy 61 LWWLFAVVPFVILKQDSEKKNVMAFFLHHIDISIGVSGKRMF 106  
 Db 61 LWWLFAVVPFVILKQDSEKKNVMAFFLHHIDISIGVSGKRMF 106

## RESULT 4

ABP59926  
 ID ABP59926 standard; protein; 106 AA.

AC ABP59926;

XX 08-SEP-2003 (first entry)

DT Human 106 amino acid neural thread protein-like protein.

DE Human; tumour; cancer; neural thread protein; NTP; cell removal;  
 KW cell destruction; antipsoriatic; antimicrobial; immunosuppressive;  
 KW antiinflammatory; dermatological; antiarteriosclerotic; vasotropic;  
 KW gene therapy.

XX Homo sapiens.

OS WO2003044053-A2.

PN 30-MAY-2003.

PD 18-NOV-2002; 2002WO-CA001757.

PF 16-NOV-2001; 2001US-0331477P.

PR (NYMO-) NYMOX CORP.

XX Averbach P, Gemmell J;

XX WPI; 2003-457592/43.

PT New neural thread protein (NTP), useful for preparing a composition for

PT treating or preventing a condition in a mammal requiring removal or  
 PT destruction of cells, e.g. psoriasis, eczema, atherosclerosis or  
 PT inflammatory disease.

XX Disclosure; Fig 3; 98pp; English.

XX The present invention relates to peptides derived from the human neural  
 CC thread protein (NTP). The peptides are useful for preparing a composition  
 CC for treating or preventing a condition in a mammal requiring removal or  
 CC destruction of cells, comprising tonsillary hypertrophy, prostatic  
 CC hyperplasia, psoriasis, eczema, dermatosis, cosmetic modification to a  
 CC breast, connective, skin, eye, ear, nose, throat, mouth or muscle tissue,  
 CC varicose veins, atherosclerosis, inflammatory, metabolic, infectious,  
 CC fibrosis, endocrine or autoimmune disease, or stenosis, restenosis,  
 CC occlusion or blockage of an artery or of a stent placed or implanted in  
 CC an artery. The present sequence is an NTP protein used to produce  
 CC peptides of the invention

XX SQ Sequence 106 AA;

Query Match 100.0%; Score 573; DB 6; Length 106;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-64;  
 Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MWTLKSSLVLLCLTCSYAFMFSSLRQKTSPEQKVPCEGHEFRIRQLPEHTQGLGSKW 60  
 Db 1 MWTLKSSLVLLCLTCSYAFMFSSLRQKTSPEQKVPCEGHEFRIRQLPEHTQGLGSKW 60  
 Qy 61 LWWLFAVVPFVILKQDSEKKNVMAFFLHHIDISIGVSGKRMF 106  
 Db 61 LWWLFAVVPFVILKQDSEKKNVMAFFLHHIDISIGVSGKRMF 106

## RESULT 5

AAE33192  
 ID AAE33192 standard; protein; 106 AA.

XX AAE33192;

XX 16-APR-2003 (first entry)

DT Neural thread protein (NTP) #3.

XX Cell death; tissue necrosis; neural thread protein; NTP; amyloidosis;  
 KW stroke; brain tumour; Pick's disease; Parkinson's disease; glaucoma;  
 KW Alzheimer's disease; gene therapy.

XX Unidentified.

XX WO200289841-A2.

XX 14-NOV-2002.

XX 06-MAY-2002; 2002WO-CA000681.

XX 04-MAY-2001; 2001US-0288463P.

XX (NYMO-) NYMOX CORP.

XX Averbach PA;

XX WPI; 2003-120506/11.

XX Preventing, controlling, modulating, ameliorating and/or treating cell  
 PT death or tissue necrosis using antibodies to neural thread proteins,  
 PT useful in disorders such as stroke, brain tumor, glaucoma and Alzheimer's  
 PT disease.

XX Disclosure; Fig 7; 60pp; English.

XX The invention relates to a method of preventing, and/or inhibiting cell  
 CC death and/or tissue necrosis in live tissue containing neural thread  
 CC proteins (NTP). The method involves contacting the live tissue with at

CC least one antibody, fragment or derivative that recognises NTP, where the  
 CC antibody, fragment or derivative is present to prevent, control,  
 CC ameliorate and/or inhibit cell death and/or tissue necrosis caused by the  
 CC presence of NTP. Methods and compositions of the invention are useful for  
 CC preventing, modulating, controlling and/or treating disorders associated  
 CC with cell death and/or tissue necrosis such as stroke, brain tumour,  
 CC Pick's disease, Parkinson's disease, amyloidosis, glaucoma and  
 CC Alzheimer's disease. The invention is useful in gene therapy. The present  
 CC sequence is NTP protein  
 XX  
 SQ Sequence 106 AA;

Query Match 100.0%; Score 573; DB 6; Length 106;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-64;  
 Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MWTLKSSLVLLCLTCSYAFMFSSLRQKTSEPOGKVPCEGHEFRIRQNLPEHTQGLGSKW 60  
 |||||  
 DB 1 MWTLKSSLVLLCLTCSYAFMFSSLRQKTSEPOGKVPCEGHEFRIRQNLPEHTQGLGSKW 60  
 |||||  
 QY 61 LLLFAVVPFVILKQDSEKKNVRMAPFFLHHIDISISGVSGKRMF 106  
 |||||  
 DB 61 LLLFAVVPFVILKQDSEKKNVRMAPFFLHHIDISISGVSGKRMF 106  
 |||||

RESULT 6  
 ABJ19448  
 ID ABJ19448 standard; protein; 106 AA.  
 XX  
 AC ABJ19448;  
 DT 27-MAR-2003 (first entry)  
 XX  
 DE 106-mer neural thread protein #1.  
 XX  
 XX Nootropic; neuroprotective; cell death; tissue necrosis; NTP;  
 KW neural thread protein; neurodegenerative disorder; Alzheimer's disease.  
 XX  
 OS Unidentified.  
 XX  
 XX WO200292115-A2.  
 XX  
 XX 21-NOV-2002.

XX  
 XX 16-MAY-2002; 2002WO-CA000712.  
 XX  
 XX 16-MAY-2001; 2001US-0290971P.  
 XX  
 XX (NYMO-) NYMOX CORP.  
 XX  
 XX Averbach PA;  
 XX  
 XX WPI; 2003-129234/12.  
 XX  
 XX Preventing and/or inhibiting cell death and/or tissue necrosis in a  
 PT tissue for treating a neurodegenerative disorder, e.g. Alzheimer's  
 PT disease, by contacting the live tissue with at least one segment of  
 PT neural thread proteins (NTP).  
 XX  
 XX Disclosure; Fig 4; 60pp; English.

XX The invention relates to a novel method for preventing and/or inhibiting  
 CC cell death and/or tissue necrosis in a tissue comprising contacting the  
 CC live tissue with at least one segment of neural thread proteins (NTP).  
 CC The methods are composition are useful for treating a neurodegenerative  
 CC disorder, such as Alzheimer's disease. This sequence represents an NTP  
 CC protein of the invention  
 XX  
 SQ Sequence 106 AA;

Query Match 100.0%; Score 573; DB 6; Length 106;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-64;  
 Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MWTLKSSLVLLCLTCSYAFMFSSLRQKTSEPOGKVPCEGHEFRIRQNLPEHTQGLGSKW 60  
 |||||  
 DB 1 MWTLKSSLVLLCLTCSYAFMFSSLRQKTSEPOGKVPCEGHEFRIRQNLPEHTQGLGSKW 60  
 |||||  
 QY 61 LLLFAVVPFVILKQDSEKKNVRMAPFFLHHIDISISGVSGKRMF 106  
 |||||  
 DB 61 LLLFAVVPFVILKQDSEKKNVRMAPFFLHHIDISISGVSGKRMF 106  
 |||||

RESULT 7  
 ADB37522  
 ID ADB37522 standard; protein; 106 AA.  
 XX  
 AC ADB37522;  
 XX  
 DT 04-DEC-2003 (first entry)  
 XX  
 DE Neural thread protein-like protein #1.

XX Cytostatic; Antitumour; Antipsoriatic; Dermatological;  
 KW Antiatherosclerotic; Antiarteriosclerotic; Vasotropic; Antiinflammatory;  
 KW Immunosuppressive; Tranquillizer; Antileptic; Virucide; AD7c-NTP;  
 KW neural thread protein; neuritic sprouting.

XX Unidentified.  
 XX  
 XX WO2003008444-A2.  
 XX  
 XX 30-JAN-2003.  
 XX  
 XX 19-JUL-2002; 2002WO-CA001106.  
 XX  
 XX 19-JUL-2001; 2001US-0306150P.  
 PR 19-JUL-2001; 2001US-0306161P.  
 PR 16-NOV-2001; 2001US-0331477P.  
 XX  
 XX (NYMO-) NYMOX CORP.

XX  
 XX Averbach PA, Gemmell J;

XX WPI; 2003-248000/24.

XX Novel Related peptide or AD7c-neural thread peptide, useful for treating  
 PT unwanted cellular proliferations, glandular hyperplasia, unwanted facial  
 PT hair, warts and unwanted fatty tissue.

XX Disclosure; Fig 4; 109pp; English.

XX The present invention relates to AD7c-neural thread protein (NTP) and  
 CC related proteins and peptides (I; ADB37528-ADB37641). The sequences are  
 CC useful for treating a condition in a patient requiring removal or  
 CC destruction of cells. The condition can be selected from benign or  
 CC malignant tumour of a tissue, hyperplasia, hypertrophy or overgrowth of a  
 CC tissue, virally, bacterially or parasitically altered tissue, Or  
 CC malformation of a tissue, where the tissue is selected from lung, breast,  
 CC stomach, pancreas, prostate, bladder, bone, ovary, skin, kidney, sinus,  
 CC colon, intestine, stomach, rectum, oesophagus, heart, spleen, salivary  
 CC gland, blood, brain and its coverings, spinal cord and its coverings,  
 CC muscle, connective tissue, adrenal, parathyroid, thyroid, uterus, testis,  
 CC pituitary, reproductive organs, liver, gall bladder, eye, ear, nose,  
 CC throat, tonsils, mouth, lymph nodes and lymphoid tissue. The condition is  
 CC preferably tonsillar hypertrophy, prostatic hyperplasia, psoriasis,  
 CC eczema, dermatosis, cosmetic modification to a tissue (skin, eye, ear,  
 CC nose, throat, mouth, muscle, connective, hair or breast tissue), vascular  
 CC disease (atherosclerosis or arteriosclerosis), haemorrhoids, varicose  
 CC veins, inflammatory disease, autoimmune disease, metabolic disease,  
 CC hereditary/genetic disease, traumatic disease or physical injury,  
 CC nutritional deficiency disease, infectious disease, amyloid disease,  
 CC fibrosis disease, storage disease, congenital malformation, enzyme  
 CC deficiency disease, poisoning, intoxication, environmental disease,  
 CC radiation disease, endocrine disease, degenerative disease and mechanical  
 CC disease. The peptides are useful for treating unwanted cellular

CC proliferations, glandular (e.g. prostate) hyperplasia, unwanted facial  
 CC hair, warts and unwanted fatty tissue, or for preparing antibodies that  
 CC recognize and/or bind to related proteins, Related peptides or NTP  
 CC peptides. The present sequence was used to illustrate the invention.

XX SQ Sequence 106 AA;

Query Match 100.0%; Score 573; DB 7; Length 106;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-64; Mismatches 0; Gaps 0;  
 Matches 106; Conservative 0; Indels 0; Gaps 0;  
 Qy 1 MWTLKSSLVLLCLTCSYAFMFSSLRQKTSBPQGVPCGEHFRIRQNLPEHTQGLGSKW 60  
 Db 1 MWTLKSSLVLLCLTCSYAFMFSSLRQKTSBPQGVPCGEHFRIRQNLPEHTQGLGSKW 60  
 Qy 61 LWLLFAVVPFVILKQDSEKNKVRMAPFFLHHIDSISGVSGKRMF 106  
 Db 61 LWLLFAVVPFVILKQDSEKNKVRMAPFFLHHIDSISGVSGKRMF 106

RESULT 8  
 ADL96024  
 ID ADL96024 standard; protein; 106 AA.

XX AC ADL96024;

DT 20-MAY-2004 (first entry)

XX DE Human neural thread protein, NTP106.

XX KW Human; neural thread protein; NTP122; NTP112; NTP106; NTP98; NTP75;  
 KW NTP68; NTP61; stenosis; stent; tumour; prostatic hyperplasia; psoriasis;  
 KW eczema; haemorrhoid; atherosclerosis; inflammatory disease;  
 KW autoimmune disease; metabolic disease; hereditary disease;  
 KW genetic disease; traumatic disease; physical injury;  
 KW nutritional deficiency disease; infectious disease; amyloid disease;  
 KW Alzheimer's disease; storage disease; congenital malformation;  
 KW enzyme deficiency disease; poisoning; intoxication;  
 KW environmental disease; radiation disease; endocrine disease;  
 KW degenerative disease; mechanical disease.

XX OS Homo sapiens.

XX PN US2003165569-A1.

XX PD 04-SEP-2003.

XX PF 15-NOV-2002; 2002US-00294891.

XX PR 16-NOV-2001; 2001US-0331477P.

XX PA (AVER/) AVERBACK P.  
 XX PA (GEMM/) GEMMELL J.

XX PI Averbach P, Gemmell J;

XX DR WPI; 2003-898099/82.

XX PT New neural thread protein or its variants, useful for treating tumors and  
 XX PT other conditions requiring the removal or destruction of cells (e.g.  
 XX PT prostatic hyperplasia, psoriasis, eczema, hemorrhoids or  
 XX PT atherosclerosis).

XX PS Disclosure; SEQ ID NO 3; 32pp; English.

CC The invention relates to a peptide, or its homologue, derivative,  
 CC fragment, variant or mimetic, comprising at least one neural thread  
 CC protein (NTP) peptide appearing as ADL96029-ADL96069, derived from  
 CC NTP122, 112, 106, 98, 75, 68 or 61. Also included are a nucleic acid  
 CC encoding an amino acid sequence corresponding to the above peptide, a  
 CC composition comprising one or more peptides or nucleic acids cited above  
 CC and a carrier, a method of treating a condition in a mammal requiring  
 CC removal or destruction of cells (comprising administering to the mammal

CC an amount of the peptide cited above) and a method of preventing or  
 CC inhibiting the stenosis, occlusion or blockage of a stent, comprising  
 CC coating the stent with an amount of the above peptide. The peptide  
 CC further comprises an amino acid in a reverse-D order based on the above  
 CC amino acid sequences. The composition and methods are useful in treating  
 CC tumours and other conditions requiring the removal or destruction of  
 CC cells (e.g. prostatic hyperplasia, psoriasis, eczema, hemorrhoids or  
 CC atherosclerosis). These may also be used in treating inflammatory  
 CC diseases, autoimmune diseases, metabolic diseases, hereditary/genetic  
 CC diseases, traumatic diseases or physical injuries, nutritional deficiency  
 CC diseases, infectious diseases, amyloid diseases e.g. Alzheimer's disease,  
 CC storage diseases, congenital malformation, enzyme deficiency diseases,  
 CC poisoning, intoxication, environmental diseases, radiation diseases,  
 CC endocrine diseases, degenerative diseases or mechanical diseases. The  
 CC present sequence is a human NTP protein from which the peptides of the  
 CC invention are derived.

XX SQ Sequence 106 AA;

Query Match 100.0%; Score 573; DB 7; Length 106;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-64;  
 Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MWTLKSSLVLLCLTCSYAFMFSSLRQKTSBPQGVPCGEHFRIRQNLPEHTQGLGSKW 60

Db 1 MWTLKSSLVLLCLTCSYAFMFSSLRQKTSBPQGVPCGEHFRIRQNLPEHTQGLGSKW 60

Qy 61 LWLLFAVVPFVILKQDSEKNKVRMAPFFLHHIDSISGVSGKRMF 106

Db 61 LWLLFAVVPFVILKQDSEKNKVRMAPFFLHHIDSISGVSGKRMF 106

RESULT 9

ABU12055

ID ABU12055 standard; protein; 171 AA.

XX AC ABU12055;

XX DT 19-FEB-2003 (first entry)

XX DE Human NOV10a CG90739-01 protein SEQ ID 30.

XX KW NOVX; human; antidiabetic; antiarteriosclerotic; anorectic; nootropic;  
 KW metabolic; antimicrobial; neuroprotective; antiparkinsonian; cardiant;  
 KW antilipemic; cytostatic; immunomodulatory; gene therapy; dyslipidaemia;  
 KW cardiomyopathy; metabolic disorder; diabetes; atherosclerosis; obesity;  
 KW anorexia; neurodegenerative disorder; Alzheimer's disease; cancer;  
 KW Parkinson's disease; haematopoietic disorder; metabolic disturbance;  
 KW metabolic syndrome X; wasting disease.

XX OS Homo sapiens.

XX PN WO200281625-A2.

XX PD 17-OCT-2002.

XX PF 03-APR-2002; 2002WO-US010366.

XX PR 03-APR-2001; 2001US-0281086P.

XX PR 05-APR-2001; 2001US-0281906P.

XX PR 06-APR-2001; 2001US-0282020P.

XX PR 10-APR-2001; 2001US-0282930P.

XX PR 12-APR-2001; 2001US-0283444P.

XX PR 12-APR-2001; 2001US-0283512P.

XX PR 13-APR-2001; 2001US-0283657P.

XX PR 13-APR-2001; 2001US-0283678P.

XX PR 13-APR-2001; 2001US-0283710P.

XX PR 17-APR-2001; 2001US-0284234P.

XX PR 19-APR-2001; 2001US-0285325P.

XX PR 20-APR-2001; 2001US-0285381P.

XX PR 24-APR-2001; 2001US-0286068P.

XX PR 25-APR-2001; 2001US-0286292P.

XX PR 07-JUN-2001; 2001US-0296692P.



```
RESULT 11
AAU68550
ID AAU68550 standard; protein: 239 AA.
XX
AC AAU68550;
XX
DT 16-JAN-2002 (first entry)
XX
DE Human novel cytokine encoded by cDNA 790CIP2D_11 #1.
XX
KW Human; cytokine; cell proliferation; cell differentiation;
KW anti-inflammatory; stem cell growth factor; activin; inhibin; cancer;
KW nervous system disease; neuropathy; Alzheimer's disease;
KW Parkinson's disease; Huntington's disease; spinal cord disorder;
KW head trauma; stroke; myeloid cell disorder; lymphoid cell disorder;
KW platelet disorder; thrombocytopaenia; stem cell disorder;
KW aplastic anaemia; tissue regeneration; wound healing; ulcer;
KW osteoporosis; osteoarthritis; bone degenerative disorder;
KW periodontal disease; fibrosis; reperfusion; immune disorder; SCID;
KW severe combined immunodeficiency; infection; autoimmune disorder;
KW multiple sclerosis; rheumatoid arthritis; diabetes mellitus; allergy;
KW asthma; coagulation disorder; haemophilia; sepsis; nephritis;
KW inflammatory bowel disease; food supplement; immunogen.
XX
OS Homo sapiens.
XX
XX WO200175093-A1.
XX
XX 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US010484.
XX
XX 31-MAR-2000; 2000US-00540217.
XX 23-AUG-2000; 2000US-00649167.
XX 22-SEP-2000; 2000US-00668680.
XX 23-OCT-2000; 2000US-00895618.
XX 30-NOV-2000; 2000US-00728711.
XX 14-MAR-2001; 2001US-00808701.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Asundi V, Zhou P, Xue AJ, Ren F, Zhang J, Wang J;
XX Xu C, Yang Y, Zahao QA, Chen R, Wang D, Goodrich RW, Liu C;
XX Drmanac RT;
XX
XX WPI: 2001-626432/72.
XX N-PSDB: AAS59642.
XX
XX New polypeptides and nucleic acids, useful for diagnosis, treatment of
XX inflammatory, autoimmune, neurological, myeloid or lymphoid cell, bone
XX degenerative disorders, cancer and promoting wound healing.
XX
XX Claim 20; Page 274; 336pp; English.
XX
XX The invention relates to isolated human polypeptides (which may be
XX cytokines) and the polynucleotides encoding them. The protein is useful
XX for identifying a compound which binds to it (e.g. modulators, agonists
XX and antagonists). The polynucleotides are useful as an array for mismatch
XX detection. The proteins and nucleic acids are useful as nutritional
XX sources or supplements. The protein exhibits activity relating
XX to cytokine, cell proliferation, cell differentiation, antiinflammatory,
XX stem cell growth factor activity, immune stimulating or immune
XX suppressing and activin or inhibin related activities. The proteins (and
XX antibodies raised against them) and nucleic acids are therefore useful in
XX the diagnosis and treatment of diseases and disorders such as cancer,
XX central and peripheral nervous system diseases and neuropathies,
XX Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
XX lateral sclerosis, spinal cord disorders, head trauma, cerebrovascular
XX diseases, stroke, myeloid or lymphoid cell disorders, platelet disorders,
XX thrombocytopaenia, stem cell disorders, aplastic anaemia, for
XX regeneration of bone, cartilage, tendon, ligament and/or nerve tissue
XX growth, and in tissue repair, healing of burns, incisions, ulcers, for
XX treating osteoporosis, osteoarthritis, bone degenerative disorders, or
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CC periodontal disease, lung or liver fibrosis, reperfusion injury in
CC various tissues, various immune deficiencies and disorders including
CC severe combined immunodeficiency (SCID), bacterial or fungal infections,
CC autoimmune disorders (e.g. multiple sclerosis, rheumatoid arthritis,
CC diabetes mellitus, myaesthesia gravis), allergic reactions and conditions,
CC such as asthma or other respiratory problems, coagulation disorders,
CC haemophilia), septic shock, sepsis, arthritis, nephritis and inflammatory
CC bowel disease, viral infection and are useful in altering bodily
CC characteristics. The present sequence represents a novel protein of the
CC invention
XX
XX SQ Sequence 239 AA;
XX
XX Query Match 75.0%; Score 430; DB 4; Length 239;
XX Best Local Similarity 90.9%; Pred. No. 5.2e-46;
XX Matches 80; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
XX
XX Qy 1 MWTKSSLVLLLCUTCSYAFMFSSLRKTSPPQKVGCEHFRIRQNLPEHTQGLGSKW 60
XX Db 69 MWTKSSLVLLLCUTCSYAFMFSSLRKTSPPQKVGCEHFRIRQNLPEHTQGLGSKW 128
XX
XX Qy 61 LWLLFAVVVPFVILKQCRDSEKNKVRMAP 88
XX Db 129 LWLLFAVVVPFVILQCRDSEKNKEQSPP 156
XX
XX RESULT 12
XX ABR58389
XX ID ABR58389 standard; protein: 239 AA.
XX
XX AC ABR58389;
XX
XX DT 07-JUL-2003 (first entry)
XX
XX DE Human NOV13a.
XX
XX KW Human; NOV; antidiabetic; anorectic; antibacterial; virucide;
XX immunomodulator; cytostatic; nootropic; neuroprotective; dyslipidaemia;
XX antiparkinsonian; antilipaeamic; gene therapy; metabolic disorder;
XX diabetes; obesity; infection; cachexia; cancer; Parkinson's disease;
XX neurodegenerative disorder; Alzheimer's disease; immune disorder;
XX haematopoietic disorder.
XX
XX OS Homo sapiens.
XX
XX PN WO2003029423-A2.
XX
XX PD 10-APR-2003.
XX
XX PF 02-OCT-2002; 2002WO-US031358.
XX
XX PR 02-OCT-2001; 2001US-0326483P.
XX PR 05-OCT-2001; 2001US-0327342P.
XX PR 09-OCT-2001; 2001US-0327917P.
XX PR 09-OCT-2001; 2001US-0328029P.
XX PR 09-OCT-2001; 2001US-0328044P.
XX PR 09-OCT-2001; 2001US-0328056P.
XX PR 12-OCT-2001; 2001US-0328849P.
XX PR 15-OCT-2001; 2001US-0329414P.
XX PR 17-OCT-2001; 2001US-0330142P.
XX PR 22-OCT-2001; 2001US-0341058P.
XX PR 24-OCT-2001; 2001US-0339266P.
XX PR 24-OCT-2001; 2001US-0343629P.
XX PR 29-OCT-2001; 2001US-0349575P.
XX PR 01-NOV-2001; 2001US-0346357P.
XX PR 12-APR-2002; 2002US-0371972P.
XX PR 12-APR-2002; 2002US-0371980P.
XX PR 17-APR-2002; 2002US-0373261P.
XX PR 19-APR-2002; 2002US-0373805P.
XX PR 23-APR-2002; 2002US-0374738P.
XX PR 16-MAY-2002; 2002US-0381101P.
XX PR 17-MAY-2002; 2002US-0381635P.
XX PR 29-MAY-2002; 2002US-0383830P.
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PR 01-OCT-2002; 2002US-00262839.
XX (CURA-) CURAGEN CORP.
PA
XX
XX Alsbrook JP, Anderson DW, Boldog FL, Burgess CE, Catterton B;
PI Edinger SR, Ellerman K, Gerlach VL, Gorman L, Guo X, Ji W,
PI Kekuda R, Leach MD, Li L, Miller CE, Patturajan M, Rieger DK;
PI Rothenberg ME, Shimkets RA, Smithson G, Spytek KA, Taupier RJ;
PI Vernet CAM, Voss EZ, Zerhusen BD, Zhong M;
XX
XX WPI: 2003-381625/36.
DR N-PSDB; ACC72103.
DR
XX
XX NOVX polypeptides and nucleic acids useful for diagnosing, preventing or
PT treating NOVX-associated disorders, e.g. diabetes, obesity, cancer or
PT dyslipidemia, and in chromosome mapping, tissue typing or
PT pharmacogenomics.
XX
XX Claim 1; Page 146; 487pp; English.
XX
XX The present invention relates to novel human NOV proteins and their
CC coding sequences (ACC72075-ACC72181 and ABR58363-ABR58469). The NOV
CC proteins are useful in manufacturing a medicament for treating a syndrome
CC associated with a human disease. The NOV proteins and coding sequences
CC may be used to diagnose, treat or prevent metabolic disorders such as
CC diabetes or obesity, infections, cachexia, cancer, neurodegenerative
CC disorders such as Alzheimer's disease or Parkinson's disease, immune
CC disorders, haematopoietic disorders and various dyslipidaemias
XX
XX Sequence 239 AA;
SQ
Query Match 75.0%; Score 430; DB 6; Length 239;
Best Local Similarity 90.9%; Pred. No. 5.2e-46;
Matches 80; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
QY 1 MWTLKSSLVLLCLTCSYAFMFSSLRQKTSEPOGKVPCEGHEFRIRQNLPEHTQGLGSKW 60
Db 69 MWTLKSSLVLLCLTCSYAFMFSSLRQKTSEPOGKVPCEGHEFRIRQNLPEHTQGLGSKW 128
QY 61 LWLLFAVVPFVILKQDSEKKNVMAP 88
Db 129 LWLLFVVVPFVILQCCORDSEKKEQSP 156
RESULT 13
ADS10718
ID ADS10718 standard; protein; 292 AA.
XX
XX ADS10718;
XX
XX 16-DEC-2004 (first entry)
XX
XX Human therapeutic protein - SEQ ID 955.
XX
XX antiinflammatory; neuroprotective; antianaemic; cytostatic; vulnery;
XX inflammatory; haematopoiesis; immunity; neurodegenerative; stem cell;
XX aplastic anaemia; cancer; wound healing, gene therapy.
XX
XX Homo sapiens.
XX
XX WO2004080148-A2.
XX
XX 23-SEP-2004.
XX
XX 30-SEP-2003; 2003WO-US030720.
XX
XX 02-OCT-2002; 2002US-0416186P.
XX
XX (NUVE-) NUVELO INC.
XX
XX Tang YT, Asundi V, Ren F, Zhang J, Zhang J, Wehrman T, Wang Z, Ma Y,
PI Wang D, Chen R, Zhao QA, Wang J, Ghosh M, Xue AJ, Weng G, Zhou P;
XX

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DR WPI; 2004-668857/65.
DR N-PSDB; ADS10034.
XX
XX New polynucleotide, useful in preparing a composition for diagnosing or
PT treating inflammatory, neurodegenerative or stem cell disorders, e.g.,
PT aplastic anemia or cancer for promoting wound healing.
XX
XX Claim 20; SEQ ID NO 955; 718pp; English.
XX
XX The invention relates to a novel isolated polynucleotide and the encoded
CC polypeptide. The molecules of the invention demonstrate antiinflammatory,
CC neuroprotective, antianaemic, cytostatic and vulnerary activities and may
CC be useful in preparing a composition for diagnosing or treating
CC inflammatory, haematopoietic, immune, neurodegenerative or stem cell
CC disorders, such as aplastic anaemia or cancer, as well as for promoting
CC wound healing. The molecules may also be utilised during gene therapy
CC procedures. The current sequence is that of a human therapeutic protein
CC of the invention. The current sequence is not shown explicitly within the
XX CC specification but can be accessed from the WIPO web-site.
SQ Sequence 292 AA;
Query Match 75.0%; Score 430; DB 8; Length 292;
Best Local Similarity 90.9%; Pred. No. 6.6e-46;
Matches 80; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
QY 1 MWTLKSSLVLLCLTCSYAFMFSSLRQKTSEPOGKVPCEGHEFRIRQNLPEHTQGLGSKW 60
Db 122 MWTLKSSLVLLCLTCSYAFMFSSLRQKTSEPOGKVPCEGHEFRIRQNLPEHTQGLGSKW 181
QY 61 LWLLFAVVPFVILKQDSEKKNVMAP 88
Db 182 LWLLFVVVPFVILQCCORDSEKKEQSP 209
RESULT 14
AAV12683
ID AAV12683 standard; protein; 101 AA.
XX
XX AAV12683;
XX
XX 21-JUN-1999 (first entry)
XX
XX Human 5' EST secreted protein SEQ ID NO:273.
XX
XX Human; secreted protein; EST; expressed sequence tag; diagnosis;
XX forensic; gene therapy; chromosome mapping; signal peptide;
XX upstream regulatory sequence; cytokine activity; cell proliferation;
XX differentiation; haematopoiesis regulation; tissue growth regulation;
XX reproductive hormone regulation; chemotactic; chemokinetic; haemostatic;
XX thrombolytic; anti-inflammatory; tumour inhibition.
XX
XX Homo sapiens.
XX
XX WO9906549-A2.
XX
XX 11-FEB-1999.
XX
XX 31-JUL-1998; 98WO-IB001231.
XX
XX 01-AUG-1997; 97US-00905279.
XX
XX (GEST ) GENSET.
XX
XX Dumas Milne Edwards J, Duclert A, Lacroix B;
PI
XX
XX WPI; 1999-153779/13.
DR N-PSDB; AAX51461.
XX
XX New nucleic acids encoding human secreted proteins - obtained from cDNA
PT libraries derived from testis, ovary, uterus and spleen tissue.
XX
XX Claim 34; Page 384; 522pp; English.
PS

```

XX AAX51459 to AAX51691 represent 5' expressed sequence tags (ESTs) for  
CC human secreted proteins, and encode the proteins given in AAX12681 to  
CC AAX12913, respectively. The proteins given represent the signal peptide  
CC and an N-terminal fragment of a secreted protein. The nucleic acid  
CC sequences can be used for producing secreted human gene products. They  
CC can also be used to develop products for diagnosis and therapy. The  
CC proteins obtained may have cytokine activity, cell  
CC proliferation/differentiation activity, haematopoiesis regulating  
CC activity, tissue growth regulating activity, reproductive hormone  
CC regulating activity, chemotactic/chemokinetic activity, haemostatic and  
CC thrombolytic activity, receptor/ligand activity, anti-inflammatory  
CC activity, tumour inhibition activity or other activities. The products  
CC can be used in forensic, gene therapy and chromosome mapping procedures.  
CC The sequences can also be used for obtaining corresponding promoter  
CC sequences. The nucleic acids encoding the signal peptide can be used for  
CC directing extracellular secretion of a polypeptide or the insertion of a  
CC polypeptide into a membrane, or importing a polypeptide into a cell  
XX  
SQ Sequence 101 AA;

Query Match 73.8%; Score 423; DB 2; Length 101;  
Best Local Similarity 89.8%; Pred. No. 1.4e-45;  
Matches 79; Conservative 2; Mismatches 7; Indels 0; Gaps 0;  
Qy 1 MWTLKSSILVLLCLTCSYAFMFSSLRQKTSPEQGVKPCGEHFRIRQNLPEHTQGLGSKW 60  
Db 1 MWTLKSSILVLLCLTCSYAFMFSSLRQKTSPEQGVKPCGEHFRIRQNLPEHTQGLGSKW 60  
Qy 61 LWLLFAVVVPFVILKCORDSEKKNVRRMAP 88  
Db 61 LWLLXVVVPFVILQCRDSEKKNQSP 88

RESULT 15  
AAG00463  
ID AAG00463 standard; protein; 101 AA.  
XX  
AC AAG00463;  
XX  
DT 06-OCT-2000 (first entry)  
XX  
DE Human secreted protein, SEQ ID NO: 4544.  
XX  
KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;  
KW gene therapy; chromosome mapping.  
XX  
OS Homo sapiens.  
XX  
FN EPI033401-A2.  
XX  
PD 06-SEP-2000.  
XX  
PF 21-FEB-2000; 2000EP-00200610.  
XX  
PR 26-FEB-1999; 99US-0122487P.  
XX  
PA (GEST ) GENSET.  
XX  
PI Dumas Milne Edwards J, Duclert A, Giordano J;  
XX  
DR WPI; 2000-500381/45.  
DR N-PSDB; AAC00469.  
XX  
PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for  
PT obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for  
PT diagnostic, forensic, gene therapy and chromosome mapping procedures.  
XX  
PS Claim 13; SEQ ID NO 4544; 71pp + Sequence Listing; English.  
XX  
XX The present sequence is a polypeptide encoded by one of a large number of  
CC 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were  
CC prepared from total human RNAs or polyA+ RNAs derived from 30 different

CC tissues. EST sequences usually correspond mainly to the 3' untranslated  
CC region (UTR) of the mRNA because they are often obtained from oligo-dT  
CC primed cDNA libraries. Such ESTs are not well suited for isolating cDNA  
CC sequences derived from the 5' ends of mRNAs and even in those cases where  
CC longer cDNA sequences have been obtained, the full 5' UTR is rarely  
CC included. 5' ESTs are derived from mRNAs with intact 5' ends and can  
CC therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs  
CC are also used in diagnostic, forensic, gene therapy and chromosome  
CC mapping procedures. They are used to obtain upstream regulatory sequences  
CC and to design expression and secretion vectors  
XX

SQ Sequence 101 AA;  
Query Match 73.8%; Score 423; DB 3; Length 101;  
Best Local Similarity 89.8%; Pred. No. 1.4e-45;  
Matches 79; Conservative 2; Mismatches 7; Indels 0; Gaps 0;  
Qy 1 MWTLKSSILVLLCLTCSYAFMFSSLRQKTSPEQGVKPCGEHFRIRQNLPEHTQGLGSKW 60  
Db 1 MWTLKSSILVLLCLTCSYAFMFSSLRQKTSPEQGVKPCGEHFRIRQNLPEHTQGLGSKW 60  
Qy 61 LWLLFAVVVPFVILKCORDSEKKNVRRMAP 88  
Db 61 LWLLXVVVPFVILQCRDSEKKNQSP 88

Search completed: October 11, 2005, 07:11:04  
Job time : 80.508 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 11, 2005, 06:57:16 ; Search time 177.706 Seconds  
(without alignments)  
248.149 Million cell updates/sec

Title: US-10-092-934-4

Perfect score: 573

Sequence: 1 MWTLKSLVLLCLTCSYAF.....APFLHHIDSISGVSGKRMF 106

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1854112 seqs, 416015017 residues

Total number of hits satisfying chosen parameters: 1854112

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*
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- 11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*
- 13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep.\*
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- 15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/2/pubpaa/US10D\_PUBCOMB.pep.\*
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- 19: /cgn2\_6/ptodata/2/pubpaa/US11A\_PUBCOMB.pep.\*
- 20: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep.\*
- 21: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*
- 22: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	573	100.0	106	14	US-10-138-516-3
2	573	100.0	106	14	US-10-146-130-5
3	573	100.0	106	14	US-10-092-934-4
4	573	100.0	106	14	US-10-153-334-4
5	573	100.0	106	14	US-10-198-069-4
6	573	100.0	106	14	US-10-198-070-4
7	573	100.0	106	14	US-10-294-891-3
8	573	100.0	106	17	US-10-920-313-3
9	453	79.1	171	14	US-10-114-153-30
10	430	75.0	171	16	US-10-821-273-70
11	430	75.0	239	9	US-09-808-701A-28

12	430	75.0	239	14	US-10-233-131-28	Sequence 28, Appl
13	430	75.0	239	15	US-10-240-145-80	Sequence 80, Appl
14	430	75.0	239	15	US-10-262-839-54	Sequence 54, Appl
15	430	75.0	239	18	US-10-291-128-80	Sequence 80, Appl
16	358	62.5	156	14	US-10-114-153-36	Sequence 36, Appl
17	358	62.5	156	14	US-10-114-153-40	Sequence 40, Appl
18	358	62.5	156	14	US-10-114-153-42	Sequence 42, Appl
19	354	61.8	156	14	US-10-114-153-38	Sequence 38, Appl
20	339	59.2	156	14	US-10-114-153-44	Sequence 44, Appl
21	252	44.0	47	14	US-10-114-153-32	Sequence 32, Appl
22	233	40.7	47	14	US-10-114-153-34	Sequence 34, Appl
23	92	16.1	15	14	US-10-294-891-26	Sequence 26, Appl
24	92	16.1	15	17	US-10-920-313-26	Sequence 26, Appl
25	87	15.2	15	14	US-10-294-891-25	Sequence 25, Appl
26	87	15.2	15	17	US-10-920-313-25	Sequence 25, Appl
27	83	14.5	16	14	US-10-294-891-29	Sequence 29, Appl
28	83	14.5	16	17	US-10-920-313-29	Sequence 29, Appl
29	80	14.0	15	14	US-10-294-891-27	Sequence 27, Appl
30	80	14.0	15	17	US-10-920-313-27	Sequence 27, Appl
31	80	14.0	545	15	US-10-112-944-480	Sequence 480, App
32	78.5	13.7	111	17	US-10-732-620-51	Sequence 51, Appl
33	78.5	13.7	111	17	US-10-732-620-52	Sequence 52, Appl
34	78	13.6	15	14	US-10-294-891-28	Sequence 28, Appl
35	78	13.6	15	17	US-10-920-313-28	Sequence 28, Appl
36	77	13.4	15	14	US-10-294-891-24	Sequence 24, Appl
37	77	13.4	15	17	US-10-920-313-24	Sequence 24, Appl
38	76	13.3	15	14	US-10-294-891-23	Sequence 23, Appl
39	76	13.3	15	17	US-10-920-313-23	Sequence 23, Appl
40	74.5	13.0	380	15	US-10-094-749-2909	Sequence 2909, Ap
41	74.5	13.0	470	11	US-09-922-181A-7	Sequence 7, Appli
42	74.5	13.0	544	11	US-09-922-181A-3	Sequence 3, Appli
43	74.5	13.0	683	18	US-10-631-467-660	Sequence 660, App
44	73.5	12.8	217	18	US-10-450-763-34428	Sequence 34428, A
45	73.5	12.8	586	18	US-10-450-763-40995	Sequence 40995, A

ALIGNMENTS

RESULT 1  
US-10-138-516-3  
; Sequence 3, Application US/10138516  
; Publication No. US20030003445A1  
; GENERAL INFORMATION:  
; APPLICANT: AVERBACK, PAUL  
; TITLE OF INVENTION: METHOD OF PREVENTING CELL DEATH USING ANTIBODIES TO  
; TITLE OF INVENTION: NEURAL THREAD PROTEINS  
; FILE REFERENCE: 59003.000004  
; CURRENT APPLICATION NUMBER: US/10/138,516  
; CURRENT FILING DATE: 2002-07-23  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 106  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-138-516-3

Query Match 100.0%; Score 573; DB 14; Length 106;  
Best Local Similarity 100.0%; Pred. No. 7.3e-60;  
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MWTLKSLVLLCLTCSYAFMFSSLRKTSPEQKVPQCGEHRIRQNLPEHTQGLGSKW	60
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Qy	61	LWLLFAVVPFVLKCORDSEKNKVRMAPFFLHHIDISISGVSGKRMF	106
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RESULT 2  
US-10-146-130-5

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; Sequence 5, Application US/10146130
; Publication No. US20030004107A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; TITLE OF INVENTION: METHOD OF PREVENTING CELL DEATH USING SEGMENTS OF
; TITLE OF INVENTION: NEURAL THREAD PROTEINS
; FILE REFERENCE: 59003.000007
; CURRENT APPLICATION NUMBER: US/10/146,130
; CURRENT FILING DATE: 2002-08-06
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-146-130-5

Query Match      100.0%; Score 573; DB 14; Length 106;
Best Local Similarity 100.0%; Pred. No. 7.3e-60;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MWTLKSSLVLLCLTCSYAFMFSSLRQKTSEPOGKVPCEGHEFRIRQNLPEHTQGLGSKW 60
Db 1 MWTLKSSLVLLCLTCSYAFMFSSLRQKTSEPOGKVPCEGHEFRIRQNLPEHTQGLGSKW 60
QY 61 LWLLFAVVPFVILKCORDSEKKNVRMAPFFLHHIDSISGVSGKRMF 106
Db 61 LWLLFAVVPFVILKCORDSEKKNVRMAPFFLHHIDSISGVSGKRMF 106

RESULT 3
US-10-092-934-4
; Sequence 4, Application US/10092934
; Publication No. US20030054990A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; TITLE OF INVENTION: METHODS OF USING NEURAL THREAD PROTEINS TO TREAT TUMORS
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 018792-0199
; CURRENT APPLICATION NUMBER: US/10/092,934
; CURRENT FILING DATE: 2002-06-05
; PRIOR FILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-092-934-4

Query Match      100.0%; Score 573; DB 14; Length 106;
Best Local Similarity 100.0%; Pred. No. 7.3e-60;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MWTLKSSLVLLCLTCSYAFMFSSLRQKTSEPOGKVPCEGHEFRIRQNLPEHTQGLGSKW 60
Db 1 MWTLKSSLVLLCLTCSYAFMFSSLRQKTSEPOGKVPCEGHEFRIRQNLPEHTQGLGSKW 60
QY 61 LWLLFAVVPFVILKCORDSEKKNVRMAPFFLHHIDSISGVSGKRMF 106
Db 61 LWLLFAVVPFVILKCORDSEKKNVRMAPFFLHHIDSISGVSGKRMF 106

RESULT 4
US-10-153-334-4
; Sequence 4, Application US/10153334
; Publication No. US20030096350A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF

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; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 59003-000006
; CURRENT APPLICATION NUMBER: US/10/153,334
; CURRENT FILING DATE: 2002-05-24
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-153-334-4

Query Match      100.0%; Score 573; DB 14; Length 106;
Best Local Similarity 100.0%; Pred. No. 7.3e-60;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MWTLKSSLVLLCLTCSYAFMFSSLRQKTSEPOGKVPCEGHEFRIRQNLPEHTQGLGSKW 60
Db 1 MWTLKSSLVLLCLTCSYAFMFSSLRQKTSEPOGKVPCEGHEFRIRQNLPEHTQGLGSKW 60
QY 61 LWLLFAVVPFVILKCORDSEKKNVRMAPFFLHHIDSISGVSGKRMF 106
Db 61 LWLLFAVVPFVILKCORDSEKKNVRMAPFFLHHIDSISGVSGKRMF 106

RESULT 5
US-10-198-069-4
; Sequence 4, Application US/10198069
; Publication No. US20030096756A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 59003.000009
; CURRENT APPLICATION NUMBER: US/10/198,069
; CURRENT FILING DATE: 2002-07-19
; PRIOR FILING DATE: 2001-07-19
; PRIOR FILING DATE: 2001-07-19
; PRIOR FILING DATE: 2001-07-19
; PRIOR FILING DATE: 2001-07-19
; PRIOR FILING DATE: 2001-07-19
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-198-069-4

Query Match      100.0%; Score 573; DB 14; Length 106;
Best Local Similarity 100.0%; Pred. No. 7.3e-60;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MWTLKSSLVLLCLTCSYAFMFSSLRQKTSEPOGKVPCEGHEFRIRQNLPEHTQGLGSKW 60
Db 1 MWTLKSSLVLLCLTCSYAFMFSSLRQKTSEPOGKVPCEGHEFRIRQNLPEHTQGLGSKW 60
QY 61 LWLLFAVVPFVILKCORDSEKKNVRMAPFFLHHIDSISGVSGKRMF 106
Db 61 LWLLFAVVPFVILKCORDSEKKNVRMAPFFLHHIDSISGVSGKRMF 106

RESULT 6
US-10-198-070-4
; Sequence 4, Application US/10198070
; Publication No. US20030109437A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; APPLICANT: GEMMELL, JACK

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; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 59003.000008
; CURRENT APPLICATION NUMBER: US/10/198,070
; CURRENT FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/306,161
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/306,150
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/331,477
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-198-070-4

Query Match      100.0%; Score 573; DB 14; Length 106;
Best Local Similarity 100.0%; Pred. No. 7.3e-60;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MWTLKSSLVLLCLTCSYAFMFSSLRQKTSBPQGVPCGEHFRIRQNLPEHTQGLGSKW 60
Db 1 MWTLKSSLVLLCLTCSYAFMFSSLRQKTSBPQGVPCGEHFRIRQNLPEHTQGLGSKW 60

Qy 61 LWLLFAVVPFVLKQORDSEKNKVRMAPFFLHHIDISGVSGKRMF 106
Db 61 LWLLFAVVPFVLKQORDSEKNKVRMAPFFLHHIDISGVSGKRMF 106

RESULT 7
US-10-294-891-3
; Sequence 3, Application US/10294891
; Publication No. US20030166569A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; APPLICANT: GENMEL, JACK
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; FILE REFERENCE: 59003.000010
; CURRENT APPLICATION NUMBER: US/10/294,891
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: 60/331,447
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-294-891-3

Query Match      100.0%; Score 573; DB 14; Length 106;
Best Local Similarity 100.0%; Pred. No. 7.3e-60;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MWTLKSSLVLLCLTCSYAFMFSSLRQKTSBPQGVPCGEHFRIRQNLPEHTQGLGSKW 60
Db 1 MWTLKSSLVLLCLTCSYAFMFSSLRQKTSBPQGVPCGEHFRIRQNLPEHTQGLGSKW 60

Qy 61 LWLLFAVVPFVLKQORDSEKNKVRMAPFFLHHIDISGVSGKRMF 106
Db 61 LWLLFAVVPFVLKQORDSEKNKVRMAPFFLHHIDISGVSGKRMF 106

RESULT 8
US-10-920-313-3
; Sequence 3, Application US/10920313
; Publication No. US20050032704A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; APPLICANT: GENMEL, JACK
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; FILE REFERENCE: 59003.000010
; CURRENT APPLICATION NUMBER: US/10/920,313
; CURRENT FILING DATE: 2004-08-18
; PRIOR APPLICATION NUMBER: 60/331,447
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-920-313-3

Query Match      100.0%; Score 573; DB 17; Length 106;
Best Local Similarity 100.0%; Pred. No. 7.3e-60;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MWTLKSSLVLLCLTCSYAFMFSSLRQKTSBPQGVPCGEHFRIRQNLPEHTQGLGSKW 60
Db 1 MWTLKSSLVLLCLTCSYAFMFSSLRQKTSBPQGVPCGEHFRIRQNLPEHTQGLGSKW 60

Qy 61 LWLLFAVVPFVLKQORDSEKNKVRMAPFFLHHIDISGVSGKRMF 106
Db 61 LWLLFAVVPFVLKQORDSEKNKVRMAPFFLHHIDISGVSGKRMF 106

RESULT 9
US-10-114-153-30
; Sequence 30, Application US/10114153
; Publication No. US20030185815A1
; GENERAL INFORMATION:
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Shenoy, Sureesh
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Rastelli, Luca
; APPLICANT: Mezes, Peter
; APPLICANT: Smithson, Glennnda
; APPLICANT: Guo, Xiaojia
; APPLICANT: Gerlach, Valerie
; APPLICANT: Casman, Stacie
; APPLICANT: Boldog, Ferenc
; APPLICANT: Li, Li
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Tchernev, Velizar
; APPLICANT: Gangolli, Esha
; APPLICANT: Vernet, Corine
; APPLICANT: Spytek, Kimberly
; APPLICANT: Malyankar, Uriel
; APPLICANT: Patturajan, Meera
; APPLICANT: Miller, Charles
; APPLICANT: Taupier, Raymond J. Jr.
; APPLICANT: Heyes, Melvyn
; APPLICANT: Ju, Jingfang
; APPLICANT: Peyman, John
; APPLICANT: Catterton, Elina
; APPLICANT: MacDougall, John
; APPLICANT: Edinger, Shlomit
; APPLICANT: Stone, David
; APPLICANT: Mazur, Ann
; TITLE OF INVENTION: NOVEL ANTIBODIES THAT BIND TO ANTIGENIC POLYPEPTIDES, NUCLEIC ACI
; TITLE OF INVENTION: ENCODING THE ANTIGENS, AND METHODS OF USE
; FILE REFERENCE: 21402-322A
; CURRENT APPLICATION NUMBER: US/10/114,153
; CURRENT FILING DATE: 2002-08-06
; PRIOR APPLICATION NUMBER: 60/281086
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281906
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/282020
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; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/282930
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/283512
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/283444
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/283657
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283710
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283678
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284234
; PRIOR FILING DATE: 2001-04-17
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 251
; SEQ ID NO 30
; LENGTH: 171
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-114-153-30

Query Match          79.1%; Score 453; DB 14; Length 171;
Best Local Similarity 94.3%; Pred. No. 2.2e-45;
Matches 83; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 MWTLKSSLVLLCLTCSYAFMFSSLRQKTSEPOGKVPCEGHEFRIRQNLPEHTQGLGSKW 60
DB 1 MWTLKSSLVLLCLTCSYAFMFSSLRQKTSEPOGKVPCEGHEFRIRQNLPEHTQGLGSKW 60

QY 61 LLLFAVVPFVILKCORDSEKKNVRMAP 88
DB 61 LLLFAVVPFVILKCORDSEKKNVRMAP 88

RESULT 10
US-10-821-273-70
; Sequence 70, Application US/10821273
; Publication No. US20040248256A1
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: Lavallie, Edward R.
; APPLICANT: Collins-Racie, Lisa A.
; APPLICANT: Evans, Cheryl
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Agostino, Michael J.
; APPLICANT: Steinger II, Robert J.
; APPLICANT: Bowman, Michael R.
; APPLICANT: Diblasio-Smith, Elizabeth
; APPLICANT: Widom, Angela
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: 00766.000101.
; CURRENT APPLICATION NUMBER: US/10/821,273
; CURRENT FILING DATE: 2004-04-09
; PRIOR APPLICATION NUMBER: US 09/306,111
; PRIOR FILING DATE: 1999-05-06
; PRIOR APPLICATION NUMBER: US 60/084,564
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: US 60/087,645
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: US 60/093,712
; PRIOR FILING DATE: 1998-07-22
; PRIOR APPLICATION NUMBER: US 60/094,935
; PRIOR FILING DATE: 1998-07-31
; PRIOR APPLICATION NUMBER: US 60/095,880
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: US 60/096,068
; PRIOR FILING DATE: 1998-08-11
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 70
; LENGTH: 171
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-273-70

Query Match          75.0%; Score 430; DB 16; Length 171;
Best Local Similarity 90.9%; Pred. No. 1.2e-42;
Matches 80; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 MWTLKSSLVLLCLTCSYAFMFSSLRQKTSEPOGKVPCEGHEFRIRQNLPEHTQGLGSKW 60
DB 1 MWTLKSSLVLLCLTCSYAFMFSSLRQKTSEPOGKVPCEGHEFRIRQNLPEHTQGLGSKW 60

QY 61 LLLFAVVPFVILKCORDSEKKNVRMAP 88
DB 61 LLLFAVVPFVILKCORDSEKKNVRMAP 88

RESULT 11
US-09-808-701A-28
; Sequence 28, Application US/09808701A
; Publication No. US20020146757A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Goodrich, Ryle
; APPLICANT: Asundi, Vinod
; APPLICANT: Dmanac, Radoje T.
; TITLE OF INVENTION: No. 6610536el Nucleic Acids and
; FILE REFERENCE: 790CIP2D
; CURRENT APPLICATION NUMBER: US/09/808,701A
; CURRENT FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: pt_FL_genes Version 2.0
; SEQ ID NO 28
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-808-701A-28

Query Match          75.0%; Score 430; DB 9; Length 239;
Best Local Similarity 90.9%; Pred. No. 1.8e-42;
Matches 80; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 MWTLKSSLVLLCLTCSYAFMFSSLRQKTSEPOGKVPCEGHEFRIRQNLPEHTQGLGSKW 60
DB 69 MWTLKSSLVLLCLTCSYAFMFSSLRQKTSEPOGKVPCEGHEFRIRQNLPEHTQGLGSKW 128

QY 61 LLLFAVVPFVILKCORDSEKKNVRMAP 88
DB 129 LLLFAVVPFVILKCORDSEKKNVRMAP 156

RESULT 12
US-10-233-131-28
; Sequence 28, Application US/10233131
; Publication No. US20030096279A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Xue, Aidong J.
; APPLICANT: Ren, Felyan
; APPLICANT: Wang, Dunrui
; APPLICANT: Chen, Rui-hong
```

APPLICANT: Drmanac, Radoje T.  
TITLE OF INVENTION: No. US20030096279A1el Nucleic Acids and  
FILE REFERENCE: 790CIP2D DIVA  
CURRENT APPLICATION NUMBER: US/10/233,131  
CURRENT FILING DATE: 2002-08-29  
PRIOR APPLICATION NUMBER: 09/808,701  
PRIOR FILING DATE: 2001-03-14  
PRIOR APPLICATION NUMBER: 09/649,167  
PRIOR FILING DATE: 2000-08-23  
PRIOR APPLICATION NUMBER: 09/540,217  
PRIOR FILING DATE: 2000-03-31  
NUMBER OF SEQ ID NOS: 34  
SOFTWARE: pt\_FL\_genes Version 2.0  
SEQ ID NO 28  
LENGTH: 239  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-233-131-28

Query Match 75.0%; Score 430; DB 14; Length 239;  
Best Local Similarity 90.9%; Pred. No. 1.8e-42;  
Matches 80; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 MWTLKSSIVLLCLTCSYAFMFSSLRKTSPPQGVKPCGGEHFRIRQNLPEHTQGLGSKW 60  
Db 69 MWTLKSSIVLLCLTCSYAFMFSSLRKTSPPQGVKPCGGEHFRIRQNLPEHTQGLGSKW 128

Qy 61 LWLFAVVVPFVILKCORDSEKNKVRMAP 88  
Db 129 LWLFAVVVPFVILQCRDSEKNKEQSPP 156

RESULT 13  
US-10-240-145-80  
Sequence 80, Application US/10240145  
Publication No. US20030235883A1  
GENERAL INFORMATION:  
APPLICANT: Hyseq, Inc  
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES  
CURRENT APPLICATION NUMBER: US/10/240,145  
CURRENT FILING DATE: 2002-09-27  
PRIOR APPLICATION NUMBER: 09/540,217  
PRIOR FILING DATE: 2000-03-31  
PRIOR APPLICATION NUMBER: 09/649,167  
PRIOR FILING DATE: 2000-08-23  
PRIOR APPLICATION NUMBER: 09/668,680  
PRIOR FILING DATE: 2000-09-22  
PRIOR APPLICATION NUMBER: 09/695,618  
PRIOR FILING DATE: 2000-10-23  
PRIOR APPLICATION NUMBER: 09/728,711  
PRIOR FILING DATE: 2000-11-30  
PRIOR APPLICATION NUMBER: NOT YET ASSIGNED  
PRIOR FILING DATE: 2000-03-14  
NUMBER OF SEQ ID NOS: 172  
SOFTWARE: Custom  
SEQ ID NO 80  
LENGTH: 239  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-240-145-80

Query Match 75.0%; Score 430; DB 15; Length 239;  
Best Local Similarity 90.9%; Pred. No. 1.8e-42;  
Matches 80; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MWTLKSSIVLLCLTCSYAFMFSSLRKTSPPQGVKPCGGEHFRIRQNLPEHTQGLGSKW 60  
Db 69 MWTLKSSIVLLCLTCSYAFMFSSLRKTSPPQGVKPCGGEHFRIRQNLPEHTQGLGSKW 128

Qy 61 LWLFAVVVPFVILKCORDSEKNKVRMAP 88  
Db 129 LWLFAVVVPFVILQCRDSEKNKEQSPP 156

Db 129 LWLFAVVVPFVILQCRDSEKNKEQSPP 156

RESULT 14  
US-10-262-839-54  
Sequence 54, Application US/10262839  
Publication No. US20040038877A1  
GENERAL INFORMATION:  
APPLICANT: Alsbrook, John,  
APPLICANT: Anderson, David W.,  
APPLICANT: Boldog, Ferenc,  
APPLICANT: Burgess, Catherine,  
APPLICANT: Catterton, Elina,  
APPLICANT: Edinger, Shlomit,  
APPLICANT: Ellerman, Karen,  
APPLICANT: Gerlach, Valerie,  
APPLICANT: Gorman, Linda,  
APPLICANT: Guo, Xiaojia,  
APPLICANT: Ji, Weizhen,  
APPLICANT: Kekuda, Ramesh,  
APPLICANT: Leach, Martin,  
APPLICANT: Li, Li,  
APPLICANT: Miller, Charles,  
APPLICANT: Patturajan, Meera,  
APPLICANT: Reiger, Daniel,  
APPLICANT: Rothenberg, Mark,  
APPLICANT: Shimkets, Richard,  
APPLICANT: Smithson, Glennda,  
APPLICANT: Spytek, Kimberly,  
APPLICANT: Taupier, Raymond, Jr.,  
APPLICANT: Vernet, Corine,  
APPLICANT: Voss, Edward,  
APPLICANT: Zerhusen, Brian,  
APPLICANT: Zhong, Mei  
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD  
FILE REFERENCE: 21402-462A  
CURRENT APPLICATION NUMBER: US/10/262,839  
CURRENT FILING DATE: 2002-10-01  
PRIOR APPLICATION NUMBER: 60/326,483  
PRIOR FILING DATE: 2001-10-02  
PRIOR APPLICATION NUMBER: 60/327,917  
PRIOR FILING DATE: 2001-10-09  
PRIOR APPLICATION NUMBER: 60/328,029  
PRIOR FILING DATE: 2001-10-09  
PRIOR APPLICATION NUMBER: 60/328,056  
PRIOR FILING DATE: 2001-10-09  
PRIOR APPLICATION NUMBER: 60/381,101  
PRIOR FILING DATE: 2002-05-16  
PRIOR APPLICATION NUMBER: 60/371,972  
PRIOR FILING DATE: 2002-04-12  
PRIOR APPLICATION NUMBER: 60/327,342  
PRIOR FILING DATE: 2001-10-05  
PRIOR APPLICATION NUMBER: 60/328,044  
PRIOR FILING DATE: 2001-10-09  
PRIOR APPLICATION NUMBER: 60/328,849  
PRIOR FILING DATE: 2001-10-12  
PRIOR APPLICATION NUMBER: 60/374,738  
PRIOR FILING DATE: 2002-04-23  
Remaining Prior Application data removed - See File wrapper or PALM.  
NUMBER OF SEQ ID NOS: 367  
SOFTWARE: Curaseqlist version 0.1  
SEQ ID NO 54  
LENGTH: 239  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-262-839-54

Query Match 75.0%; Score 430; DB 15; Length 239;  
Best Local Similarity 90.9%; Pred. No. 1.8e-42;  
Matches 80; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 MWTLKSSIVLLCLTCSYAFMFSSLRKTSPPQGVKPCGGEHFRIRQNLPEHTQGLGSKW 60  
Db 129 LWLFAVVVPFVILQCRDSEKNKEQSPP 156

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Db      69  MMTLKSSLLVLLCLTCSYAFMFSSLRQNTSEPOGKVQYGEHFRIRQNLPEHTQGLGSKW 128

Qy      61  LMLLFAWPFVILKCQDSEKQKVRMAP 88
         ||||| |||||:||||| : |
Db      129 LMLLFWVPFVILQCDSEKQKESPP 156

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RESULT 15

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US-10-291-128-80
; Sequence 80, Application US/10291128
; Publication No. US2005020422A1
; GENERAL INFORMATION:
; APPLICANT: Nuvelo, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP4
; CURRENT APPLICATION NUMBER: US/10/291.128
; CURRENT FILING DATE: 2002-11-08
; PRIORITY APPLICATION NUMBER: PCT/US01/10484
; PRIORITY FILING DATE: 2001-03-30
; PRIORITY APPLICATION NUMBER: 09/540,217
; PRIORITY FILING DATE: 2000-03-31
; PRIORITY APPLICATION NUMBER: 09/649,167
; PRIORITY FILING DATE: 2000-08-23
; PRIORITY APPLICATION NUMBER: 09/668,680
; PRIORITY FILING DATE: 2000-09-22
; PRIORITY APPLICATION NUMBER: 09/695,618
; PRIORITY FILING DATE: 2000-10-23
; PRIORITY APPLICATION NUMBER: 09/728,711
; PRIORITY FILING DATE: 2000-11-30
; PRIORITY APPLICATION NUMBER: 09/808,701
; PRIORITY FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 172
; SOFTWARE: Custom
; SEQ ID NO 80
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-291-128-80

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Query Match      75.0%; Score 430; DB 18; Length 239;
Best Local Similarity 90.9%; Pred. No. 1.8e-42;
Matches 80; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
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Db	69	MWTLKSSVLLLLCLTCSVAFNPSSLRKTSPOGKVGCBHFRIQNLPHTQGNLGSKW	128
Qy	61	LWLLFAVVPFVILKCQDSEKNKVRMAP	88
Db	129	LWLLFAVVPFVILKCQDSEKNKVRMAP	156

Search completed: October 11, 2005, 07:39:44  
Job time : 178.706 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 11, 2005, 06:57:19 ; Search time 24.2326 Seconds  
(without alignments)  
326.535 Million cell updates/sec

Title: US-10-092-934-4  
Perfect score: 573  
Sequence: 1 MWTKSSLVLLCLTCSYAF.....APFLKHIDISGVSGKRMF 106

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	430	75.0	239	4	US-09-808-701A-28
2	423	73.8	101	4	US-09-513-999C-4544
3	422	73.6	138	4	US-09-621-976-3898
4	74.5	13.0	698	4	US-09-949-016-11419
5	69	12.0	248	4	US-09-270-767-44243
6	68	11.9	1125	4	US-09-949-016-10194
7	67	11.7	508	4	US-09-328-352-6467
8	66.5	11.6	1021	4	US-09-252-991A-19205
9	66	11.5	733	4	US-09-949-016-7651
10	65.5	11.4	270	4	US-09-107-532A-5444
11	65.5	11.4	364	4	US-09-270-767-42122
12	65	11.3	625	4	US-09-949-016-9694
13	64	11.2	421	4	US-09-252-991A-17417
14	64	11.2	810	4	US-09-538-092-1275
15	63.5	11.1	639	4	US-09-949-016-9434
16	63.5	11.1	685	4	US-09-949-016-8627
17	63.5	11.1	1290	4	US-09-538-092-956
18	63.5	11.1	1312	4	US-09-949-016-10141
19	62.5	10.9	403	4	US-10-017-372E-21
20	62.5	10.9	407	4	US-10-017-372E-17
21	62	10.8	542	4	US-09-389-956-78
22	62	10.8	714	4	US-09-492-709A-253
23	62	10.8	733	4	US-09-489-039A-12568
24	61	10.6	285	1	US-08-292-045-5
25	61	10.6	543	4	US-09-362-123A-4
26	60.5	10.6	173	1	US-08-157-005-8
27	60.5	10.6	173	2	US-08-799-464A-24

28	60.5	10.6	173	3	US-08-747-863-8	Sequence 8, Appli
29	60.5	10.6	173	4	US-09-565-864-8	Sequence 8, Appli
30	60.5	10.6	173	4	US-08-301-435-24	Sequence 24, Appli
31	60.5	10.6	173	4	US-10-226-065-8	Sequence 8, Appli
32	60.5	10.6	173	5	PCT-US95-09927-24	Sequence 24, Appli
33	60.5	10.6	173	5	PCT-US95-10904-24	Sequence 24, Appli
34	60.5	10.6	295	2	US-08-481-956A-9	Sequence 9, Appli
35	60.5	10.6	295	2	US-08-629-291A-9	Sequence 9, Appli
36	60.5	10.6	295	2	US-08-658-335B-9	Sequence 9, Appli
37	60.5	10.6	295	4	US-09-406-640-9	Sequence 9, Appli
38	60.5	10.6	642	4	US-09-949-016-6986	Sequence 6986, Ap
39	60.5	10.6	648	4	US-09-949-016-10374	Sequence 10374, A
40	60.5	10.6	1214	4	US-09-949-016-6885	Sequence 6885, Ap
41	60.5	10.6	1318	4	US-09-949-016-7130	Sequence 7130, Ap
42	60.5	10.6	1464	1	US-08-026-138E-1	Sequence 1, Appli
43	60.5	10.6	1464	3	US-08-436-328B-10	Sequence 10, Appli
44	60.5	10.6	1464	4	US-08-217-704C-2	Sequence 2, Appli
45	60.5	10.6	1464	4	US-09-949-016-8311	Sequence 8311, Ap

ALIGNMENTS

RESULT 1

US-09-808-701A-28  
; Sequence 28, Application US/09808701A  
; Patent No. 6610536  
; GENERAL INFORMATION:  
; APPLICANT: Tang, Y. Tom  
; APPLICANT: Goodrich, Ryle  
; APPLICANT: Asundi, Vinod  
; APPLICANT: Drmanac, Radoje T.  
; TITLE OF INVENTION: No. 6610536el Nucleic Acids and  
; TITLE OF INVENTION: Polypeptides  
; FILE REFERENCE: 790CIP2D  
; CURRENT APPLICATION NUMBER: US/09/808,701A  
; CURRENT FILING DATE: 2002-03-14  
; PRIOR APPLICATION NUMBER: 09/649,167  
; PRIOR FILING DATE: 2000-08-23  
; PRIOR APPLICATION NUMBER: 09/540,217  
; PRIOR FILING DATE: 2000-03-31  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: pc\_fl\_genes Version 2.0  
; SEQ ID NO 28  
; LENGTH: 239  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-808-701A-28

Query Match 75.0%; Score 430; DB 4; Length 239;  
Best Local Similarity 90.9%; Pred. No. 1.7e-46;  
Matches 80; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Oy	1	MWTKSSLVLLCLTCSYAFMFSSLRKTSPOQKVPQCGEHFRIRQNLPEHTQGLGSKW	60
Db	69	MWTKSSLVLLCLTCTAFMFSSLRKTSPOQKVPQCGEHFRIRQNLPEHTQGLGSKW	128
Oy	61	LWLLFAVVVPFVILKCORDSEKNKVRMAP	88
Db	129	LWLLFAVVVPFVILKCORDSEKNKQSP	156

RESULT 2

US-09-513-999C-4544  
; Sequence 4544, Application US/09513999C  
; Patent No. 6783961  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Duclert, A.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
; Patent No. 6783961  
; FILE REFERENCE: 59. US2.REG





Qy 62 WLLFAVVPFVILKCQDS 79  
: || | || | :  
Db 452 TMLFELVETIVILALDHT 469

[illegible]



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; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 17417
; LENGTH: 421
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-17417

Query Match      11.2%; Score 64; DB 4; Length 421;
Best Local Similarity 44.7%; Pred. No. 12;
Matches 17; Conservative 5; Mismatches 12; Indels 4; Gaps 1;

Qy 31 EPQGVKPCGEHFRIRQNLPEHTQGLGSKWLWLLFAVV 68
Db 2 EPFRGGSGPHWRVRGLP---CRPGVEALFQLFAVV 35

RESULT 14
US-09-538-092-1275
; Sequence 1275, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Giot, Loic
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CuratPatSeqFormatter Version 0.9
; SEQ ID NO 1275
; LENGTH: 810
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number Q06730
US-09-538-092-1275

Query Match      11.2%; Score 64; DB 4; Length 810;
Best Local Similarity 27.8%; Pred. No. 28;
Matches 22; Conservative 10; Mismatches 31; Indels 16; Gaps 4;

Qy 13 CLTCSYAFMFSS---LRQKTS---EPQGVKPCGEHFRIRQNLPEHTQGLGSKWLWLLFA 66
Db 414 CNACGKTFCKQSDLTGKHQTHHTGLKPYECYCGSKSFRVTSHLKVHQRTHTGK----- 466

Qy 67 VVPFVILKCORD-SEKNKV 84
Db 467 --PFECLCGKSFSEKSNL 483

RESULT 15
US-09-949-016-9434
; Sequence 9434, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9434
; LENGTH: 639
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9434

Query Match      11.1%; Score 63.5; DB 4; Length 639;
Best Local Similarity 25.3%; Pred. No. 24;
Matches 19; Conservative 12; Mismatches 29; Indels 15; Gaps 3;

Qy 13 CLTCSYAFMF--SSLRQKTSBPQGVKVP-----CGEHFRIRQNLPEHTQGLGSKWLWLLFA 66
Db 416 CKECGKSFYNSLSLTHVTRTHTEIPEYECNECGKAFKYSSSLTKCHMIHTGK----- 468

Qy 67 VVPFVILKCORDSEK 81
Db 469 --PFECECGKAFSK 481

Search completed: October 11, 2005, 07:42:49
Job time : 26.2326 secs
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 11, 2005, 06:57:07 ; Search time 16.4385 Seconds  
(without alignments)  
620.432 Million cell updates/sec

Title: US-10-092-934-5  
Perfect score: 582  
Sequence: 1 MFFVLRRFCFPETESHSL.....VQGGKQKLYISADLVHLIA 106

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79:\*  
1: Pirl:\*  
2: Pirl2:\*  
3: Pirl3:\*  
4: Pirl4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	183.5	31.5	613	4 C40201	artifact-warning s
2	161.5	27.7	673	4 F40201	artifact-warning s
3	158	27.1	627	4 A40201	artifact-warning s
4	145	24.9	46	2 I54375	gene NF2 protein -
5	135	23.2	39	2 I34374	gene NF2 protein -
6	132	22.7	53	2 A42442	integrin beta-1 ch
7	108	18.6	597	4 E40201	artifact-warning s
8	104	17.9	100	2 A46010	X-linked retinopat
9	92	15.8	522	2 T08711	gamma-adaptin homo
10	90	15.5	440	2 A26359	decay-accelerating
11	86	14.8	773	2 T00502	probable receptor-
12	73.5	12.6	588	2 E96633	probable Serine/Th
13	72.5	12.5	447	2 A96639	protein t1f9.18 [i
14	71	12.2	652	2 T10576	hypothetical prote
15	71	12.2	766	2 B85440	receptor kinase-li
16	71	12.2	2302	2 T14328	protein-tyrosine-p
17	70	12.0	668	2 T26724	hypothetical prote
18	70	12.0	907	2 T04820	aconitate hydratase
19	68.5	11.8	2183	2 T42764	coagulation factor
20	68	11.7	4302	2 A38971	polycystic kidney
21	67.5	11.6	130	2 B72702	hypothetical prote
22	67.5	11.6	854	1 QRHYLD	LDL receptor precu
23	67.5	11.6	879	1 QRRTLD	LDL receptor precu
24	66.5	11.4	556	2 T24690	hypothetical prote
25	65.5	11.3	1192	2 T48499	receptor-like prot
26	65	11.2	424	2 JC5921	non-selective cati
27	65	11.2	898	2 T10101	aconitate hydratase
28	64.5	11.1	321	2 I61749	phormone receptor
29	64.5	11.1	356	2 A11954	hypothetical prote

30	64.5	11.1	520	2 S14600	E2 glycoprotein pr
31	64.5	11.1	593	1 GYHU	granulin precursor
32	64.5	11.1	980	2 T05414	protein kinase hom
33	64	11.0	507	2 H82378	probable long-chai
34	63.5	10.9	427	2 A71612	translation releas
35	63.5	10.9	454	2 T42680	hypothetical prote
36	63.5	10.9	2529	2 A56923	transcription fact
37	63.5	10.9	2578	2 A56922	transcription fact
38	63	10.8	331	2 T31998	hypothetical prote
39	63	10.8	386	2 AG0081	conserved hypothe
40	63	10.8	837	1 A29512	LDL receptor precu
41	62.5	10.7	236	2 S31058	hypothetical prote
42	62.5	10.7	329	1 A48754	B7-2 antigen - hum
43	62.5	10.7	606	2 S35427	env polypotein -
44	62.5	10.7	640	2 F75553	hypothetical prote
45	62.5	10.7	647	2 T35931	probable gamma-glu

ALIGNMENTS

RESULT 1

C40201  
artifact-warning sequence (translated ALU class C) - human  
C:Species: Homo sapiens (man)  
C:Date: 31-Mar-1992 #sequence\_revision 11-Aug-1995 #text\_change 19-May-2000  
C:Accession: C40201  
R:Claverie, J.M.  
personal communication, 1992

A:Reference number: A40201  
A:Accession: C40201  
A:Molecule type: DNA  
A:Residues: 1-613 <CLA>  
R:Claverie, J.M.  
Genomics 12, 838-841, 1992

A:Title: Identifying coding exons by similarity search: Alu-derived and other potential  
A:Reference number: A40200; MUID:92241891; PMID:1572661  
A:Contents: annotation  
C:Comment: This "warning" entry is a conceptual translation in all 6 reading frames of o  
in-frame stop codons are shown as 'X'.  
C:Comment: Any significant similarity of a predicted protein sequence to a portion of th

Query Match 31.5%; Score 183.5; DB 4; Length 613;  
Best Local Similarity 62.3%; Pred. No. 3.2e-12;  
Matches 38; Conservative 4; Mismatches 16; Indels 3; Gaps 2;

Qy	8	FCFCFFETESHSLTQAGVQWCELGSPOLPSGFKRFSCLSLSSWDSHEP	65
Db	310	FFFFFETESHVTOAGVQWRDLGSLQAPPPGFMFSCLSLRTWDY-RRPHHAQLIFCI	368

Qy	66	F 66
Db	369	F 369

RESULT 2

F40201  
artifact-warning sequence (translated ALU class F) - human

C:Species: Homo sapiens (man)  
C:Date: 31-Mar-1992 #sequence\_revision 11-Aug-1995 #text\_change 19-May-2000  
C:Accession: F40201  
R:Claverie, J.M.  
personal communication, 1992

A:Reference number: A40201  
A:Accession: F40201  
A:Molecule type: DNA  
A:Residues: 1-673 <CLA>  
R:Claverie, J.M.  
Genomics 12, 838-841, 1992

A:Title: Identifying coding exons by similarity search: Alu-derived and other potential  
A:Reference number: A40200; MUID:92241891; PMID:1572661  
A:Contents: annotation



artifact-warning sequence (translated ALU class E) - human  
C;Species: Homo sapiens (man)  
C;Date: 31-Mar-1992 #sequence\_revision 11-Aug-1995 #text\_change 19-May-2000  
C;Accession: E40201  
R;Claverie, J.M.  
A:Reference number: A40201  
A:Accession: E40201  
A:Molecule type: DNA  
A;Residues: 1-597 <CUA>  
R;Claverie, J.M.  
Genomics 12, 838-841, 1992  
A;Title: Identifying coding exons by similarity search: Alu-derived and other potentially  
A;Reference number: A40200; MUID:92241891; PMID:1572661  
A;Contents: annotation  
C;Comment: This "warning" entry is a conceptual translation in all 6 reading frames of c  
in-frame stop codons are shown as 'X'.  
C;Comment: Any significant similarity of a predicted protein sequence to a portion of th  
.  
Query Match 18.6%; Score 108; DB 4; Length 597;  
Best Local Similarity 43.8%; Pred. No. 0.00063;  
Matches 28; Conservative 5; Mismatches 19; Indels 12; Gaps 3;  
QY 12 FFETESHSL-TQAGVQWCELGSPQPLPSGKRF-----SCLSLSSWDYSHRPHPVICS 65  
DB 502 FFLRRSFALVAQAGVRW-----HNLTFANFASWQAILCSLSPSSWDYRHAPRPANFI 555  
QY 66 FLME 69  
DB 556 FLVE 559  
RESULT 8  
A46010  
X-linked retinopathy protein (C-terminal, clone XEH.8c) - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 21-Sep-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004  
C;Accession: A46010  
R;Wong, P.; MacDonald, I.M.; Sood, R.; Smith, C.; Pilon, R.; Tennisswood, M.  
Genomics 15, 467-471, 1993  
A;Title: Identification and partial characterization of a candidate gene for X-linked re  
A;Reference number: A46010; MUID:93224131; PMID:8468040  
A;Accession: A46010  
A;Status: preliminary  
A:Molecule type: nucleic acid  
A;Residues: 1-100 <WON>  
A;Cross-references: UNIPROT:Q07826; GB:S58722; NID:g299470; PIDN:AAB26149.1; PID:g299471  
A;Note: sequence extracted from NCBI backbone (NCBIN:129339, NCBIPI:129340)  
Query Match 17.9%; Score 104; DB 2; Length 100;  
Best Local Similarity 62.5%; Pred. No. 0.00025;  
Matches 20; Conservative 4; Mismatches 8; Indels 0; Gaps 0;  
QY 8 FCFEFTESHSLTQAGVQWCELGSPQPLPSG 39  
DB 1 FFFFEFTESCVAEAGVQWCDLGLSKSPPPG 32  
RESULT 9  
T08711  
gamma-adaptin homolog DKFZp564D066.1 - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 13-Aug-1999  
C;Accession: T08711  
R;Wambutt, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.  
submitted to the Protein Sequence Database, March 1999  
A;Reference number: Z16471  
A;Accession: T08711  
A:Molecule type: mRNA  
A;Residues: 1-522 <WAM>  
A;Cross-references: EMBL:AL050025  
A;Experimental source: fetal brain; clone DKFZp564D066

C;Genetics:  
A;Note: DKFZp564D066.1  
C;Keywords: membrane trafficking  
Query Match 15.8%; Score 92; DB 2; Length 522;  
Best Local Similarity 66.7%; Pred. No. 0.031;  
Matches 18; Conservative 3; Mismatches 6; Indels 0; Gaps 0;  
QY 15 TESHSLTQAGVQWCELGSPQPLPSGFK 41  
DB 496 TGSHSVSQAGVQWDLGSLQLPAPFR 522  
RESULT 10  
A26359  
decay-accelerating factor, splice form 1 precursor - human  
N;Alternate names: decay-accelerating factor 5; decay-accelerating factor secreted form  
C;Species: Homo sapiens (man)  
C;Date: 05-Oct-1998 #sequence\_revision 05-Oct-1988 #text\_change 09-Jul-2004  
C;Accession: A26359; A39702; S16187; S23138; A27258  
R;Caras, I.W.; Davitz, M.A.; Rhee, L.; Weddell, G.; Martin Jr., D.W.; Nussenzweig, V.  
Nature 325, 545-549, 1987  
A;Title: Cloning of decay-accelerating factor suggests novel use of splicing to generate  
A;Reference number: A26359; MUID:87115845; PMID:2433596  
A;Accession: A26359  
A:Molecule type: mRNA  
A;Residues: 1-440 <CAR>  
A;Cross-references: UNIPROT:P08174; GB:M30142  
R;Ewulonu, U.K.; Ravi, L.; Medof, M.E.  
Proc. Natl. Acad. Sci. U.S.A. 88, 4675-4679, 1991  
A;Title: Characterization of the decay-accelerating factor gene promoter region.  
A;Reference number: A39702; MUID:91271256; PMID:1711208  
A;Accession: A39702  
A:Molecule type: DNA  
A;Residues: 1-79,'T',81-104 <EWU>  
A;Cross-references: GB:M64356  
A;Note: the authors translated the codon AGT for residue 85 as Met  
R;Nakano, Y.; Sugita, Y.; Ishikawa, Y.; Choi, N.H.; Tobe, T.; Tomita, M.  
Biochim. Biophys. Acta 1074, 326-330, 1991  
A;Title: Isolation of two forms of decay-accelerating factor (DAF) from human urine.  
A;Reference number: S16187; MUID:91291869; PMID:1712233  
A;Accession: S16187  
A;Status: preliminary  
A:Molecule type: protein  
A;Residues: 35-47 <BIO>  
R;Nakano, Y.; Sumida, K.; Kikuta, N.; Miura, N.H.; Tobe, T.; Tomita, M.  
Biochim. Biophys. Acta 1116, 235-240, 1992  
A;Title: Complete determination of disulfide bonds localized within the short consensus  
A;Reference number: S23138; MUID:92305034; PMID:1377029  
A;Accession: S23138  
A;Status: preliminary  
A:Molecule type: protein  
A;Residues: 35-41;65-68;79-81;93-103;128-134;143-145;155-159;162-168;188-192;203-204;211  
R;Sugita, Y.; Negoro, T.; Matsuda, T.; Sakamoto, T.; Tomita, M.  
J. Biochem. 100, 143-150, 1986  
A;Title: Improved method for the isolation and preliminary characterization of human DAF  
A;Reference number: A27258; MUID:87008461; PMID:2428813  
A;Accession: A27258  
A:Molecule type: protein  
A;Residues: 35,'X',37,'G',39-51,'P',53-55,'X',57-58,'X',60-63 <SUG>  
A;Note: Gly-35 and Leu-38 were also found  
C;Comment: For an alternative splice form, see PIR:B26359  
C;Genetics:  
A;Gene: GDB:DAF  
A;Cross-references: GDB:119088; OMIM:125240  
A;Map position: 1q32-1q32  
C;Superfamily: decay-accelerating factor; complement factor H repeat homology  
C;Keywords: alternative splicing; glycoprotein  
F:1-34/Domain: signal sequence #status predicted <SIG>  
F:35-44/Product: decay-accelerating factor 1 #status predicted <MAT>  
F:36-94/Domain: complement factor H repeat homology <FH01>  
F:98-158/Domain: complement factor H repeat homology <FH02>  
F:163-220/Domain: complement factor H repeat homology <FH03>







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OM protein - protein search, using sw model

Run on: October 11, 2005, 06:57:07 ; Search time 63.6283 Seconds  
(without alignments)  
853.085 Million cell updates/sec

Title: US-10-092-934-5

Perfect score: 582

Sequence: 1 MFFVLYRFCFFPTEHSL.....VQQGRKQLYISADLVHLIA 106

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	234.5	40.3	375	2 O60448	homo sapien
2	220.5	37.9	124	2 Q6ZVF6	homo sapien
3	211	36.3	132	2 Q6ZNU7	homo sapien
4	207	35.6	131	2 Q6ZTD3	homo sapien
5	203	34.9	135	2 Q95KE1	macaca fasc
6	203	34.9	151	2 Q9HA67	homo sapien
7	203	34.9	165	2 Q6ZSS3	homo sapien
8	203	34.9	165	2 Q6ZT71	homo sapien
9	203	34.9	195	2 Q6ZUW2	homo sapien
10	201	34.5	124	2 Q6ZSG7	homo sapien
11	201	34.5	158	2 Q9NAL9	homo sapien
12	201	34.5	176	2 Q6ZTU6	homo sapien
13	200	34.4	165	2 Q6ZS21	homo sapien
14	199.5	34.3	591	1 ALU08 HUMAN	homo sapien
15	199	34.2	122	2 Q6ZVH4	homo sapien
16	198	34.0	299	2 Q6ZRN6	homo sapien
17	196.5	33.8	170	2 Q6ZV14	homo sapien
18	196	33.7	129	2 Q6ZS06	homo sapien
19	194.5	33.4	152	2 Q9NX85	homo sapien
20	192.5	33.1	117	2 Q8EU02	homo sapien
21	192	33.0	61	2 Q9UI48	homo sapien
22	192	33.0	151	2 Q9N287	homo sapien
23	191.5	32.9	137	2 Q6ZS97	homo sapien
24	191	32.8	132	2 Q6ZS28	homo sapien
25	190.5	32.7	129	2 Q6ZM43	homo sapien
26	189	32.5	163	2 Q96MM0	homo sapien
27	188	32.3	123	2 Q6ZMQ3	homo sapien
28	187	32.1	102	2 Q9P147	homo sapien
29	187	32.1	593	1 ALU6 HUMAN	homo sapien
30	186	32.0	83	2 Q96ID7	homo sapien
31	186	32.0	120	2 Q6ZSU7	homo sapien

#### RESULT 1

O60448 ID O60448 PRELIMINARY; PRT; 375 AA.

AC O60448;

DT 01-AUG-1998 (TrEMBLrel. 07, Created)

DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE Neuronal thread protein AD7C-NTP.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Neuronal;

RX MEDLINE=98064067; PubMed=9399956;

RA Monte S.M., Ghanbari H.A., Wands J.R.;

RA Hauser S.L., Ghanbari H.A., Wands J.R.;

RT "Characterization of the AD7C-NTP cDNA expression in Alzheimer's

RT disease and measurement of a 41-KD protein in cerebrospinal fluid.";

RL J. Clin. Invest. 100:3093-3104(1997).

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=Neuronal;

RA de la Monte S.M., Wands J.R.;

RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF010144; AAC08737.1; -

DR GO; GO:0005615; C:extracellular space; TAS.

DR GO; GO:0016021; C:integral to membrane; TAS.

DR GO; GO:0006915; P:apoptosis; TAS.

DR GO; GO:0007417; P:central nervous system development; TAS.

SO SEQUENCE 375 AA; 41720 MW; 955443950A5BFED CRC64;

Query Match 40.3%; Score 234.5; DB 2; Length 375;

Best Local Similarity 72.1%; Pred. No. 1.9e-17;

Matches 44; Conservative 2; Mismatches 14; Indels 1; Gaps 1;

Qy 8 FCFCFFTEHSHSTQAGVQMCGLSGPPLSGFRFCCLSLSSWDYSHPEHPHV-ICSF 66

Db 297 FNFLCFEMESHVSQTQAGVQWPNLGLQLPLPPLKRFCSCLSPSSWDYCHLPPHPANFCIF 356

Qy 67 L 67

Db 357 I 357

#### RESULT 2

O6ZVF6 ID O6ZVF6 PRELIMINARY; PRT; 124 AA.

AC O6ZVF6;

DT 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE Hypothetical protein FLJ42633.

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OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Cerebellum;
RA Ninomiya K., Wagatsuma M., Kanda K., Kondo H., Yokoi T., Kodaira H.,
RA Furuya T., Takahashi M., Kikkawa E., Omura Y., Abe K., Kamihara K.,
RA Katsuta N., Sato K., Tanikawa M., Yamazaki M., Sugiyama T., Irie R.,
RA Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M.,
RA Murakawa K., Kanehori K., Sugiyama A., Kawakami B., Suzuki Y.,
RA Sugano S., Nagahara K., Masuho Y., Nagai K., Isogai T.;
RA Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B.,
RA Suzuki Y., Sugano S., Nagahara K., Masuho Y., Nagai K., Isogai T.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: AK124624; BAC85905.1; -.
DR GO: GO:0004872; F:receptor activity; IEA.
DR InterPro: IPR000152; ASX_hydroxyl_S.
DR PROSITE: PS00010; ASX_HYDROXYL; UNKNOWN_1.
KW Receptor.
SQ SEQUENCE 124 AA; 14173 MW; 108AA891087A31B4 CRC64;

Query Match 37.9%; Score 220.5; DB 2; Length 124;
Best Local Similarity 54.2%; Pred. No. 2.1e-16;
Matches 45; Conservative 9; Mismatches 18; Indels 11; Gaps 4;

QY 3 FVLVRFCCFFETESHLSLTQAGVQWCELGSPOPLPSGFKRFSCLSLSSWDYSHEPPHP 61
DB 26 FCFCFCFCFFETESHLSLTQAGVQWCELGSPOPLPSGFKRFSCLSLSSWDYSHEPPHP 83

QY 62 VICSLMEKCLILYKPGDITGP 84
DB 84 --C--LANFCIF---SRDSVSP 98

RESULT 3
Q6ZNU7 PRELIMINARY; PRT; 132 AA.
AC Q6ZNU7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein FLJ27113.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Tanai H., Watanabe S., Ishida S., Ono Y., Hotuta T., Watanabe M.,
RA Suzuki Y., Hata H., Nakagawa K., Mizuno S., Morinaga M., Kawamura M.,
RA Sugiyama T., Irie R., Otsuki T., Sato H., Nishikawa T., Sugiyama A.,
RA Kawakami B., Nagai K., Isogai T., Sugano S.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: AK130623; BAC85397.1; -.
SQ SEQUENCE 132 AA; 14490 MW; EFB6797A7A143BF6 CRC64;

Query Match 36.3%; Score 211; DB 2; Length 132;
Best Local Similarity 50.5%; Pred. No. 2.6e-15;
Matches 47; Conservative 6; Mismatches 30; Indels 10; Gaps 3;

QY 8 FCRCFFETESHLSLTQAGVQWCELGSPOPLPSGFKRFSCLSLSSWDYSHEPPHPICSP 66
DB 19 FLFFFFLRRFVLVAQGVQWCELGSPOPLPSGFKRFSCLSLSSWDYSHEPPHPANFLF 78

QY 67 LME-----KCLILYKPGDITGPILVQGGK 92
DB 79 LVETGLHVQAGLEFVTSQDP--PALASQAR 109

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RESULT 4
ID Q6ZTD3 PRELIMINARY; PRT; 131 AA.
AC Q6ZTD3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein FLJ44770.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Cerebellum;
RA Oshina A., Takahashi-Fujii A., Tanase T., Imose N., Takeuchi K.,
RA Arita M., Musashino K., Yuuki H., Hara H., Sugiyama T., Irie R.,
RA Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M.,
RA Murakawa K., Kanehori K., Sugiyama A., Kawakami B., Suzuki Y.,
RA Sugano S., Nagahara K., Masuho Y., Nagai K., Isogai T.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: AK126724; BAC86659.1; -.
SQ SEQUENCE 131 AA; 15492 MW; B85276F6B7E13795 CRC64;

Query Match 35.6%; Score 207; DB 2; Length 131;
Best Local Similarity 54.2%; Pred. No. 7.1e-15;
Matches 45; Conservative 7; Mismatches 21; Indels 10; Gaps 2;

QY 2 FVLVRFCCFFETESHLSLTQAGVQWCELGSPOPLPSGFKRFSCLSLSSWDYSHEPPHP 61
DB 35 YFFSLF-FFFFETESCVTQAGVQWRDLGSLPLPGFTQFCLSLPSSWDYRHPPCP 93

QY 62 VICSLMEKCLILYKPGDITGP 84
DB 94 -----ANFLYFSDRVSP 107

RESULT 5
ID Q95KE1 PRELIMINARY; PRT; 135 AA.
AC Q95KE1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Frontal lobe left;
RA Hashimoto K., Osada N., Hida M., Kusuda J., Sugano S.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB062934; BAB60728.1; -.
DR InterPro: IPR000173; GAP_dhdrogenase.
DR PROSITE: PS00071; GAPDH; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 135 AA; 15411 MW; 94DA9FF8025670DF CRC64;

Query Match 34.9%; Score 203; DB 2; Length 135;
Best Local Similarity 64.4%; Pred. No. 2e-14;
Matches 38; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY 3 FVLVRFCCFFETESHLSLTQAGVQWCELGSPOPLPSGFKRFSCLSLSSWDYSHEPPHP 61
DB 71 FSFLSFFFFFKTESCVSQAGVQWRDLGSLPQPPPPRFTQFCLSLPSSWDYRHPPCP 129

RESULT 6

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Q9HA67
ID Q9HA67 PRELIMINARY; PRT; 151 AA.
AC Q9HA67;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein FLJ12155.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
TX TISSU= Mammary gland;
RX PubMed=14702039; DOI=10.1038/ngl1285;
RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahara K.,
RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
RA Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
RA Abe K., Kamihara K., Katsuta M., Sato K., Tanikawa M., Yamazaki M.,
RA Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
RA Tanai H., Kimata M., Watanabe M., Hiraoa K., Chiba Y., Ishida S.,
RA Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,
RA Kanehori K., Takahashi-Fujii A., Hara H., Tanase T., Nomura Y.,
RA Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
RA Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohara T., Sano S.,
RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA Hishigaki H., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA Yanazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Ohtani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
RT "Complete sequencing and characterization of 21,243 full-length human
RT cDNAs";
RL Natl. Genet. 36:40-45(2004).
DR EMBL; AK022217; BAB13989.1; --
SQ SEQUENCE 151 AA; 16972 MW; ECB65BBD50DF2811 CRC64;

Query Match 34.9%; Score 203; DB 2; Length 151;
Best Local Similarity 54.5%; Pred. No. 2.3e-14;
Matches 42; Conservative 5; Mismatches 10; Indels 20; Gaps 3;

Qy 9 CFC-----FFETESHSLTQAGVQWCELGSPQPLPSGKRFSCSLSSWDYSHE 57
Db 12 CICKHYAPPTAPHLPPFFETESHVSTQAGVQWCDLGLSLQSPGPKQFSCSLSRSDYRVR 71

Qy 58 PPHPVIC-----SFLME 69
Db 72 P-----LCLANFIVFLVE 84

RESULT 7
ID Q6ZS53 PRELIMINARY; PRT; 165 AA.
AC Q6ZS53;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein FLJ45823.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Tanigami A., Fujiwara T., Shibahara T., Goto Y., Hirao M., Shimizu F.,
RA Wakebe H., Ono T., Hishigaki H., Watanabe T., Ozaki K., Sugiyama T.,
RA Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J.,
RA Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K.,
RA Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,
RA Wagatsuma M., Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A.,
RA Masuho Y., Nagai K., Isogai T.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK127723; BAC87102.1; --
SQ SEQUENCE 165 AA; 19319 MW; 84BC643864656574 CRC64;

Query Match 34.9%; Score 203; DB 2; Length 165;
Best Local Similarity 56.8%; Pred. No. 2.5e-14;
Matches 42; Conservative 7; Mismatches 23; Indels 2; Gaps 2;

Qy 1 MPFVLYRFCFC-FFETESHSLTQAGVQWCELGSPQPLPSGKRFSCSLSSWDYSHEPP 59
Db 59 VFFPFFYFLSFPPFETESLSVAQAGVQWHDGLSLQPRPPGPKQFSCSLSPSSWDYGHPTPQ 118

Qy 60 HPV-ICSFLEKCL 72
Db 119 RSANFCIFRKDRVL 132

RESULT 8
Q6ZT71 PRELIMINARY; PRT; 165 AA.
ID Q6ZT71;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein FLJ44907.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSU= Amygdala;
RA Oshima A., Musashino K., Yuuki H., Hara H., Sugiyama T., Irie R.,
RA Arita M., Musashino K., Yuuki H., Hara H., Sugiyama T., Irie R.,
RA Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M.,
RA Murakawa K., Kanehori K., Sugiyama A., Kawakami B., Suzuki Y.,
RA Sugano S., Nagahara K., Masuho Y., Nagai K., Isogai T.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK126855; BAC86723.1; --
SQ SEQUENCE 165 AA; 19309 MW; 2BBEB4386467B575 CRC64;

Query Match 34.9%; Score 203; DB 2; Length 165;
Best Local Similarity 56.8%; Pred. No. 2.5e-14;
Matches 42; Conservative 7; Mismatches 23; Indels 2; Gaps 2;

Qy 1 MPFVLYRFCFC-FFETESHSLTQAGVQWCELGSPQPLPSGKRFSCSLSSWDYSHEPP 59
Db 59 VFFPFFYFLSFPPFETESLSVAQAGVQWHDGLSLQPRPPGPKQFSCSLSPSSWDYGHPTPQ 118

Qy 60 HPV-ICSFLEKCL 72
Db 119 RSANFCIFRKDRVL 132

RESULT 9
Q6ZUW2 PRELIMINARY; PRT; 195 AA.
ID Q6ZUW2;
AC Q6ZUW2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

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DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein FLJ43278.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Oshima A., Takahashi-Fujii A., Tanase T., Imose N., Takeuchi K.,
RA Arita M., Musashino K., Yuuki H., Hara H., Sugiyama T., Irie R.,
RA Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Waga-
RA Murakawa K., Kanehori K., Sugiyama A., Kawakami B., Suzuki Y.,
RA Sugano S., Nagahara K., Masuho Y., Nagai K., Isogai T.,
RA Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
RL EMBL; AK125268; BAC86106.1; -.
DR EMBL; AK125268; BAC86106.1; -.
SQ SEQUENCE 195 AA; 21399 MW; 6C4225556FE990B1 CRC64;

Query Match 34.9%; Score 203; DB 2; Length 195;
Best Local Similarity 51.1%; Pred. No. 3e-14;
Matches 47; Conservative 7; Mismatches 26; Indels 12; Gaps 3;

QY 4 VLYRFCFFETESHSLTQAGVQVCELGSPQLPSGPKRFSCLSLSSWDYSHPPHPV- 62
DB 77 ILGLFVILFFEMSCSVALGQVHGLGSLQPPGPKRFSCLSLSSWDYSHPPHPAS 136
QY 63 ICSFLMEK-----CLILYKNGDTIGPI 85
DB 137 LPFLMPKRYIYVLTCTLL--PVLSUGTI 166

RESULT 10
ID Q6ZSG7 PRELIMINARY; PRT; 124 AA.
AC Q6ZSG7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein FLJ45543.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Thalamus;
RA Ota T., Nakagawa S., Senoh A., Mizuguchi H., Inagaki H., Sugiyama T.,
RA Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J.,
RA Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K.,
RA Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,
RA Waga-uma M., Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A.,
RA Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahara K.,
RA Masuho Y., Nagai K., Isogai T.;
RA Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
RL EMBL; AK127451; BAC86986.1; -.
DR EMBL; AK127451; BAC86986.1; -.
SQ SEQUENCE 124 AA; 14502 MW; 07D5313B6E1DE897 CRC64;

Query Match 34.58%; Score 201; DB 2; Length 124;
Best Local Similarity 63.2%; Pred. No. 3.1e-14;
Matches 36; Conservative 6; Mismatches 15; Indels 0; Gaps 0;

QY 5 LYRFFCFETESHSLTQAGVQVCELGSPQLPSGPKRFSCLSLSSWDYSHPPHP 61
DB 1 MWFFVILFETESHVLTQAGVQVQCNLSLQPPPPWPKQFSCLSPSSWNRHLPPCP 57

RESULT 11
Q8NAL9
ID AC Q8NAL9 PRELIMINARY; PRT; 158 AA.
AC Q8NAL9;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)

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DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein FLJ35131.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Sekine M., Obyashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahara K.,
RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
RA Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
RA Abe K., Kamiyama K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
RA Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
RA Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y., Ishida S.,
RA Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,
RA Kanehori K., Takahashi-Fujii A., Hara H., Tanase T., Nomura Y.,
RA Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
RA Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukushima Y.,
RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
RA Kawabata R., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
RT "Complete sequencing and characterization of 21,243 full-length human
RT cDNAs."
RL Nat. Genet. 36:40-45(2004).
DR EMBL; AK092450; BAC03893.1; -.
SQ SEQUENCE 158 AA; 17414 MW; E151503015F2FE34 CRC64;

Query Match 34.5%; Score 201; DB 2; Length 158;
Best Local Similarity 67.8%; Pred. No. 4e-14;
Matches 40; Conservative 2; Mismatches 13; Indels 4; Gaps 1;

QY 16 ESHSLTQAGVQVQVCELGSPQLPSGPKRFSCLSLSSWDYSHPP-HPVICSLMEK 70
DB 2 ESHSVTQAGVQVQVCELGSLQPLPPGPKRFTCLSLSSWDYRRVPPPLANCFIPSF 60

RESULT 12
Q6ZTU6
ID AC Q6ZTU6 PRELIMINARY; PRT; 176 AA.
AC Q6ZTU6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein FLJ44211.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Thymus;
RA Kanehori K., Ishibashi T., Chiba Y., Fujimori K., Hiraoka S.,
RA Tanai H., Watanabe S., Ishida S., Ono Y., Hotuta T., Watanabe M.,
RA Sugiyama T., Irie R., Otsuki T., Sato H., Ota T., Wakamatsu A.,
RA Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T.,

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 11, 2005, 06:57:07 ; Search time 78.508 Seconds  
(without alignments)  
522.196 Million cell updates/sec

Title: US-10-092-934-5  
Perfect score: 582  
Sequence: 1 MFFVLXRFCCFPETESHSL.....VQQKQKLYISADLVHLIA 106

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5  
Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A Geneseq\_l6Dec04:.\*  
1: Geneseqp1980s:.\*  
2: Geneseqp1990s:.\*  
3: Geneseqp2000s:.\*  
4: Geneseqp2001s:.\*  
5: Geneseqp2002s:.\*  
6: Geneseqp2003as:.\*  
7: Geneseqp2003bs:.\*  
8: Geneseqp2004as:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	582	100.0	106	AAE29146	Neural th
2	582	100.0	106	ABR63244	106 amino
3	582	100.0	106	ABU02976	Human neu
4	582	100.0	106	AAE33193	Neural th
5	582	100.0	106	ABJ19449	106-mer n
6	582	100.0	106	ABJ19449	Neural th
7	237.5	40.8	119	AAO06149	Human pol
8	234.5	40.3	85	AB28760	Peptide #
9	234.5	40.3	375	AB013399	Neuron-as
10	234.5	40.3	375	ABB81538	Neural th
11	234.5	40.3	375	AAE29142	AD7C-NTP
12	234.5	40.3	375	ABR63268	AD7C-neur
13	234.5	40.3	375	ADA84017	Human POM
14	234.5	40.3	375	ABU03024	Human neu
15	234.5	40.3	375	ABB99774	Amino aci
16	234.5	40.3	375	ABJ19445	AD7C-neur
17	234.5	40.3	375	ADB37642	Human neu
18	234.5	40.3	375	ADR14409	Human NP-
19	231.5	39.8	76	AB75336	Gene 47 h
20	230.5	39.6	89	ABG09800	Novel hum
21	230.5	39.6	123	AB63958	Human pro
22	226	38.8	97	ABB11638	Human sec
23	223.5	38.4	100	ADA55476	Human pro
24	223.5	38.4	396	AAU30455	Novel hum
25	223	38.3	133	ABB97994	Human cyc

26	221	38.0	168	5	ADK34256	Novel hum
27	221	38.0	1026	6	ABU12314	Human PAT
28	220.5	37.9	124	8	ADQ65229	Novel hum
29	219	37.6	131	4	AAU32027	Novel hum
30	218.5	37.5	101	6	ADA54613	Human pro
31	218	37.5	861	6	ABU12316	Human PAT
32	218	37.5	895	6	ABU12304	Human PAT
33	218	37.5	933	6	ABU12307	Human PAT
34	218	37.5	993	6	ABU12300	Human PAT
35	218	37.5	1044	6	ABU12310	Human PAT
36	217.5	37.4	92	5	ADK34934	Novel hum
37	215.5	37.0	146	4	ABG08195	Novel hum
38	215.5	37.0	219	4	AAG66500	Human neu
39	215.5	37.0	433	7	ADC87285	Human GPC
40	214.5	36.9	114	7	ADB64269	Human pro
41	214	36.8	397	2	AAO95913	Neural th
42	213.5	36.7	129	4	AAO08006	Human pol
43	213	36.6	132	4	ABG08282	Novel hum
44	212.5	36.5	92	5	ABB99219	Human try
45	212.5	36.5	93	4	AAO96679	Human rep

## ALIGNMENTS

## RESULT 1

AAE29146  
ID AAE29146 standard; protein; 106 AA.

XX	AAE29146;	
AC		
XX		
DT	27-JAN-2003 (first entry)	
XX		
DE	Neural thread protein (NTP) #4.	
XX		
KW	Neural thread protein; NTP; hyperplasia; hypertrophy; arteriosclerosis;	
KW	haemorrhoid; gene therapy; tumour; vascular disease; atherosclerosis;	
KW	inflammatory disease; nutritional deficiency disease; genetic disease;	
KW	autoimmune disease; metabolic disease; traumatic disease; intoxication;	
KW	infectious disease; congenital malformation; enzyme deficiency disease;	
KW	amyloid disease; fibrosis disease; storage disease; radiation disease;	
KW	poisoning; environmental disease; endocrine disease; protein therapy;	
KW	degenerative disease; mechanical disease.	
XX		
OS	Unidentified.	
XX		
PN	WO200274323-A2.	
XX		
PD	26-SEP-2002.	
XX		
PF	08-MAR-2002; 2002WO-IB001959.	
XX		
PR	08-MAR-2001; 2001US-0273957P.	
XX		
PA	(AVER/) AVERBACK P.	
XX		
PI	Averback P;	
XX		
DR	WPI; 2002-759864/82.	
XX		
PT	Treating a condition in a patient requiring removal or destruction of	
PT	cells, such as a benign or malignant tumor of a tissue or an inflammatory	
PT	disease, comprises administering a neural thread protein (NTP) or a NTP	
PT	gene to a mammal.	
XX		
PS	Claim 23; Fig 5; 70pp; English.	
XX		
CC	The invention relates to a method for treating a condition in a patient	
CC	requiring removal or destruction of cells. The method involves	
CC	administering to a mammal a neural thread protein (NTP), or administering	
CC	to a tumour or other target cell a NTP gene, where the expression of the	
CC	NTP gene is induced resulting in expression of the NTP protein. The	
CC	method and NTP are useful for treating a condition in a patient requiring	

CC removal or destruction of cells, such as a benign or malignant tumour of  
CC a tissue, a hyperplasia, hypertrophy, or overgrowth of a tissue,  
CC preferably tonsillar hypertrophy or prostatic hyperplasia, a virally,  
CC bacterially, or parasitically altered tissue, or a malformation of a  
CC tissue. Other conditions include a cosmetic modification to a tissue,  
CC such as removal of unwanted facial hair, warts or unwanted fatty tissue,  
CC a vascular disease, particularly atherosclerosis or arteriosclerosis,  
CC haemorrhoids, or varicose veins, an inflammatory disease, autoimmune  
CC disease, metabolic disease, hereditary/genetic disease, traumatic disease  
CC or physical injury, nutritional deficiency disease, infectious disease,  
CC congenital malformation, amyloid disease, fibrosis disease, storage  
CC disease, enzyme deficiency disease, poisoning, intoxication, degenerative  
CC disease, radiation disease, environmental disease, endocrine disease or  
CC mechanical disease. The invention is useful in protein therapy and gene  
CC therapy. The present sequence is NTP protein  
XX  
SQ Sequence 106 AA;

Query Match 100.0%; Score 582; DB 5; Length 106;  
Best Local Similarity 100.0%; Pred. No. 2.1e-63;  
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFFVLYRFCFCFFETESHSLTQAGVQWCELGSPQLPSGPKRFSCLSLSSWDYSHEPPH 60  
Db 1 MFFVLYRFCFCFFETESHSLTQAGVQWCELGSPQLPSGPKRFSCLSLSSWDYSHEPPH 60

QY 61 PVICSFMEKCLILYKPNGDTIGPILVQOGKROKLYISADLVHLIA 106  
Db 61 PVICSFMEKCLILYKPNGDTIGPILVQOGKROKLYISADLVHLIA 106

## RESULT 2

ABR63244  
ID ABR63244 standard; protein; 106 AA.

XX ABR63244;

XX 28-AUG-2003 (first entry)

DE 106 amino acid neural thread protein.

XX Cytostatic; Antibacterial; Immunosuppressive; Antiinflammatory;  
KW neural thread protein; NTP; tumour.

XX Unidentified.

XX W02003008443-A2.

XX 30-JAN-2003.

XX 19-JUL-2002; 2002WO-CA001105.

XX 19-JUL-2001; 2001US-0306150P.

XX 19-JUL-2001; 2001US-0306161P.

XX 16-NOV-2001; 2001US-0331477P.

XX (NYMO-) NYMOX CORP.

XX Averbach PA;

XX WPI; 2003-247995/24.

XX Novel neural thread protein peptide, referred as cell death peptide,  
PT useful for treating prostatic hyperplasia, psoriasis, eczema, dermatosis,  
PT atherosclerosis, cosmetic modification to skin, throat, mouth, muscle.

XX Disclosure; Fig 5; 77pp; English.

XX The present invention relates to a neural thread protein (NTP) peptide  
CC referred to as cell death peptide. Thought to be cytostatic,  
CC antibacterial, immunosuppressive and antiinflammatory. It is useful for  
CC treating a condition in a patient requiring removal or destruction of  
CC cells, for treating a condition such as benign or malignant tumor,

CC inflammatory disease, autoimmune disease and infectious disease. The  
CC peptide useful for treatment is derived from the amino acid sequence for  
CC a pancreatic thread protein. The peptide is conjugated, linked or bound  
CC to a molecule chosen from antibody or its fragment, antibody-like binding  
CC molecule, where the molecule has a higher affinity for binding to a tumor  
CC or other target than binding to other cells. Treatment using NTP peptides  
CC can remove benign tumors with less risk and fewer of the undesirable side  
CC effects of surgery. The present sequence is an NTP amino acid sequence  
XX  
SQ Sequence 106 AA;

Query Match 100.0%; Score 582; DB 6; Length 106;  
Best Local Similarity 100.0%; Pred. No. 2.1e-63;  
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFFVLYRFCFCFFETESHSLTQAGVQWCELGSPQLPSGPKRFSCLSLSSWDYSHEPPH 60  
Db 1 MFFVLYRFCFCFFETESHSLTQAGVQWCELGSPQLPSGPKRFSCLSLSSWDYSHEPPH 60

QY 61 PVICSFMEKCLILYKPNGDTIGPILVQOGKROKLYISADLVHLIA 106  
Db 61 PVICSFMEKCLILYKPNGDTIGPILVQOGKROKLYISADLVHLIA 106

## RESULT 3

ABU02976

ID ABU02976 standard; protein; 106 AA.

XX ABU02976;

XX 20-JAN-2003 (first entry)

XX Human neural thread protein AD7C-NTP, protein fragment #4.

XX Neural thread protein; NTP-peptide; AD7C-NTP; surgical excision;  
KW transplantation; grafting; chemotherapy; immunotherapy; vaccination;  
KW ablation; cryotherapy; laser therapy; phototherapy; gene therapy;  
KW radiation; tumour; hyperplasia; hypertrophy; overgrowth of tissue;  
KW malformation of tissue; tonsillary hypertrophy; prostatic hyperplasia;  
KW cosmetic modification; vascular disease; atherosclerosis;  
KW arteriosclerosis; haemorrhoid; varicose vein; inflammatory disease;  
KW autoimmune disease; metabolic disease; traumatic disease;  
KW physical injury; nutritional deficiency disease; infectious disease;  
KW amyloid disease; fibrosis disease; storage disease;  
KW congenital malformation; enzyme deficiency disease; poisoning;  
KW intoxication; environmental disease; radiation disease;  
KW endocrine disease; degenerative disease; mechanical disease.

XX Homo sapiens.

XX W0200297030-A2.

XX 05-DEC-2002.

XX 24-MAY-2002; 2002WO-CA000759.

XX 25-MAY-2001; 2001US-0293156P.

XX (NYMO-) NYMOX CORP.

XX Averbach PA;

XX WPI; 2003-041406/03.

XX Novel peptides similar in amino acid sequence to neural thread proteins  
PT (NTP), useful for treating unwanted cellular proliferations such as  
PT malignant tumors and prostatic hyperplasia.

XX Disclosure; Fig 5; 78pp; English.

XX The invention describes an NTP-peptide (I) comprising at least one amino  
CC acid sequence corresponding to part of the amino acid sequence of a  
CC neural thread protein, AD7C-NTP. The invention provides a method of

CC treating a condition requiring removal or destruction of cells of a  
 CC mammal comprising administering to a mammal, a therapeutic amount of (I).  
 CC The treatment is administered to the mammal before, during or after  
 CC surgical excision, transplantation, grafting, chemotherapy,  
 CC immunotherapy, vaccination, thermal or electrical ablation, cryotherapy,  
 CC laser therapy, phototherapy, gene therapy and/or radiation. The method is  
 CC useful for treatment of benign or malignant tumour; hyperplasia,  
 CC hypertrophy or overgrowth of tissue; virally, bacterially or  
 CC parasitically altered tissue; malformation of tissue selected from lung,  
 CC breast, stomach, pancreas, prostate, bladder, bone, ovary, skin, kidney,  
 CC sinus, colon, intestine, rectum, esophagus, heart, spleen, salivary  
 CC gland, blood, brain and its coverings, spinal cord, muscle, connective  
 CC tissue, adrenal, parathyroid, thyroid, uterus, testis, pituitary,  
 CC reproductive organs, liver, hair, gall bladder, eye, ear, nose, throat,  
 CC tonsils, mouth and lymph nodes and lymphoid system; consiliary  
 CC hyper trophy; prostatic hyperplasia; cosmetic modification to a tissue;  
 CC vascular disease (atherosclerosis or arteriosclerosis); haemorrhoids;  
 CC varicose veins; inflammatory disease; autoimmune disease; metabolic  
 CC disease; hereditary/genetic disease; traumatic disease; physical injury;  
 CC nutritional deficiency disease; infectious disease; amyloid disease;  
 CC fibrosis disease; storage disease; congenital malformation; enzyme  
 CC deficiency disease; poisoning; intoxication; environmental disease;  
 CC radiation disease; endocrine disease; degenerative disease and mechanical  
 CC disease. This is the amino acid sequence of a human neural thread protein  
 CC AD7C-NTP protein fragment  
 CC  
 CC Sequence 106 AA;

Query Match 100.0%; Score 582; DB 6; Length 106;  
 Best Local Similarity 100.0%; Pred. No. 2.1e-63;  
 Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFFVLYRFCFCFFETESHSLTQAGVQWCELGSPQLPSGFKRFSCLSLSSWDYSHPEPPH 60  
 Db 1 MFFVLYRFCFCFFETESHSLTQAGVQWCELGSPQLPSGFKRFSCLSLSSWDYSHPEPPH 60

Qy 61 PVICSFLMEKCLILYKPNKGTIGPILVQOGKQKLYISADLVHLIA 106  
 Db 61 PVICSFLMEKCLILYKPNKGTIGPILVQOGKQKLYISADLVHLIA 106

RESULT 4  
 AA333193  
 ID AA333193 standard; protein; 106 AA.  
 AC AA333193;  
 XX  
 XX 16-APR-2003 (first entry)  
 DT  
 XX Neural thread protein (NTP) #4.  
 XX  
 XX Cell death; tissue necrosis; neural thread protein; NTP; amyloidosis;  
 KW stroke; brain tumour; Pick's disease; Parkinson's disease; glaucoma;  
 KW Alzheimer's disease; gene therapy.  
 XX  
 XX Unidentified.  
 OS  
 XX WO200289841-A2.  
 XX  
 XX 14-NOV-2002.  
 PD  
 XX  
 XX 06-MAY-2002; 2002WO-CA000681.  
 PF  
 XX  
 XX 04-MAY-2001; 2001US-0288463P.  
 PR  
 XX  
 XX (NYMO-) NYMOX CORP.  
 PA  
 XX  
 XX Averbach PA;  
 PI  
 XX  
 XX WPI; 2003-120506/11.  
 DR  
 XX  
 XX Preventing, controlling, modulating, ameliorating and/or treating cell  
 PT death or tissue necrosis using antibodies to neural thread proteins,

PT useful in disorders such as stroke, brain tumor, glaucoma and Alzheimer's  
 PT disease.  
 XX  
 XX Disclosure; Fig 8; 60pp; English.  
 XX  
 XX The invention relates to a method of preventing, and/or inhibiting cell  
 CC death and/or tissue necrosis in live tissue containing neural thread  
 CC proteins (NTP). The method involves contacting the live tissue with at  
 CC least one antibody, fragment or derivative that recognises NTP, where the  
 CC antibody, fragment or derivative is present to prevent, control,  
 CC ameliorate and/or inhibit cell death and/or tissue necrosis caused by the  
 CC presence of NTP. Methods and compositions of the invention are useful for  
 CC preventing, modulating, controlling and/or treating disorders associated  
 CC with cell death and/or tissue necrosis such as stroke, brain tumour,  
 CC Pick's disease, Parkinson's disease, amyloidosis, glaucoma and  
 CC Alzheimer's disease. The invention is useful in gene therapy. The present  
 CC sequence is NTP protein

SQ Sequence 106 AA;

Query Match 100.0%; Score 582; DB 6; Length 106;  
 Best Local Similarity 100.0%; Pred. No. 2.1e-63;  
 Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFFVLYRFCFCFFETESHSLTQAGVQWCELGSPQLPSGFKRFSCLSLSSWDYSHPEPPH 60  
 Db 1 MFFVLYRFCFCFFETESHSLTQAGVQWCELGSPQLPSGFKRFSCLSLSSWDYSHPEPPH 60

Qy 61 PVICSFLMEKCLILYKPNKGTIGPILVQOGKQKLYISADLVHLIA 106  
 Db 61 PVICSFLMEKCLILYKPNKGTIGPILVQOGKQKLYISADLVHLIA 106

RESULT 5  
 ABJ19449  
 ID ABJ19449 standard; protein; 106 AA.  
 XX  
 AC ABJ19449;  
 XX  
 XX 27-MAR-2003 (first entry)  
 DT  
 XX 106-mer neural thread protein #2.  
 DE  
 XX Nootropic; neuroprotective; cell death; tissue necrosis; NTP;  
 KW neural thread protein; neurodegenerative disorder; Alzheimer's disease.  
 KW  
 XX Unidentified.  
 OS  
 XX WO200292115-A2.  
 XX  
 XX 21-NOV-2002.  
 PD  
 XX  
 XX 16-MAY-2002; 2002WO-CA000712.  
 PF  
 XX  
 XX 16-MAY-2001; 2001US-0290971P.  
 PR  
 XX  
 XX (NYMO-) NYMOX CORP.  
 PA  
 XX  
 XX Averbach PA;  
 PI  
 XX  
 XX WPI; 2003-129234/12.  
 DR  
 XX  
 XX Preventing and/or inhibiting cell death and/or tissue necrosis in a  
 PT tissue for treating a neurodegenerative disorder, e.g. Alzheimer's  
 PT disease, by contacting the live tissue with at least one segment of  
 PT neural thread proteins (NTP).  
 PT  
 XX Disclosure; Fig 5; 60pp; English.

PS The invention relates to a novel method for preventing and/or inhibiting  
 XX cell death and/or tissue necrosis in a tissue comprising contacting the  
 CC live tissue with at least one segment of neural thread proteins (NTP).  
 CC The methods are composition are useful for treating a neurodegenerative

CC disorder, such as Alzheimer's disease. This sequence represents an NTP  
 CC protein of the invention  
 XX  
 SQ Sequence 106 AA;

Query Match 100.0%; Score 582; DB 6; Length 106;  
 Best Local Similarity 100.0%; Pred. No. 2.1e-63;  
 Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFFVLYRFCFCFPETESHSLTQAGVQWCELGSPQLPSGFKRFSCLSLSSWDYSHEPPH 60  
 |||||  
 DB 1 MFFVLYRFCFCFPETESHSLTQAGVQWCELGSPQLPSGFKRFSCLSLSSWDYSHEPPH 60  
 |||||

QY 61 PVICFLMEKCLILYKPNGDTIGPILVQOGKQKLYISADLVHLIA 106  
 |||||  
 DB 61 PVICFLMEKCLILYKPNGDTIGPILVQOGKQKLYISADLVHLIA 106  
 |||||

RESULT 6  
 ADB37523  
 ID ADB37523 standard; protein; 106 AA.  
 XX  
 AC ADB37523;  
 XX  
 DT 04-DEC-2003 (first entry)  
 XX  
 DE Neural thread protein-like protein #2.  
 XX  
 KW Cytostatic; Antitumour; Antipsoriatic; Dermatological;  
 KW Antiatherosclerotic; Antiarteriosclerotic; Vasotropic; Antiinflammatory;  
 KW Immunosuppressive; Tranquillizer; Antiemetic; Virucide; AD7c-NTP;  
 KW neural thread protein; neuritic sprouting.  
 XX  
 OS Unidentified.  
 XX  
 PN WO2003008444-A2.  
 XX  
 PD 30-JAN-2003.  
 XX  
 PF 19-JUL-2002; 2002WO-CA001106.  
 XX  
 PR 19-JUL-2001; 2001US-0306150P.  
 PR 19-JUL-2001; 2001US-0306161P.  
 PR 16-NOV-2001; 2001US-0331477P.  
 XX  
 PA (NYMO-) NYMOX CORP.  
 XX  
 PI Averbach PA, Gemmell J;  
 XX  
 DR WPI; 2003-248000/24.  
 XX  
 PT Novel Related peptide or AD7c-neural thread peptide, useful for treating  
 PT unwanted cellular proliferations, glandular hyperplasia, unwanted facial  
 PT hair, warts and unwanted fatty tissue.  
 XX  
 PS Disclosure; Fig 5; 109pp; English.  
 XX  
 CC The present invention relates to AD7c-neural thread protein (NTP) and  
 CC related proteins and peptides (I; ADB37528-ADB37641). The sequences are  
 CC useful for treating a condition in a patient requiring removal or  
 CC destruction of cells. The condition can be selected from benign or  
 CC malignant tumour of a tissue, hyperplasia, hypertrophy or overgrowth of a  
 CC tissue, virally, bacterially or parasitically altered tissue, or  
 CC malformation of a tissue, where the tissue is selected from lung, breast,  
 CC stomach, pancreas, prostate, bladder, bone, ovary, skin, kidney, sinus,  
 CC colon, intestine, stomach, rectum, oesophagus, heart, spleen, salivary  
 CC gland, blood, brain and its coverings, spinal cord and its coverings,  
 CC muscle, connective tissue, adrenal, parathyroid, thyroid, uterus, testis,  
 CC pituitary, reproductive organs, liver, gall bladder, eye, ear, nose,  
 CC throat, tonsils, mouth, lymph nodes and lymphoid tissue. The condition is  
 CC preferably consiliary hypertrophy, prostatic hyperplasia, psoriasis,  
 CC eczema, dermatosis, cosmetic modification to a tissue (skin, eye, ear,  
 CC nose, throat, mouth, muscle, connective, hair or breast tissue), vascular

CC disease (atherosclerosis or arteriosclerosis), haemorrhoids, varicose  
 CC veins, inflammatory disease, autoimmune disease, metabolic disease,  
 CC hereditary/genetic disease, traumatic disease or physical injury,  
 CC nutritional deficiency disease, infectious disease, amyloid disease,  
 CC fibrosis disease, storage disease, congenital malformation, enzyme  
 CC deficiency disease, poisoning, intoxication, environmental disease,  
 CC radiation disease, endocrine disease, degenerative disease and mechanical  
 CC disease. The peptides are useful for treating unwanted cellular  
 CC proliferations, glandular (e.g. prostate) hyperplasia, unwanted facial  
 CC hair, warts and unwanted fatty tissue, or for preparing antibodies that  
 CC recognize and/or bind to Related proteins, Related peptides or NTP  
 CC peptides. The present sequence was used to illustrate the invention.  
 XX

SQ Sequence 106 AA;

Query Match 100.0%; Score 582; DB 7; Length 106;  
 Best Local Similarity 100.0%; Pred. No. 2.1e-63;  
 Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFFVLYRFCFCFPETESHSLTQAGVQWCELGSPQLPSGFKRFSCLSLSSWDYSHEPPH 60  
 |||||

DB 1 MFFVLYRFCFCFPETESHSLTQAGVQWCELGSPQLPSGFKRFSCLSLSSWDYSHEPPH 60  
 |||||

QY 61 PVICFLMEKCLILYKPNGDTIGPILVQOGKQKLYISADLVHLIA 106  
 |||||

DB 61 PVICFLMEKCLILYKPNGDTIGPILVQOGKQKLYISADLVHLIA 106  
 |||||

RESULT 7  
 AAO06149  
 ID AAO06149 standard; protein; 119 AA.

XX AAO06149;

DT 06-NOV-2001 (first entry)

XX Human polypeptide SEQ ID NO 20041.

XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;  
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;  
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;  
 KW nervous system disorders; arthritis; inflammation.

XX Homo sapiens.

XX WO200164835-A2.

XX 07-SEP-2001.

XX 26-FEB-2001; 2001WO-US0004927.

XX 28-FEB-2000; 2000US-00515126.

XX 18-MAY-2000; 2000US-00577409.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Drmanac RT;

XX WPI; 2001-514838/56.

XX N-PSDB; AAI86080.

PT Isolated nucleic acids and polypeptides, useful for preventing diagnosing

XX and treating e.g. leukemia, inflammation and immune disorders.

PS Claim 20; SEQ ID NO 20041; 1399pp + Sequence Listing; English.

XX The invention relates to human polynucleotides (AAI79941-AAI93841) and  
 CC the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to  
 CC cytokine, cell proliferation or cell differentiation or which may induce  
 CC production of other cytokines in other cell populations. The  
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or  
 CC peptide therapy. The polypeptides have various cytokine-like activities,  
 CC e.g. stem cell growth factor activity, haematopoiesis regulating

CC activity, tissue growth factor activity, immunomodulatory activity and  
CC activin/inhibin activity and may be useful in the diagnosis and/or  
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and  
CC inflammation. Note: The sequence data for this patent did not form part  
CC of the printed specification, but was obtained in electronic format  
CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 119 AA;  
  
Query Match 40.8%; Score 237.5; DB 4; Length 119;  
Best Local Similarity 72.1%; Pred. No. 6.7e-21;  
Matches 44; Conservative 4; Mismatches 10; Indels 3; Gaps 1;  
  
Qy 12 FFEFESHSLTQAGVQWVCELGSPQLPSGFRFSCLSLLSSWDYSHEPPHPV---ICSFLLM 68  
Db 2 FFEFESHVAQAGVQWVCDLGLSLQPLGLKFEFSCLSLLSSWDYRHTPPHPANLFFVFSFLV 61  
  
Qy 69 E 69  
Db 62 E 62  
  
RESULT 8  
AAB28760  
ID AAB28760 standard; protein; 85 AA.  
XX  
AC AAB28760;  
XX  
DT 30-JAN-2001 (first entry)  
XX  
DE Peptide #5.  
XX  
KW Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;  
KW antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer;  
KW vulnerable; anticonvulsant; antibacterial; antifungal; antiparasitic;  
KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;  
KW neurological disease; infection; human; secreted protein.  
XX  
OS Homo sapiens.  
XX  
PN WO200055198-A1.  
XX  
PD 21-SEP-2000.  
XX  
PF 09-MAR-2000; 2000WO-US006012.  
XX  
PR 12-MAR-1999; 99US-0124093P.  
PR 23-NOV-1999; 99US-0166989P.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Rosen CA, Ruben SM, Komatsoulis G;  
XX  
DR WPI; 2000-587520/55.  
XX  
PT Human secreted proteins and the nucleic acids that encode them, useful in  
PT gene therapy protocols and recombinant nucleic acid based procedures.  
XX  
PS Disclosure; Page 369; 391pp; English.  
XX  
CC Sequences AAB28702-B28751 represent the amino acid sequences of 50 human  
CC secreted proteins encoded by the genes AAC59907-C59956. The genes and  
CC proteins are useful for preventing, ameliorating or treating medical  
CC conditions, e.g. by protein or gene therapy. The genes are isolated from  
CC a range of human tissues disclosed in the specification. The nucleic  
CC acids, proteins, antibodies and (ant)agonists are useful in the  
CC diagnosis, treatment and prevention of: (a) cancer, e.g. breast and  
CC ovarian cancer, and other cancers of the adrenal gland, bone, bone  
CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b)  
CC immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic  
CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,  
CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)  
CC cardiovascular disorders such as myocardial ischaemia; (d) wound healing

CC ; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f)  
CC infectious diseases such as viral, bacterial, fungal and parasitic  
CC infections. The present sequence was used in the invention  
XX  
SQ Sequence 85 AA;  
  
Query Match 40.1%; Score 234.5; DB 3; Length 85;  
Best Local Similarity 72.1%; Pred. No. 1e-20;  
Matches 44; Conservative 2; Mismatches 14; Indels 1; Gaps 1;  
  
Qy 8 FCFEFETESHSLTQAGVQWVCELGSPQLPSGFRFSCLSLLSSWDYSHEPPHPV-ICSF 66  
Db 7 FNFCLFEMESHSLTQAGVQWVQPLGLKRFSCLSLPSGWDYGHLPHPANFCIF 66  
  
Qy 67 L 67  
Db 67 I 67  
  
RESULT 9  
AAB01399  
ID AAB01399 standard; protein; 375 AA.  
XX  
AC AAB01399;  
XX  
DT 20-OCT-2000 (first entry)  
XX  
DE Neuron-associated protein.  
XX  
KW Neuron associated protein; NEUAP; neurological disorder; epilepsy;  
KW ischemic cerebrovascular disease; stroke; cerebral neoplasm;  
KW Alzheimer's disease; Pick's disease; Huntington's disease; dementia;  
KW Parkinson's disease; demyelinating disease; meningitis; prion disease;  
KW kuru; Creutzfeldt-Jakob disease; neurofibromatosis; cerebral palsy;  
KW muscular dystrophy; central nervous system; CNS;  
KW peripheral nervous system; PNS; myopathy; schizophrenia;  
KW actinic keratosis; arteriosclerosis; atherosclerosis; bursitis;  
KW cirrhosis; hepatitis; mixed connective tissue disease; MCTD;  
KW myelofibrosis; paroxysmal nocturnal haemoglobinuria; cancer;  
KW autoimmune disease; inflammation; acquired immunodeficiency syndrome;  
KW AIDS; Addison's disease; adult respiratory distress syndrome; allergy;  
KW ankylosing spondylitis; amyloidosis; anaemia; asthma;  
KW werner syndrome, trauma; human.  
XX  
OS Homo sapiens.  
XX  
PN WO200034477-A2.  
XX  
PD 15-JUN-2000.  
XX  
PF 10-DEC-1999; 99WO-US030408.  
XX  
PR 11-DEC-1998; 98US-00210083.  
PR 09-FEB-1999; 99US-0119365P.  
PR 16-MAR-1999; 99US-0124687P.  
XX  
XX (INCY-) INCYTE PHARM INC.  
XX  
XX Tang YT, Yue H, Baughn MR, Hillman JL, Lal P, Au-Young J;  
XX Yang J, Lu DAM, Azimzai Y;  
XX  
XX WPI; 2000-423423/36.  
XX  
XX New human neuron-associated proteins and polynucleotides encoding them,  
XX useful for diagnosis, treatment and prevention of cell proliferative  
XX disorders including cancer, neuronal and neurological disorders.  
XX  
XX Disclosure; Page 143-144; 145pp; English.  
XX  
XX Human neuron-associated proteins (NEUAP) can be used for treating or  
XX preventing a disorder associated with decreased expression or activity of  
XX NEUAP. Antagonists of NEUAP are useful for treating or preventing  
XX disorder associated with increased expression or activity of NEUAP. NEUAP



PT cells, such as a benign or malignant tumor of a tissue or an inflammatory  
PT disease, comprises administering a neural thread protein (NTP) or a NTP  
XX gene to a mammal.

PS Example 2; Fig 1; 70pp; English.

XX The invention relates to a method for treating a condition in a patient  
CC requiring removal or destruction of cells. The method involves  
CC administering to a mammal a neural thread protein (NTP), or administering  
CC to a tumour or other target cell a NTP gene, where the expression of the  
CC NTP gene is induced resulting in expression of the NTP protein. The  
CC method and NTP are useful for treating a condition in a patient requiring  
CC removal or destruction of cells, such as a benign or malignant tumour of  
CC a tissue, a hyperplasia, hypertrophy, or overgrowth of a tissue,  
CC preferably tonsillar hypertrophy or prostatic hyperplasia, a virally,  
CC bacterially, or parasitically altered tissue, or a malformation of a  
CC tissue. Other conditions include a cosmetic modification to a tissue,  
CC such as removal of unwanted facial hair, warts or unwanted fatty tissue,  
CC a vascular disease, particularly atherosclerosis or arteriosclerosis,  
CC haemorrhoids, or varicose veins, an inflammatory disease, autoimmune  
CC disease, metabolic disease, hereditary/genetic disease, traumatic disease  
CC or physical injury, nutritional deficiency disease, infectious disease,  
CC congenital malformation, amyloid disease, fibrosis disease, storage  
CC disease, enzyme deficiency disease, poisoning, intoxication, degenerative  
CC disease, radiation disease, environmental disease, endocrine disease or  
CC mechanical disease. The invention is useful in protein therapy and gene  
CC therapy. The present sequence is AD7c-NTP protein

XX Sequence 375 AA;

Query Match 40.3%; Score 234.5; DB 5; Length 375;  
Best Local Similarity 72.1%; Pred. No. 6.7e-20;  
Matches 44; Conservative 2; Mismatches 14; Indels 1; Gaps 1;

Qy 8 FCFCFFETESHSLTQAGVQWCELGSPQLPSGFKRFSCLSLSSWDYSHEPPHPV-ICSP 66  
Db 297 FNFLCFEMESHVSVTQAGVQWPNLGSLOPLPGLKRFSCSLSPSSWDYGHLPHPANFCIF 356

Qy 67 L 67  
Db 357 I 357

RESULT 12  
ABR63268  
ID ABR63268 standard; protein; 375 AA.

XX ABR63268;

XX 28-AUG-2003 (first entry)

XX AD7c-NTP protein.

XX Cytostatic; Antibacterial; Immunosuppressive; Antiinflammatory;  
XX neural thread protein; NTP; tumour.

XX Unidentified.

XX WO2003008443-A2.

XX 30-JAN-2003.

XX 19-JUL-2002; 2002WO-CA001105.

XX 19-JUL-2001; 2001US-0306150P.

XX 19-JUL-2001; 2001US-0306161P.

XX 16-NOV-2001; 2001US-0331477P.

XX (NYMO-) NYMOX CORP.

XX Averbach PA;

XX WPI; 2003-247999/24.

XX  
PT  
XX  
XX  
PS

Novel neural thread protein peptide, referred as cell death peptide,  
useful for treating prostatic hyperplasia, psoriasis, eczema, dermatosis,  
atherosclerosis, cosmetic modification to skin, throat, mouth, muscle.

Disclosure; Fig 1; 77pp; English.

XX The present invention relates to a neural thread protein (NTP) peptide  
CC referred to as cell death peptide. Thought to be cytostatic,  
CC antibacterial, immunosuppressive and antiinflammatory. It is useful for  
CC treating a condition in a patient requiring removal or destruction of  
CC cells, for treating a condition such as benign or malignant tumor,  
CC inflammatory disease, autoimmune disease and infectious disease. The  
CC peptide useful for treatment is derived from the amino acid sequence for  
CC a pancreatic thread protein. The peptide is conjugated, linked or bound  
CC to a molecule chosen from antibody or its fragment, antibody-like binding  
CC molecule, where the molecule has a higher affinity for binding to a tumor  
CC or other target than binding to other cells. Treatment using NTP peptides  
CC can remove benign tumors with less risk and fewer of the undesirable side  
CC effects of surgery. The present sequence is an NTP amino acid sequence

XX Sequence 375 AA;

Query Match 40.3%; Score 234.5; DB 6; Length 375;  
Best Local Similarity 72.1%; Pred. No. 6.7e-20;  
Matches 44; Conservative 2; Mismatches 14; Indels 1; Gaps 1;

Qy 8 FCFCFFETESHSLTQAGVQWCELGSPQLPSGFKRFSCLSLSSWDYSHEPPHPV-ICSP 66  
Db 297 FNFLCFEMESHVSVTQAGVQWPNLGSLOPLPGLKRFSCSLSPSSWDYGHLPHPANFCIF 356

Qy 67 L 67  
Db 357 I 357

RESULT 13

ADA84017

ID ADA84017 standard; protein; 375 AA.

XX ADA84017;

XX 20-NOV-2003 (first entry)

XX Human POM80 protein.

XX human; marker; expressed sequence tag; EST; arabidopsis; tumour;  
XX stress-induced phenotype; hyperosmotic stress; colon cancer; immunogen;  
XX vaccine.

XX Homo sapiens.

XX WO2002103028-A2.

XX 27-DEC-2002.

XX 30-MAY-2002; 2002WO-IB004189.

XX 30-MAY-2001; 2001US-0293999P.

XX 22-OCT-2001; 2001US-0330457P.

XX 19-FEB-2002; 2002US-0357144P.

XX (BIOM-) BIOMEDICAL CENT.

XX Baranova AV, Yankovsky NK, Kozlov AP, Lobashev AV, Krukovskaya LL;

XX WPI; 2003-175241/17.

XX N-PSDB; ADA84016.

XX Determining if a nucleic acid is a marker for a phenotype/cell type of  
PT interest, by global comparison of expressed sequence tags known to be  
PT expressed in the phenotype/cell type with all ESTs expressed in normal  
PT tissue.



XX Claim 29; Page 398-400; 516pp; English.

XX The invention relates to a novel method for determining if a nucleic acid

CC is a marker for a predetermined phenotype/cell type of interest from a

CC biological species. The method comprises performing a global comparison

CC of a group of expressed sequence tags (ESTs) known to be expressed in the

CC phenotype/cell type of interest with all ESTs expressed in normal tissue

CC in order to identify ESTs that are preferentially expressed in the

CC phenotype/cell of interest. A method of the invention is useful for

CC determining whether a nucleic acid is a marker for a predetermined

CC phenotype or cell type of interest from a biological species, preferably

CC Arabidopsis or human. The cell type of interest is an abnormal cell such

CC as a tumour cell, and the predetermined phenotype is a stress-induced

CC phenotype such as hypersensitive stress or high salt conditions. A method

CC of the invention is also useful for determining the progression of colon

CC cancer in a human, for detecting a tumour cell, and for regulating or

CC preventing the growth of a tumour cell. An antibody of the invention is

CC useful for detecting the absence or presence of peptides encoded by

CC tumour-associated markers. A polypeptide of the invention is useful as an

CC immunogen for vaccinating an animal. The present sequence represents a

CC tumour-associated antigen of the invention.

XX Sequence 375 AA;

XX Query Match 40.3%; Score 234.5; DB 6; Length 375;

XX Best Local Similarity 72.1%; Pred. No. 6.7e-20;

XX Matches 44; Conservative 2; Mismatches 14; Indels 1; Gaps 1;

QY 8 FCFCFFETESHSLTQAGVQWVCELGSPQLPSGFKRFSCLLSLSSWDYSHPEHPHV-ICSF 66

Db 297 FNFCLFEMESHSHVTQAGVQWVQPNLGSLOPLPGLKRFSCLSLPSSWDYGHLPHPANFCIF 356

QY 67 L 67

Db 357 I 357

RESULT 14

ID ABU03024 standard; protein; 375 AA.

XX ABU03024;

XX 20-JAN-2003 (first entry)

XX Human neural thread protein AD7C-NTP.

XX Neural thread protein; NTP-peptide; AD7C-NTP; surgical excision;

XX transplantation; grafting; chemotherapy; immunotherapy; vaccination;

XX ablation; cryotherapy; laser therapy; phototherapy; gene therapy;

XX radiation; tumour; hyperplasia; hypertrophy; overgrowth of tissue;

XX malformation of tissue; tonsillary hypertrophy; prostatic hyperplasia;

XX cosmetic modification; vascular disease; atherosclerosis;

XX arteriosclerosis; haemorrhoid; varicose vein; inflammatory disease;

XX autoimmune disease; metabolic disease; traumatic disease;

XX physical injury; nutritional deficiency disease; infectious disease;

XX amyloid disease; fibrosis disease; storage disease;

XX congenital malformation; enzyme deficiency disease; poisoning;

XX intoxication; environmental disease; radiation disease;

XX endocrine disease; degenerative disease; mechanical disease.

XX Homo sapiens.

XX W0200297030-A2.

XX 05-DEC-2002.

XX 24-MAY-2002; 2002WO-CA000759.

XX 25-MAY-2001; 2001US-0293156P.

XX (NYMO-) NYMOX CORP.

XX

XX Averback PA;

XX WPI; 2003-041406/03.

XX Novel peptides similar in amino acid sequence to neural thread proteins

PT (NTP), useful for treating unwanted cellular proliferations such as

PT malignant tumors and prostatic hyperplasia.

XX Disclosure; Fig 1; 78pp; English.

XX The invention describes an NTP-peptide (I) comprising at least one amino

CC acid sequence corresponding to part of the amino acid sequence of a

CC neural thread protein, AD7C-NTP. The invention provides a method of

CC treating a condition requiring removal or destruction of cells of a

CC mammal comprising administering to a mammal, a therapeutic amount of (I).

CC The treatment is administered to the mammal before, during or after

CC surgical excision, transplantation, grafting, chemotherapy,

CC immunotherapy, vaccination, thermal or electrical ablation, cryotherapy,

CC laser therapy, phototherapy, gene therapy and/or radiation. The method is

CC useful for treatment of benign or malignant tumour; hyperplasia,

CC hypertrophy or overgrowth of tissue; virally, bacterially or

CC parasitically altered tissue; malformation of tissue selected from lung,

CC breast, stomach, pancreas, prostate, bladder, bone, ovary, skin, kidney,

CC sinus, colon, intestine, rectum, esophagus, heart, spleen, salivary

CC gland, blood, brain and its coverings, spinal cord, muscle, connective

CC tissue, adrenal, parathyroid, thyroid, uterus, testis, pituitary,

CC reproductive organs, liver, hair, gall bladder, eye, ear, nose, throat,

CC tonsils, mouth and lymph nodes and lymphoid system; tonsillary

CC hypertrophy; prostatic hyperplasia; cosmetic modification to a tissue;

CC vascular disease (atherosclerosis or arteriosclerosis); haemorrhoids;

CC varicose veins; inflammatory disease; autoimmune disease; metabolic

CC disease; hereditary/genetic disease; traumatic disease; physical injury;

CC nutritional deficiency disease; infectious disease; amyloid disease;

CC fibrosis disease; storage disease; congenital malformation; enzyme

CC deficiency disease; poisoning; intoxication; environmental disease;

CC radiation disease; endocrine disease; degenerative disease and mechanical

CC disease. This is the amino acid sequence of the human neural thread

CC protein AD7C-NTP

XX Sequence 375 AA;

XX Query Match 40.3%; Score 234.5; DB 6; Length 375;

XX Best Local Similarity 72.1%; Pred. No. 6.7e-20;

XX Matches 44; Conservative 2; Mismatches 14; Indels 1; Gaps 1;

QY 8 FCFCFFETESHSLTQAGVQWVCELGSPQLPSGFKRFSCLLSLSSWDYSHPEHPHV-ICSF 66

Db 297 FNFCLFEMESHSHVTQAGVQWVQPNLGSLOPLPGLKRFSCLSLPSSWDYGHLPHPANFCIF 356

QY 67 L 67

Db 357 I 357

RESULT 15

AB999774

ID ABB99774 standard; protein; 375 AA.

XX ABB99774;

XX 24-MAR-2003 (first entry)

XX Amino acid sequence of human neuronal thread protein AD7C-NTP.

XX Human; neuronal thread protein; AD7C-NTP; Alzheimer's disease; histone;

XX neurodegeneration; in vivo gene expression; amphipathic compound;

XX gene therapy.

XX Homo sapiens.

XX W0200299036-A2.

XX



PD 12-DEC-2002.  
XX  
PF 28-MAY-2002; 2002WO-US016429.  
XX  
PR 01-JUN-2001; 2001US-00872968.  
XX  
PA (RHOD-) RHODE ISLAND HOSPITAL.  
XX  
PI Wands JR, De La Monte SM;  
XX  
DR WPI; 2003-140605/13.  
DR N-PSDB; ABZ23236.  
XX  
PT Inducing prolonged in vivo gene expression in mammal by contacting  
PT neuronal tissue with composition comprising Alzheimer's disease-  
PT associated neural thread protein 7c antisense nucleic acid, histone,  
PT amphipathic compound.  
XX  
PS Disclosure; Page 35; 69pp; English.  
XX  
CC The present sequence represents a human neuronal thread protein AD7c-NTP.  
CC AD7c-NTP is overexpressed in brains with Alzheimer's disease at early and  
CC intermediate stages of neurodegeneration. The expression of AD7c-NTP may  
CC be reduced using the method of the invention. The specification describes  
CC a method for inducing prolonged in vivo gene expression in a mammal. The  
CC method comprises contacting a non-muscular tissue with a composition  
CC comprising a nucleic acid, histone and an amphipathic compound. The  
CC method is useful for inducing prolonged in vivo gene expression in non-  
CC muscular tissue of a mammal, e.g. neuronal tissue, central nervous system  
CC (CNS) tissue, tissue comprising a post-mitotic neuronal cell, cortical  
CC neuronal cell or hippocampal neuronal cell, glial cell, or vascular  
CC endothelial cell. The method is useful in gene therapy applications to  
CC treat Alzheimer's disease, where the composition comprises antisense  
CC AD7c-NTP nucleic acid  
XX  
SQ Sequence 375 AA;  
  
Query Match 40.3%; Score 234.5; DB 6; Length 375;  
Best Local Similarity 72.1%; Pred. No. 6.7e-20;  
Matches 44; Conservative 2; Mismatches 14; Indels 1; Gaps 1;  
  
Qy 8 FCFCFFETESHSLTQAGVQWCELGSPQLPSGFKRFSCLSLLSSWDYSHEPPHPV-ICSF 66  
Db 297 FNFCLFEMESHVSVTQAGVQWNLGSLQLPLPGLKRFSCLSLPSSWDYGHLPHPANFCIF 356  
  
Qy 67 L 67  
Db 357 I 357

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
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#### SUMMARIES

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4	582	100.0	106	14	US-10-153-334-5
5	582	100.0	106	14	US-10-198-069-5
6	582	100.0	106	14	US-10-198-070-5
7	234.5	40.3	375	9	US-09-964-666-2
8	234.5	40.3	375	9	US-09-964-412-2
9	234.5	40.3	375	10	US-09-964-667-2
10	234.5	40.3	375	10	US-09-872-368-2
11	234.5	40.3	375	10	US-09-964-678A-2

12	234.5	40.3	375	14	US-10-146-130-2	Sequence 2, Appli
13	234.5	40.3	375	14	US-10-092-934-10	Sequence 10, Appli
14	234.5	40.3	375	14	US-10-153-334-1	Sequence 1, Appli
15	234.5	40.3	375	14	US-10-198-069-1	Sequence 1, Appli
16	234.5	40.3	375	14	US-10-157-031-299	Sequence 299, App
17	234.5	40.3	375	14	US-10-198-070-1	Sequence 1, Appli
18	234.5	40.3	375	16	US-10-755-889-410	Sequence 410, App
19	234.5	40.3	375	17	US-10-910-173-2	Sequence 2, Appli
20	230.5	39.6	89	18	US-10-450-763-40159	Sequence 40159, A
21	230.5	39.6	123	15	US-10-104-047-2112	Sequence 2112, Ap
22	226	38.8	97	15	US-10-276-774-2008	Sequence 2008, Ap
23	223.5	38.4	100	15	US-10-094-749-3044	Sequence 3044, Ap
24	218.5	37.5	101	15	US-10-094-749-2181	Sequence 2181, Ap
25	215.5	37.0	146	18	US-10-450-763-38554	Sequence 38554, A
26	215.5	37.0	433	14	US-10-017-161-2092	Sequence 2092, Ap
27	215.5	37.0	433	15	US-10-292-798-1738	Sequence 1738, Ap
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30	212.5	36.5	93	10	US-09-764-891-5337	Sequence 5337, Ap
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37	203.5	35.0	116	13	US-10-001-835-161	Sequence 161, App
38	203	34.9	151	14	US-10-198-070-22	Sequence 22, Appli
39	201	34.5	135	15	US-10-424-599-24280	Sequence 24280, A
40	201	34.5	158	15	US-10-104-047-3047	Sequence 3047, Ap
41	199.5	34.3	105	15	US-10-108-260A-3988	Sequence 3988, Ap
42	199	34.2	127	15	US-10-108-260A-2558	Sequence 2558, Ap
43	198	34.0	62	15	US-10-001-885-98	Sequence 98, Appli
44	198	34.0	62	20	US-11-057-447-98	Sequence 98, Appli
45	198	34.0	74	15	US-10-276-774-1929	Sequence 1929, Ap

#### ALIGNMENTS

##### RESULT 1

US-10-138-516-4  
; Sequence 4, Application US/10138516  
; Publication No. US20030003445A1  
; GENERAL INFORMATION:  
; APPLICANT: AVERBACK, PAUL  
; TITLE OF INVENTION: METHOD OF PREVENTING CELL DEATH USING ANTIBODIES TO  
; TITLE OF INVENTION: NEURAL THREAD PROTEINS  
; FILE REFERENCE: 59003.000004  
; CURRENT APPLICATION NUMBER: US/10/138.516  
; CURRENT FILING DATE: 2002-07-23  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 106  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-138-516-4

Query Match 100.0%; Score 582; DB 14; Length 106;  
Best Local Similarity 100.0%; Pred. No. 2.5e-59;  
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFFVLYRFCFFETESHSLTQAGVQWCELGSPQLPSGFKRFSCLSLSSWDSYSHPEPH 60  
Db 1 MFFVLYRFCFFETESHSLTQAGVQWCELGSPQLPSGFKRFSCLSLSSWDSYSHPEPH 60

Qy 61 PVI CSFLMEKCLILYKNGDTIGPILVQOGRKQKLYISADLVHLIA 106  
Db 61 PVI CSFLMEKCLILYKNGDTIGPILVQOGRKQKLYISADLVHLIA 106

RESULT 2  
US-10-146-130-6

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; Sequence 6, Application US/10146130
; Publication No. US20030004107A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; TITLE OF INVENTION: METHOD OF PREVENTING CELL DEATH USING SEGMENTS OF
; TITLE OF INVENTION: NEURAL THREAD PROTEINS
; FILE REFERENCE: 59003.000007
; CURRENT APPLICATION NUMBER: US/10/146.130
; CURRENT FILING DATE: 2002-08-06
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-146-130-6

Query Match      100.0%; Score 582; DB 14; Length 106;
Best Local Similarity 100.0%; Pred. No. 2.5e-59;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFFVLYRFCFCFFETESHSLTQAGVQWCELGSPQLPSGFKRFSCLSLSSWDYSHEPPH 60
Db 1 MFFVLYRFCFCFFETESHSLTQAGVQWCELGSPQLPSGFKRFSCLSLSSWDYSHEPPH 60

Qy 61 PVICFLMEKCLILYKPNGDTIGPILVQOQKROKLYISADLVHLIA 106
Db 61 PVICFLMEKCLILYKPNGDTIGPILVQOQKROKLYISADLVHLIA 106

RESULT 3
US-10-092-934-5
; Sequence 5, Application US/10092934
; Publication No. US20030054990A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; TITLE OF INVENTION: METHODS OF USING NEURAL THREAD PROTEINS TO TREAT TUMORS
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 018792-0199
; CURRENT APPLICATION NUMBER: US/10/092.934
; CURRENT FILING DATE: 2002-06-05
; PRIOR APPLICATION NUMBER: 60/273,957
; PRIOR FILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-092-934-5

Query Match      100.0%; Score 582; DB 14; Length 106;
Best Local Similarity 100.0%; Pred. No. 2.5e-59;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFFVLYRFCFCFFETESHSLTQAGVQWCELGSPQLPSGFKRFSCLSLSSWDYSHEPPH 60
Db 1 MFFVLYRFCFCFFETESHSLTQAGVQWCELGSPQLPSGFKRFSCLSLSSWDYSHEPPH 60

Qy 61 PVICFLMEKCLILYKPNGDTIGPILVQOQKROKLYISADLVHLIA 106
Db 61 PVICFLMEKCLILYKPNGDTIGPILVQOQKROKLYISADLVHLIA 106

RESULT 4
US-10-153-334-5
; Sequence 5, Application US/10153334
; Publication No. US20030096350A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF
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; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 59003-000006
; CURRENT APPLICATION NUMBER: US/10/153.334
; CURRENT FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: 60/293,156
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-153-334-5

Query Match      100.0%; Score 582; DB 14; Length 106;
Best Local Similarity 100.0%; Pred. No. 2.5e-59;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFFVLYRFCFCFFETESHSLTQAGVQWCELGSPQLPSGFKRFSCLSLSSWDYSHEPPH 60
Db 1 MFFVLYRFCFCFFETESHSLTQAGVQWCELGSPQLPSGFKRFSCLSLSSWDYSHEPPH 60

Qy 61 PVICFLMEKCLILYKPNGDTIGPILVQOQKROKLYISADLVHLIA 106
Db 61 PVICFLMEKCLILYKPNGDTIGPILVQOQKROKLYISADLVHLIA 106

RESULT 5
US-10-198-069-5
; Sequence 5, Application US/10198069
; Publication No. US20030096756A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 59003.000009
; CURRENT APPLICATION NUMBER: US/10/198.069
; CURRENT FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/306,161
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/306,150
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/331,477
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-198-069-5

Query Match      100.0%; Score 582; DB 14; Length 106;
Best Local Similarity 100.0%; Pred. No. 2.5e-59;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFFVLYRFCFCFFETESHSLTQAGVQWCELGSPQLPSGFKRFSCLSLSSWDYSHEPPH 60
Db 1 MFFVLYRFCFCFFETESHSLTQAGVQWCELGSPQLPSGFKRFSCLSLSSWDYSHEPPH 60

Qy 61 PVICFLMEKCLILYKPNGDTIGPILVQOQKROKLYISADLVHLIA 106
Db 61 PVICFLMEKCLILYKPNGDTIGPILVQOQKROKLYISADLVHLIA 106

RESULT 6
US-10-198-070-5
; Sequence 5, Application US/10198070
; Publication No. US20030109437A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; APPLICANT: GEMMELL, JACK
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; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 59003.000008
; CURRENT APPLICATION NUMBER: US/10/198,070
; CURRENT FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/306,161
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/306,150
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/331,477
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-198-070-5

Query Match      100.0%; Score 582; DB 14; Length 106;
Best Local Similarity 100.0%; Pred. No. 2.5e-59;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFFVLYRFCFFETESHSLTQAGVQWCELGSPQLPSGFKRFSCLLSLSSWDYSHEPPH 60
Db 1 MFFVLYRFCFFETESHSLTQAGVQWCELGSPQLPSGFKRFSCLLSLSSWDYSHEPPH 60

Qy 61 PVICFLMEKCLILYKNGDGTIGPLVQOGRKQKLYISADLVHLIA 106
Db 61 PVICFLMEKCLILYKNGDGTIGPLVQOGRKQKLYISADLVHLIA 106

RESULT 7
US-09-964-666-2
; Sequence 2, Application US/09964666
; Patent No. US20020104108A1
; GENERAL INFORMATION:
; APPLICANT: de la Monte, Suzanne
; Wands, Jack R.
; TITLE OF INVENTION: Transgenic Animals and Cell Lines for
; Screening Drugs Effective for the Treatment or Prevention
; of Alzheimer's Disease
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
; STREET: 1100 New York Ave., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/964,666
; FILING DATE: 28-Sep-2001
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 0609.4370000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 375 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-09-964-666-2
Query Match      40.3%; Score 234.5; DB 9; Length 375;
Best Local Similarity 72.1%; Pred. No. 2.1e-18;
Matches 44; Conservative 2; Mismatches 14; Indels 1; Gaps 1;

Qy 8 FCFCFFETESHSLTQAGVQWCELGSPQLPSGFKRFSCLLSLSSWDYSHEPPHV-ICSF 66
Db 297 FNFCLEFEMESHVLTQAGVQWPNLGSLOPLPGLKRFCSCLSLPSSWDYGHLPHPANFCIF 356

Qy 67 L 67
Db 357 I 357

RESULT 8
US-09-964-412-2
; Sequence 2, Application US/09964412
; Patent No. US20020129391A1
; GENERAL INFORMATION:
; APPLICANT: de la Monte, Suzanne
; Wands, Jack R.
; TITLE OF INVENTION: Transgenic Animals and Cell Lines for
; Screening Drugs Effective for the Treatment or Prevention
; of Alzheimer's Disease
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
; STREET: 1100 New York Ave., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/964,412
; FILING DATE: 28-Sep-2001
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 0609.4370000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 375 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-09-964-412-2
Query Match      40.3%; Score 234.5; DB 9; Length 375;
Best Local Similarity 72.1%; Pred. No. 2.1e-18;
Matches 44; Conservative 2; Mismatches 14; Indels 1; Gaps 1;

Qy 8 FCFCFFETESHSLTQAGVQWCELGSPQLPSGFKRFSCLLSLSSWDYSHEPPHV-ICSF 66
Db 297 FNFCLEFEMESHVLTQAGVQWPNLGSLOPLPGLKRFCSCLSLPSSWDYGHLPHPANFCIF 356

Qy 67 L 67
Db 357 I 357

RESULT 9
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; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-964-666-2

Query Match      40.3%; Score 234.5; DB 9; Length 375;
Best Local Similarity 72.1%; Pred. No. 2.1e-18;
Matches 44; Conservative 2; Mismatches 14; Indels 1; Gaps 1;

Qy 8 FCFCFFETESHSLTQAGVQWCELGSPQLPSGFKRFSCLLSLSSWDYSHEPPHV-ICSF 66
Db 297 FNFCLEFEMESHVLTQAGVQWPNLGSLOPLPGLKRFCSCLSLPSSWDYGHLPHPANFCIF 356

Qy 67 L 67
Db 357 I 357

RESULT 8
US-09-964-412-2
; Sequence 2, Application US/09964412
; Patent No. US20020129391A1
; GENERAL INFORMATION:
; APPLICANT: de la Monte, Suzanne
; Wands, Jack R.
; TITLE OF INVENTION: Transgenic Animals and Cell Lines for
; Screening Drugs Effective for the Treatment or Prevention
; of Alzheimer's Disease
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
; STREET: 1100 New York Ave., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/964,412
; FILING DATE: 28-Sep-2001
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 0609.4370000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 375 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-09-964-412-2
Query Match      40.3%; Score 234.5; DB 9; Length 375;
Best Local Similarity 72.1%; Pred. No. 2.1e-18;
Matches 44; Conservative 2; Mismatches 14; Indels 1; Gaps 1;

Qy 8 FCFCFFETESHSLTQAGVQWCELGSPQLPSGFKRFSCLLSLSSWDYSHEPPHV-ICSF 66
Db 297 FNFCLEFEMESHVLTQAGVQWPNLGSLOPLPGLKRFCSCLSLPSSWDYGHLPHPANFCIF 356

Qy 67 L 67
Db 357 I 357

RESULT 9
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US-09-964-667-2  
; Sequence 2, Application US/09964667  
; Publication No. US20030033621A1  
; GENERAL INFORMATION:  
; APPLICANT: de la Monte, Suzanne  
; Wands, Jack R.  
; TITLE OF INVENTION: Transgenic Animals and Cell Lines for  
; Screening Drugs Effective for the Treatment or Prevention  
; of Alzheimer's Disease  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.  
; STREET: 1100 New York Ave., Suite 600  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/964,667  
; FILING DATE: 28-Sep-2001  
; CLASSIFICATION: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Esmond, Robert W.  
; REGISTRATION NUMBER: 32,893  
; REFERENCE/DOCKET NUMBER: 0609.4370000  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-2600  
; TELEFAX: 202-371-2540  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 375 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-09-964-667-2

Query Match 40.3%; Score 234.5; DB 10; Length 375;  
Best Local Similarity 72.1%; Pred. No. 2.1e-18;  
Matches 44; Conservative 2; Mismatches 14; Indels 1; Gaps 1;  
Qy 8 FCFCFFETESHSLTQAGVQWCELGSPQLPSGFKRFSCLSLLSSWDYSHPEPPHPV-ICSF 66  
Db 297 FNFCLFEMESHVQTQAGVQWPNLGSLOPLPPGLKRFSCLSLPSSWDYGHLPHPANFCIF 356  
Qy 67 L 67  
Db 357 I 357

RESULT 10  
US-09-872-968-2  
; Sequence 2, Application US/09872968  
; Publication No. US20030050262A1  
; GENERAL INFORMATION:  
; APPLICANT: Wands, Jack R  
; APPLICANT: de la Monte, Suzanne M  
; TITLE OF INVENTION: Inhibition of Neurodegeneration  
; FILE REFERENCE: 21486-047  
; CURRENT APPLICATION NUMBER: US/09/872,968  
; CURRENT FILING DATE: 2001-06-01  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 375  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-872-968-2

Query Match 40.3%; Score 234.5; DB 10; Length 375;  
Best Local Similarity 72.1%; Pred. No. 2.1e-18;  
Matches 44; Conservative 2; Mismatches 14; Indels 1; Gaps 1;  
Qy 8 FCFCFFETESHSLTQAGVQWCELGSPQLPSGFKRFSCLSLLSSWDYSHPEPPHPV-ICSF 66  
Db 297 FNFCLFEMESHVQTQAGVQWPNLGSLOPLPPGLKRFSCLSLPSSWDYGHLPHPANFCIF 356  
Qy 67 L 67  
Db 357 I 357  
RESULT 11  
US-09-964-678A-2  
; Sequence 2, Application US/09964678A  
; Publication No. US20030066097A1  
; GENERAL INFORMATION:  
; APPLICANT: de la Monte, Suzanne  
; APPLICANT: Wands, Jack R.  
; TITLE OF INVENTION: Transgenic Animals and Cell Lines for Screening Drugs  
; TITLE OF INVENTION: Effective for the Treatment or Prevention of  
; TITLE OF INVENTION: Alzheimer's Disease  
; FILE REFERENCE: 0609.4370002  
; CURRENT APPLICATION NUMBER: US/09/964,678A  
; CURRENT FILING DATE: 2001-09-28  
; PRIOR APPLICATION NUMBER: 09/380,203  
; PRIOR FILING DATE: 2000-04-25  
; PRIOR APPLICATION NUMBER: PCT/US98/03685  
; PRIOR FILING DATE: 1998-02-26  
; PRIOR APPLICATION NUMBER: 60/038,908  
; PRIOR FILING DATE: 1997-02-26  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 375  
; TYPE: PRT  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: AD7c-NTP cDNA  
US-09-964-678A-2

Query Match 40.3%; Score 234.5; DB 10; Length 375;  
Best Local Similarity 72.1%; Pred. No. 2.1e-18;  
Matches 44; Conservative 2; Mismatches 14; Indels 1; Gaps 1;  
Qy 8 FCFCFFETESHSLTQAGVQWCELGSPQLPSGFKRFSCLSLLSSWDYSHPEPPHPV-ICSF 66  
Db 297 FNFCLFEMESHVQTQAGVQWPNLGSLOPLPPGLKRFSCLSLPSSWDYGHLPHPANFCIF 356  
Qy 67 L 67  
Db 357 I 357  
RESULT 12  
US-10-146-130-2  
; Sequence 2, Application US/10146130  
; Publication No. US20030004107A1  
; GENERAL INFORMATION:  
; APPLICANT: AVERBACK, PAUL  
; TITLE OF INVENTION: METHOD OF PREVENTING CELL DEATH USING SEGMENTS OF  
; FILE REFERENCE: 59003.000007  
; CURRENT APPLICATION NUMBER: US/10/146,130  
; CURRENT FILING DATE: 2002-08-06  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 375  
; TYPE: PRT  
; ORGANISM: Homo sapiens

## US-10-146-130-2

Query Match 40.3%; Score 234.5; DB 14; Length 375;  
Best Local Similarity 72.1%; Pred. No. 2.1e-18;  
Matches 44; Conservative 2; Mismatches 14; Indels 1; Gaps 1;  
Qy 8 FCFCFFETESHSLTQAGVQWVONLGSQPLPSGFKRFSCLSLSSWDYSHPEHPV-ICSF 66  
Db 297 FNFLCFEMESHVTOAGVQWVONLGSQPLPSGFKRFSCLSLSSWDYSHPEHPV-ICSF 356  
Qy 67 L 67  
Db 357 I 357

## RESULT 13

US-10-092-934-10  
; Sequence 10, Application US/10092934  
; Publication No. US20030054990A1  
; GENERAL INFORMATION:  
; APPLICANT: AVERBACK, PAUL  
; TITLE OF INVENTION: METHODS OF USING NEURAL THREAD PROTEINS TO TREAT TUMORS  
; TITLE OF INVENTION: AND CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF  
; TITLE OF INVENTION: CELLS  
; FILE REFERENCE: 018792-0199  
; CURRENT APPLICATION NUMBER: US/10/092,934  
; CURRENT FILING DATE: 2002-06-05  
; PRIOR APPLICATION NUMBER: 60/273,957  
; PRIOR FILING DATE: 2001-03-08  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 10  
; LENGTH: 375  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-092-934-10

Query Match 40.3%; Score 234.5; DB 14; Length 375;  
Best Local Similarity 72.1%; Pred. No. 2.1e-18;  
Matches 44; Conservative 2; Mismatches 14; Indels 1; Gaps 1;  
Qy 8 FCFCFFETESHSLTQAGVQWVONLGSQPLPSGFKRFSCLSLSSWDYSHPEHPV-ICSF 66  
Db 297 FNFLCFEMESHVTOAGVQWVONLGSQPLPSGFKRFSCLSLSSWDYSHPEHPV-ICSF 356  
Qy 67 L 67  
Db 357 I 357

## RESULT 14

US-10-153-334-1  
; Sequence 1, Application US/10153334  
; Publication No. US20030096350A1  
; GENERAL INFORMATION:  
; APPLICANT: AVERBACK, PAUL  
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER  
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF  
; TITLE OF INVENTION: CELLS  
; FILE REFERENCE: 59003-000006  
; CURRENT APPLICATION NUMBER: US/10/153,334  
; CURRENT FILING DATE: 2002-05-24  
; PRIOR APPLICATION NUMBER: 60/293,156  
; PRIOR FILING DATE: 2001-05-25  
; NUMBER OF SEQ ID NOS: 53  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 375  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-153-334-1

Query Match 40.3%; Score 234.5; DB 14; Length 375;

Best Local Similarity 72.1%; Pred. No. 2.1e-18;  
Matches 44; Conservative 2; Mismatches 14; Indels 1; Gaps 1;  
Qy 8 FCFCFFETESHSLTQAGVQWVONLGSQPLPSGFKRFSCLSLSSWDYSHPEHPV-ICSF 66  
Db 297 FNFLCFEMESHVTOAGVQWVONLGSQPLPSGFKRFSCLSLSSWDYSHPEHPV-ICSF 356  
Qy 67 L 67  
Db 357 I 357

## RESULT 15

US-10-198-069-1  
; Sequence 1, Application US/10198069  
; Publication No. US20030096756A1  
; GENERAL INFORMATION:  
; APPLICANT: AVERBACK, PAUL  
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER  
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF  
; TITLE OF INVENTION: CELLS  
; FILE REFERENCE: 59003.000009  
; CURRENT APPLICATION NUMBER: US/10/198,069  
; CURRENT FILING DATE: 2002-07-19  
; PRIOR APPLICATION NUMBER: 60/306,161  
; PRIOR FILING DATE: 2001-07-19  
; PRIOR APPLICATION NUMBER: 60/306,150  
; PRIOR FILING DATE: 2001-07-19  
; PRIOR APPLICATION NUMBER: 60/331,477  
; PRIOR FILING DATE: 2001-11-16  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 375  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-198-069-1

Query Match 40.3%; Score 234.5; DB 14; Length 375;  
Best Local Similarity 72.1%; Pred. No. 2.1e-18;  
Matches 44; Conservative 2; Mismatches 14; Indels 1; Gaps 1;  
Qy 8 FCFCFFETESHSLTQAGVQWVONLGSQPLPSGFKRFSCLSLSSWDYSHPEHPV-ICSF 66  
Db 297 FNFLCFEMESHVTOAGVQWVONLGSQPLPSGFKRFSCLSLSSWDYSHPEHPV-ICSF 356  
Qy 67 L 67  
Db 357 I 357

Search completed: October 11, 2005, 07:39:45  
Job time : 178.706 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 11, 2005, 06:57:19 ; Search time 24.2326 Seconds  
(without alignments)  
326.535 Million cell updates/sec

Title: US-10-092-934-5  
Perfect score: 582  
Sequence: 1 MFFVLRFPCFETESHSL.....VQGGKQKLYISADLVHLIA 106

Scoring table:  
BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	234.5	40.3	375	2	US-08-454-557C-121
2	234.5	40.3	375	2	US-08-340-426D-121
3	234.5	40.3	375	2	US-08-450-673C-121
4	234.5	40.3	375	4	US-09-872-968-2
5	214	36.8	397	5	PCT-US95-1711A-121
6	206	35.4	61	4	US-09-513-999C-4581
7	194.5	33.4	87	4	US-09-205-258-342
8	194.5	33.4	119	4	US-09-513-999C-7867
9	184	31.6	60	4	US-09-513-999C-7075
10	184	31.6	67	4	US-09-621-976-5968
11	182	31.3	96	4	US-09-513-999C-6065
12	182	31.3	102	4	US-09-621-976-6112
13	181.5	31.2	97	4	US-09-513-999C-4770
14	180.5	31.0	66	4	US-09-621-976-5606
15	180	30.9	60	4	US-09-513-999C-7143
16	179	30.8	87	4	US-09-621-976-4482
17	179	30.8	121	4	US-09-513-999C-7874
18	174	29.9	108	4	US-09-513-999C-7878
19	172.5	29.6	64	4	US-09-621-976-5588
20	172	29.6	54	4	US-09-513-999C-7519
21	172	29.6	76	4	US-09-621-976-6338
22	170	29.2	58	4	US-09-513-999C-4523
23	170	29.2	59	4	US-09-471-276-1317
24	168	28.9	65	4	US-09-513-999C-6665
25	168	28.9	92	4	US-09-248-796A-16335
26	166	28.5	90	4	US-09-621-976-4397
27	165	28.4	70	4	US-09-513-999C-6561

28	164.5	28.3	132	4	US-09-636-215-573	Sequence 573, App
29	164.5	28.3	132	4	US-09-685-166A-573	Sequence 573, App
30	164.5	28.3	132	4	US-09-679-426-573	Sequence 573, App
31	164.5	28.3	132	4	US-09-759-143-573	Sequence 573, App
32	164.5	28.3	132	4	US-09-651-236-573	Sequence 573, App
33	164.5	28.3	135	4	US-09-685-166A-884	Sequence 884, App
34	164.5	28.3	135	4	US-09-679-426-884	Sequence 884, App
35	164.5	28.3	135	4	US-09-759-143-884	Sequence 884, App
36	160	27.5	91	4	US-09-621-976-5929	Sequence 5929, App
37	159	27.3	63	4	US-09-621-976-6005	Sequence 6005, App
38	159	27.3	103	4	US-09-513-999C-5327	Sequence 5327, App
39	158.5	27.2	776	4	US-10-020-079-24	Sequence 24, Appl
40	158.5	27.2	789	4	US-10-020-079-22	Sequence 22, Appl
41	158.5	27.2	863	4	US-10-020-079-32	Sequence 32, Appl
42	158.5	27.2	876	4	US-10-020-079-30	Sequence 30, Appl
43	158.5	27.2	889	4	US-10-020-079-20	Sequence 20, Appl
44	158.5	27.2	895	4	US-10-020-079-18	Sequence 18, Appl
45	158.5	27.2	976	4	US-10-020-079-28	Sequence 28, Appl

ALIGNMENTS

RESULT 1  
US-08-454-557C-121  
; Sequence 121, Application US/08454557C  
; Patent No. 5830670  
; GENERAL INFORMATION:  
; APPLICANT: de la Monte, Suzanne  
; APPLICANT: Wands, Jack R.  
; TITLE OF INVENTION: Neutral Thread Protein Gene Expression and Detection  
; NUMBER OF SEQUENCES: 121  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.  
; STREET: 1100 New York Avenue, Suite 600  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/454,557C  
; FILING DATE: 30-MAY-1995  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ludwig, Steven R.  
; REGISTRATION NUMBER: 36,203  
; REFERENCE/DOCKET NUMBER: 0609.3840003  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 371-2600  
; TELEFAX: (202) 371-2540  
; INFORMATION FOR SEQ ID NO. 121:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 375 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-454-557C-121

Query Match 40.3%; Score 234.5; DB 2; Length 375;  
Best Local Similarity 72.1%; Pred. No. 3.3e-21;  
Matches 44; Conservative 2; Mismatches 14; Indels 1; Gaps 1;  
QY 8 FCFCFFETESHSLTQAGVQWCELGSPDLPSCGFKRFSCLLSLSSWDYSHEPHPV-ICSF 66  
DB 297 FNFLCFEMESHVSVTQAGVQWPNLGLSLOPLPGLKRFKFSCLLSLSSWDYSHEPHPV-ICSF 356  
QY 67 L 67

Db 357 I 357

RESULT 2

US-08-340-426D-121

Sequence 121, Application US/08340426D

Patent No. 5948634

GENERAL INFORMATION:

APPLICANT: de la Monte, Suzanne

APPLICANT: Wands, Jack R.

TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection

TITLE OF INVENTION: of Alzheimer's Disease

NUMBER OF SEQUENCES: 121

CORRESPONDENCE ADDRESS:

ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.

STREET: 1100 New York Avenue, Suite 600

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/340,426D

FILING DATE: 14-NOV-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Ludwig, Steven R.

REGISTRATION NUMBER: 36,203

REFERENCE/DOCKET NUMBER: 0609.3840002

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 371-2600

TELEFAX: (202) 371-2540

INFORMATION FOR SEQ ID NO: 121:

SEQUENCE CHARACTERISTICS:

LENGTH: 375 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-340-426D-121

Query Match 40.3%; Score 234.5; DB 2; Length 375;

Best Local Similarity 72.1%; Pred. No. 3.3e-21;

Matches 44; Conservative 2; Mismatches 14; Indels 1; Gaps 1;

QY 8 FCFCFFETESHSLTQAGVQWVCELGSPQLPSGFKRFSCLSLSSWDYSHEPPHPV-ICSP 66

Db 297 FNFCLFEMESHVTVQAGVQWVNLGSLQPLPGLKRFSCSLSPSSWDYGHLPHPANFCIF 356

QY 67 L 67

Db 357 I 357

RESULT 3

US-08-450-673C-121

Sequence 121, Application US/08450673C

Patent No. 5948888

GENERAL INFORMATION:

APPLICANT: de la Monte, Suzanne

APPLICANT: Wands, Jack R.

TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection

TITLE OF INVENTION: of Alzheimer's Disease

NUMBER OF SEQUENCES: 121

CORRESPONDENCE ADDRESS:

ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.

STREET: 1100 New York Avenue, Suite 600

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/450,673C

FILING DATE: 30-MAY-1995

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Ludwig, Steven R.

REGISTRATION NUMBER: 36,203

REFERENCE/DOCKET NUMBER: 0609.3840004

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 371-2600

TELEFAX: (202) 371-2540

INFORMATION FOR SEQ ID NO: 121:

SEQUENCE CHARACTERISTICS:

LENGTH: 375 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-450-673C-121

Query Match 40.3%; Score 234.5; DB 4; Length 375;

Best Local Similarity 72.1%; Pred. No. 3.3e-21;

Matches 44; Conservative 2; Mismatches 14; Indels 1; Gaps 1;

QY 8 FCFCFFETESHSLTQAGVQWVCELGSPQLPSGFKRFSCLSLSSWDYSHEPPHPV-ICSP 66

Db 297 FNFCLFEMESHVTVQAGVQWVNLGSLQPLPGLKRFSCSLSPSSWDYGHLPHPANFCIF 356

QY 67 L 67

Db 357 I 357

RESULT 4

US-09-872-968-2

Sequence 2, Application US/09872968

Patent No. 6770797

GENERAL INFORMATION:

APPLICANT: Wands, Jack R

APPLICANT: de la Monte, Suzanne M

TITLE OF INVENTION: Inhibition of Neurodegeneration

FILE REFERENCE: 21486-047

CURRENT APPLICATION NUMBER: US/09/872,968

CURRENT FILING DATE: 2001-06-01

NUMBER OF SEQ ID NOS: 2

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 2

LENGTH: 375

TYPE: PRT

ORGANISM: Homo sapiens

US-09-872-968-2

Query Match 40.3%; Score 234.5; DB 4; Length 375;

Best Local Similarity 72.1%; Pred. No. 3.3e-21;

Matches 44; Conservative 2; Mismatches 14; Indels 1; Gaps 1;

QY 8 FCFCFFETESHSLTQAGVQWVCELGSPQLPSGFKRFSCLSLSSWDYSHEPPHPV-ICSP 66

Db 297 FNFCLFEMESHVTVQAGVQWVNLGSLQPLPGLKRFSCSLSPSSWDYGHLPHPANFCIF 356

QY 67 L 67

Db 357 I 357

RESULT 5

PCT-US95-17111A-121

; Sequence 121, Application PC/TUS9517111A  
; GENERAL INFORMATION:  
; APPLICANT: de la Monte, Suzanne  
; APPLICANT: Wands, Jack R.  
; TITLE OF INVENTION: Neural Thread Protein Gene Expression and  
; TITLE OF INVENTION: Detection of Alzheimer's Disease  
; NUMBER OF SEQUENCES: 121  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.  
; STREET: 1100 New York Avenue, Suite 600  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/17111A  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/340,426  
; FILING DATE: 14-NOV-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ludwig, Steven R.  
; REGISTRATION NUMBER: 36,203  
; REFERENCE/DOCKET NUMBER: 0609.3840002  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 371-2600  
; TELEFAX: (202) 371-2540  
; INFORMATION FOR SEQ ID NO: 121:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 397 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; PCT-US95-17111A-121

Query Match 36.8%; Score 214; DB 5; Length 397;  
Best Local Similarity 67.7%; Pred. No. 1.4e-18;  
Matches 42; Conservative 3; Mismatches 17; Indels 0; Gaps 0;

Qy 8 FCFCTESHSLTQAGVQWCELGSPQLPSGFKRFSCLSLSSWDYSHEPPHVICSEFL 67  
Db 298 FNFCLFEMESHVSTQAGVQWPNLGLQPLPGLKRFKFSCLSLPSSWDYGHLLHTPLIFVFS 357

Qy 68 ME 69

Db 358 LE 359

RESULT 6  
US-09-513-999C-4581  
; Sequence 4581, Application US/09513999C  
; Patent No. 6783961  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Duclert, A.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
; Patent No. 6783961  
; FILE REFERENCE: 59.US2.REG  
; CURRENT APPLICATION NUMBER: US/09/513.999C  
; CURRENT FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/122,487  
; PRIOR FILING DATE: 1999-02-26  
; NUMBER OF SEQ ID NOS: 36681  
; SOFTWARE: Patent.pm  
; SEQ ID NO 4581  
; LENGTH: 61

; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SIGNAL  
; LOCATION: -16...-1  
; OTHER INFORMATION: score 7.5  
; OTHER INFORMATION: seq LFCLSVCLFEVES/HS  
US-09-513-999C-4581  
  
Query Match 35.4%; Score 206; DB 4; Length 61;  
Best Local Similarity 69.6%; Pred. No. 1.3e-18;  
Matches 39; Conservative 1; Mismatches 14; Indels 2; Gaps 1;

Qy 8 FCFCTESHSLTQAGVQWCELGSPQLPSGFKRFSCLSLSSWDYSHEPPHP 61  
Db 5 FCLSVCLFEVESHTQAGVQWHSGLPGLNLPFGKRFKFSCLSLSSWDYRHAPPPP 60

RESULT 7  
US-09-205-258-342  
; Sequence 342, Application US/09205258  
; Patent No. 6525174  
; GENERAL INFORMATION:  
; APPLICANT: Young et al.  
; TITLE OF INVENTION: 207 Human Secreted Proteins  
; FILE REFERENCE: P2007P1  
; CURRENT APPLICATION NUMBER: US/09/205,258  
; CURRENT FILING DATE: 1998-12-04  
; EARLIER APPLICATION NUMBER: PCT/US98/11422  
; EARLIER FILING DATE: 1998-06-04  
; EARLIER APPLICATION NUMBER: 60/048,885  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/049,375  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,881  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,880  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,896  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/049,020  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,876  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,895  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,884  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,894  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,971  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,964  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,882  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,899  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,893  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,900  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,901  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,892  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,915  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/049,019  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,970  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,972

EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,916  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,373  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,875  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,374  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,917  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,949  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,974  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,883  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,897  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,898  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,962  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,963  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,877  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,878  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/070,923  
EARLIER FILING DATE: 1997-12-18  
EARLIER APPLICATION NUMBER: 60/092,921  
EARLIER FILING DATE: 1998-07-15  
EARLIER APPLICATION NUMBER: 60/094,657  
EARLIER FILING DATE: 1998-07-30  
NUMBER OF SEQ ID NOS: 1227  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 342  
LENGTH: 87  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: SITE  
LOCATION: (87)  
OTHER INFORMATION: Xaa equals stop translation  
US-09-205-258-342

Query Match 33.4%; Score 194.5; DB 4; Length 87;  
Best Local Similarity 61.2%; Pred. No. 5.9e-17;  
Matches 41; Conservative 4; Mismatches 17; Indels 5; Gaps 3;  
QY 8 FC---FCF-PETESHSLTQAGVQWCELGSPQPLPSGPKRFSCLSLLSSWDYSHEPPHV- 62  
DB 4 FCFVLCFVEMSSSVTQAGVQWCDLGSLQAPPSPGPFSCLSLSSWDYRRPPRPN 63  
QY 63 ICSFLME 69  
DB 64 FLYFLVE 70

RESULT 8  
US-09-513-999C-7867  
Sequence 7867, Application US/09513999C  
Patent No. 6783961  
GENERAL INFORMATION:  
APPLICANT: Dumas Milne Edwards, J.B.  
APPLICANT: Duclert, A.  
APPLICANT: Giordano, J.Y.  
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
Patent No. 6783961  
FILE REFERENCE: 59.US2.REG  
CURRENT APPLICATION NUMBER: US/09/513,999C  
CURRENT FILING DATE: 2000-02-24

PRIOR APPLICATION NUMBER: US 60/122,487  
PRIOR FILING DATE: 1999-02-26  
NUMBER OF SEQ ID NOS: 36681  
SOFTWARE: Patent.pm  
SEQ ID NO 7867  
LENGTH: 119  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: SIGNAL  
LOCATION: -16..-1  
OTHER INFORMATION: score 6.5  
OTHER INFORMATION: seq VLXLVCLFETES/XS  
FEATURE:  
NAME/KEY: UNSURE  
LOCATION: -11  
OTHER INFORMATION: Xaa=Phe or His or Leu or Tyr  
FEATURE:  
NAME/KEY: UNSURE  
LOCATION: 1  
OTHER INFORMATION: Xaa=Gly or Arg  
US-09-513-999C-7867

Query Match 33.4%; Score 194.5; DB 4; Length 119;  
Best Local Similarity 67.8%; Pred. No. 8.8e-17;  
Matches 40; Conservative 3; Mismatches 15; Indels 1; Gaps 1;  
QY 1 MFFVLVRFCCFPETESHSLTQAGVQWCELGSPQPLPSGPKRFSCLSLLSSWDYSHEPP 59  
DB 1 MIFVLXLF-VCLFETESXSVARAGVQWHLVLSURLPLPPGPKRFSCLSLLSSWDYRRVPP 58

RESULT 9  
US-09-513-999C-7075  
Sequence 7075, Application US/09513999C  
Patent No. 6783961  
GENERAL INFORMATION:  
APPLICANT: Dumas Milne Edwards, J.B.  
APPLICANT: Duclert, A.  
APPLICANT: Giordano, J.Y.  
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
Patent No. 6783961  
FILE REFERENCE: 59.US2.REG  
CURRENT APPLICATION NUMBER: US/09/513,999C  
CURRENT FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: US 60/122,487  
PRIOR FILING DATE: 1999-02-26  
NUMBER OF SEQ ID NOS: 36681  
SOFTWARE: Patent.pm  
SEQ ID NO 7075  
LENGTH: 60  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-513-999C-7075

Query Match 31.6%; Score 184; DB 4; Length 60;  
Best Local Similarity 60.3%; Pred. No. 7.9e-16;  
Matches 35; Conservative 4; Mismatches 19; Indels 0; Gaps 0;  
QY 2 FFVLVRFCCFPETESHSLTQAGVQWCELGSPQPLPSGPKRFSCLSLLSSWDYSHEPP 59  
DB 3 YIYIYIFLFFVFMNSCCFQAQGVQWRDLGSLQPPSPGPKQFSCLSLLSSWDYRRHPP 60

RESULT 10  
US-09-621-976-5968  
Sequence 5968, Application US/09621976  
Patent No. 6639063  
GENERAL INFORMATION:  
APPLICANT: Dumas Milne Edwards, J.B.  
APPLICANT: Jobert, S.  
APPLICANT: Giordano, J.Y.  
TITLE OF INVENTION: ESTs and Encoded Human Proteins.

```
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 5968
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-621-976-5968

Query Match      31.6%; Score 184; DB 4; Length 87;
Best Local Similarity 52.7%; Pred. No. 1.3e-15;
Matches 39; Conservative 5; Mismatches 18; Indels 12; Gaps 2;

Qy 12 FFETESHSLTOAGVQWCELGSPQLPSGFKRFSCLSLSSWDYSHPPHPV-ICSFLEMEK 70
Db 24 FFETFCVAEAKVWCDLGSLOPLPGFKRFSCHLSLSSWDCRHLPPHQAFCIF---- 79

Qy 71 CLILYKPNGDTIGP 84
Db 80 -----SGDGVSP 86

RESULT 11
US-09-513-999C-6065
; Sequence 6065, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 6065
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-513-999C-6065

Query Match      31.3%; Score 182; DB 4; Length 96;
Best Local Similarity 60.0%; Pred. No. 2.6e-15;
Matches 36; Conservative 4; Mismatches 20; Indels 0; Gaps 0;

Qy 20 LTQAGVQWCELGSPQLPSGFKRFSCLSLSSWDYSHPPHPVICSFLEMEKCLILYKPNG 79
Db 6 VAQAGVQWRDLGSPQLPPGPKRFSCLSPSSWDYRHVPLLPANLVFLVENGFLHVGPGAG 65

RESULT 12
US-09-621-976-6112
; Sequence 6112, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 6112
; LENGTH: 102
; TYPE: PRT

; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 5968
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-621-976-6112

Query Match      31.3%; Score 182; DB 4; Length 102;
Best Local Similarity 59.0%; Pred. No. 2.8e-15;
Matches 36; Conservative 6; Mismatches 17; Indels 2; Gaps 2;

Qy 7 RFCEFCFFETESHSLTOAGVQWCELGSPQLPSGFKRFSCLSLSSWDYSHPPHPV-ICS 65
Db 32 KICL-FFETEAHCVALAXVQWRDIGSLQPLGLKQSSCLSLSSWDYRLPPHPANFCI 90

Qy 66 F 66
Db 91 F 91

RESULT 13
US-09-513-999C-4770
; Sequence 4770, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 4770
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 8
; OTHER INFORMATION: Xaa=Ala or Glu or Gly or Val
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 82
; OTHER INFORMATION: Xaa=Ala or Pro
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 94
; OTHER INFORMATION: Xaa=Asn or Thr
US-09-513-999C-4770

Query Match      31.2%; Score 181.5; DB 4; Length 97;
Best Local Similarity 45.6%; Pred. No. 3e-15;
Matches 41; Conservative 8; Mismatches 24; Indels 17; Gaps 3;

Qy 1 MFFVL-----YRFCEFCFFETESHSLTOAGVQWCELGSPQLPSGFKRFSCLSLSSWDYS 55
Db 1 MSFILINXVFLFLFIYFETGSHFVTQAGGKMRGLGSLQPLPGFRRSSCLSLSSGWDGCG 60

Qy 56 HEPPHPV-ICSFLEMEKCLILYKPNGDTIGP 84
Db 61 LAPPSANFCIF-----SGDGVSP 79

RESULT 14
US-09-621-976-5606
; Sequence 5606, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 11, 2005, 06:57:07 ; Search time 15.1979 Seconds  
(without alignments)  
620.432 Million cell updates/sec

Title: US-10-092-934-6  
Perfect score: 531  
Sequence: 1 EAYYTMHLPTTNRKIAHC.....SRTSNSTPTNSPLWTSSKPR 98

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79:.\*  
1: Pirl:.\*  
2: Pirl2:.\*  
3: Pirl3:.\*  
4: Pirl4:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	88	16.6	400	2 S58222	PQ-rich protein -
2	82	15.4	215	2 T45846	zinc-finger-like p
3	81	15.3	340	1 WMBEL1	latency-related pr
4	80.5	15.2	365	2 T15478	hypothetical prote
5	80.5	15.2	670	1 S50591	myb-related protei
6	79.5	15.0	239	2 B86346	F16F4.1 protein -
7	79	14.9	1173	2 I50620	prockr2 - chicken
8	77.5	14.6	728	2 T43632	serine/threonine p
9	77.5	14.6	792	2 T43630	serine/threonine p
10	77.5	14.6	1080	2 T27622	hypothetical prote
11	77.5	14.6	7576	2 T17428	FK506 polyketide s
12	77	14.5	437	2 S18407	acrosin (EC 3.4.21
13	76.5	14.4	257	2 T03136	hypothetical prote
14	76.5	14.4	258	2 T51689	probable transcrip
15	76.5	14.4	365	2 D86470	F21H2.9 protein -
16	76.5	14.4	1370	2 T19188	hypothetical prote
17	75.5	14.2	6420	2 T30283	polyketide synthas
18	75	14.1	317	2 D72700	hypothetical prote
19	75	14.1	639	2 T13151	adapter protein CM
20	74	13.9	323	2 T06506	glutenin low molec
21	74	13.9	374	2 T37676	zinc-finger protei
22	74	13.9	671	2 S51599	OM(2D) protein - f
23	74	13.9	733	2 S44876	ZC21.4 protein - C
24	74	13.9	859	2 S64195	HRK1 protein - yea
25	74	13.9	1093	1 S50614	regulatory protein B
26	73.5	13.8	640	2 A41726	homeotic protein B
27	73.5	13.8	642	2 S27806	homeotic protein B
28	73.5	13.8	1221	2 T13283	probable transcrip
29	73	13.7	1013	2 G71460	probable outer mem

30	72.5	13.7	628	2 S01955	hypothetical prote
31	72.5	13.7	628	2 S19150	hypothetical prote
32	72.5	13.7	1043	2 T13172	gag-like protein p
33	72	13.6	1029	2 S64731	serine/threonine-s
34	71.5	13.5	493	2 A34220	homeotic protein A
35	71	13.4	318	2 T33874	hypothetical prote
36	71	13.4	668	2 S39836	hypothetical prote
37	70.5	13.3	435	2 T30114	hypothetical prote
38	70	13.2	121	2 G82853	hypothetical prote
39	70	13.2	230	2 T28284	hypothetical prote
40	70	13.2	491	2 A32584	Abd-B protein - fr
41	70	13.2	525	1 S39834	myb-related protei
42	70	13.2	544	2 S15664	transcription fact
43	70	13.2	548	2 S52735	CW17R protein - mo
44	70	13.2	901	2 S50987	SOK1 protein - yea
45	70	13.2	1061	2 JC7116	Xscl-3 protein - A

ALIGNMENTS

RESULT 1

S58222  
PQ-rich protein - human  
C:Species: Homo sapiens (man)  
C:Date: 13-Jan-1996 #sequence\_revision 01-Mar-1996 #text\_change 09-Jul-2004  
C:Accession: S58222  
R;Wagner, F.F.; Flegel, W.A.  
submitted to the EMBL Data Library, July 1995  
A:Description: A cDNA, which predicts a protein with PQ-rich repeats, isolated from a ph  
A:Reference number: S58222  
A:Accession: S58222  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-400 <WAG>  
A:Cross-references: UNIPROT:Q15184; EMBL:Z50194; NID:G929659; PIDN:CAA90576.1; PID:G9296

Query Match 16.6%; Score 88; DB 2; Length 400;  
Best Local Similarity 34.7%; Pred. No. 0.22; Mismatches 6; Indels 16; Gaps 4;  
Matches 25; Conservative

QY	14	RPKIAHCILFNQPHSPRSNSHSHPNLKLHRRSHSHNRPRAYILITILPSKLKLRTHSQS	73
DB	343	QPQQLHPYPHPHPH-PHSHPHSHPHP---HPHPHPHQIHPHPH-----PQPHSQP	387
QY	74	H-HNPLSRTSNS	84
DB	388	HGHRLLRSTSNS	399

RESULT 2

T45846  
zinc-finger-like protein - Arabidopsis thaliana  
N:Alternate names: protein F3A4.10  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 04-Feb-2000 #sequence\_revision 04-Feb-2000 #text\_change 09-Jul-2004  
C:Accession: T45846  
R;Bargues, M.; Collado, M.C.; Navarro, P.; Terol, J.; Perez-Alonso, M.; Mewes, H.W.; May  
submitted to the Protein Sequence Database, December 1999  
A:Reference number: Z23007  
A:Accession: T45846  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-215 <BAR>  
A:Cross-references: UNIPROT:Q9SN24; EMBL:AL132978  
A:Experimental source: cultivar Columbia; BAC clone F3A4  
C:Genetics:  
A:Map position: 3  
A:Note: F3A4.10

Query Match 15.4%; Score 82; DB 2; Length 215;  
Best Local Similarity 29.5%; Pred. No. 0.45; Mismatches 13; Indels 14; Gaps 4;  
Matches 26; Conservative





```
Qy 78 LSR-----TSNSTPTNSFLMTSSKPR 98
Db 82 VQRLTGKTSTSTSSYSSTTSAPK 106

RESULT 7
I50620
Prockr2 - chicken (fragment)
C:Species: Gallus gallus (Chicken)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C:Accession: I50620
R:Schutz, B.; Niessing, J.
Gene 148, 227-236, 1994
A:Title: Cloning and structure of a chicken zinc finger cDNA: restricted expression in d
A:Reference number: I50620; MUID:95047430; PMID:7958949
A:Accession: I50620
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1173 <SCH>
A:Cross-references: UNIPROT:Q90783; EMBL:X56805; NID:G577018; PIDN:CAA40140.1; PID:G5770
C:Genetics:
A:Gene: ckr2

Query Match 14.9%; Score 79; DB 2; Length 1173;
Best Local Similarity 30.0%; Pred. No. 5.4;
Matches 27; Conservative 12; Mismatches 21; Indels 30; Gaps 5;

Qy 11 TTNRP-KIAHCILFNQHPSPNSHSHPNPLKLRHRRSHSHNR-----PRAYILITILP 62
Db 118 TGERPYACSHC-----SKTFTSSNLLLLHQRTSHRSHKCPACPKAFV----- 161

Qy 63 SKLKLRTHSQSH-----HNPLSTNSSTP 86
Db 162 SDACLQKHLQSHAAAPLLPSLPSPQLSP 191

RESULT 8
T43632
serine/threonine protein kinase MIG-15 - Caenorhabditis elegans (fragment)
C:Species: Caenorhabditis elegans
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C:Accession: T43632
R:Zhu, X.; Acharya, P.; Hedgecock, E.
Submitted to the EMBL Data Library, August 1998
A:Description: MIG-15, a NIK ortholog of the STE20 family of serine/threonine protein ki
A:Reference number: Z22584
A:Accession: T43632
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-728 <ZHU>
A:Cross-references: UNIPROT:Q9XYC4; EMBL:AF0871133; PIDN:AAD14595.1
C:Genetics:
A:Map position: X
A:Note: mig-15
C:Function:
A:Description: probably involved in cell migration and signal transduction

Query Match 14.6%; Score 77.5; DB 2; Length 728;
Best Local Similarity 27.9%; Pred. No. 4.6;
Matches 24; Conservative 13; Mismatches 32; Indels 17; Gaps 3;

Qy 29 PRNSHSHPNPLKLRHRRSHSHNRPRAYILITILPSKCLKLRT-----HSQSHH-NPLS 79
Db 52 PRHSPASRPVPVSHHQSPQOSHAPAPHLADLANYEKKRRSRERERERERQAHHAMPIA 111

Qy 80 RTSNSTP-----TNSFLMTSSKP 97
Db 112 RVASVPAPOQSRKMSEPLLITHVKP 137

RESULT 9
T43630
serine/threonine protein kinase homolog - Caenorhabditis elegans (fragment)
C:Species: Caenorhabditis elegans
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C:Accession: T43630
R:Zhu, X.; Acharya, P.; Hedgecock, E.
Submitted to the EMBL Data Library, August 1998
A:Description: MIG-15, a NIK ortholog of the STE20 family of serine/threonine protein ki
A:Reference number: Z22584
A:Accession: T43630
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-792 <ZHU>
A:Cross-references: UNIPROT:Q9UAN7; EMBL:AF0871132; PIDN:AAD14594.1
C:Genetics:
A:Map position: X
A:Note: mig-15

Query Match 14.6%; Score 77.5; DB 2; Length 792;
Best Local Similarity 27.9%; Pred. No. 5;
Matches 24; Conservative 13; Mismatches 32; Indels 17; Gaps 3;

Qy 29 PRNSHSHPNPLKLRHRRSHSHNRPRAYILITILPSKCLKLRT-----HSQSHH-NPLS 79
Db 125 PRHSPASRPVPVSHHQSPQOSHAPAPHLADLANYEKKRRSRERERERERQAHHAMPIA 184

Qy 80 RTSNSTP-----TNSFLMTSSKP 97
Db 185 RVASVPAPOQSRKMSEPLLITHVKP 210

RESULT 10
T27622
hypothetical protein ZC504.4a - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T27622
R:Kershaw, J.
Submitted to the EMBL Data Library, July 1995
A:Reference number: Z20394
A:Accession: T27622
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1080 <WIL>
A:Cross-references: UNIPROT:Q23356; EMBL:Z50029; PIDN:CAA90344.1; GSPDB:GN00028; CESP:Z
A:Experimental source: clone ZC504
C:Genetics:
A:Gene: CESP:ZC504.4a
A:Map position: X
A:Introns: 15/3; 71/3; 137/3; 211/1; 259/1; 388/2; 428/3; 614/3; 643/3; 680/3; 841/3; 95

Query Match 14.6%; Score 77.5; DB 2; Length 1080;
Best Local Similarity 27.9%; Pred. No. 6.9;
Matches 24; Conservative 13; Mismatches 32; Indels 17; Gaps 3;

Qy 29 PRNSHSHPNPLKLRHRRSHSHNRPRAYILITILPSKCLKLRT-----HSQSHH-NPLS 79
Db 413 PRHSPASRPVPVSHHQSPQOSHAPAPHLADLANYEKKRRSRERERERERQAHHAMPIA 472

Qy 80 RTSNSTP-----TNSFLMTSSKP 97
Db 473 RVASVPAPOQSRKMSEPLLITHVKP 498

RESULT 11
T17428
PK506.polyketide synthase - Streptomyces sp. (strain MA6548)
C:Species: Streptomyces sp.
A:Variety: strain MA6548
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 12-Jul-2004
C:Accession: T17428
R:Motamedi, H.; Shafiee, A.
Eur. J. Biochem. 256, 528-534, 1998
A:Title: The biosynthetic gene cluster for the macrolactone ring of the immunosuppressan
```

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serine/threonine protein kinase homolog - Caenorhabditis elegans (fragment)
C:Species: Caenorhabditis elegans
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C:Accession: T43630
R:Zhu, X.; Acharya, P.; Hedgecock, E.
Submitted to the EMBL Data Library, August 1998
A:Description: MIG-15, a NIK ortholog of the STE20 family of serine/threonine protein ki
A:Reference number: Z22584
A:Accession: T43630
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-792 <ZHU>
A:Cross-references: UNIPROT:Q9UAN7; EMBL:AF0871132; PIDN:AAD14594.1
C:Genetics:
A:Map position: X
A:Note: mig-15

Query Match 14.6%; Score 77.5; DB 2; Length 792;
Best Local Similarity 27.9%; Pred. No. 5;
Matches 24; Conservative 13; Mismatches 32; Indels 17; Gaps 3;

Qy 29 PRNSHSHPNPLKLRHRRSHSHNRPRAYILITILPSKCLKLRT-----HSQSHH-NPLS 79
Db 125 PRHSPASRPVPVSHHQSPQOSHAPAPHLADLANYEKKRRSRERERERERQAHHAMPIA 184

Qy 80 RTSNSTP-----TNSFLMTSSKP 97
Db 185 RVASVPAPOQSRKMSEPLLITHVKP 210

RESULT 10
T27622
hypothetical protein ZC504.4a - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T27622
R:Kershaw, J.
Submitted to the EMBL Data Library, July 1995
A:Reference number: Z20394
A:Accession: T27622
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1080 <WIL>
A:Cross-references: UNIPROT:Q23356; EMBL:Z50029; PIDN:CAA90344.1; GSPDB:GN00028; CESP:Z
A:Experimental source: clone ZC504
C:Genetics:
A:Gene: CESP:ZC504.4a
A:Map position: X
A:Introns: 15/3; 71/3; 137/3; 211/1; 259/1; 388/2; 428/3; 614/3; 643/3; 680/3; 841/3; 95

Query Match 14.6%; Score 77.5; DB 2; Length 1080;
Best Local Similarity 27.9%; Pred. No. 6.9;
Matches 24; Conservative 13; Mismatches 32; Indels 17; Gaps 3;

Qy 29 PRNSHSHPNPLKLRHRRSHSHNRPRAYILITILPSKCLKLRT-----HSQSHH-NPLS 79
Db 413 PRHSPASRPVPVSHHQSPQOSHAPAPHLADLANYEKKRRSRERERERERQAHHAMPIA 472

Qy 80 RTSNSTP-----TNSFLMTSSKP 97
Db 473 RVASVPAPOQSRKMSEPLLITHVKP 498

RESULT 11
T17428
PK506.polyketide synthase - Streptomyces sp. (strain MA6548)
C:Species: Streptomyces sp.
A:Variety: strain MA6548
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 12-Jul-2004
C:Accession: T17428
R:Motamedi, H.; Shafiee, A.
Eur. J. Biochem. 256, 528-534, 1998
A:Title: The biosynthetic gene cluster for the macrolactone ring of the immunosuppressan
```



```
Query Match          14.4%; Score 76.5; DB 2; Length 258;
Best Local Similarity 27.5%; Pred. No. 1.9;
Matches 22; Conservative 17; Mismatches 36; Indels 5; Gaps 3;

Qy 9 LPTNRPKIAHCILFNQPHSPNSHSHNPPLKLRHSHSH--NRPRVILITILPSKL 65
   ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 156 LPSQGDPLLDH-VPFSLQTLNSEDHFDNLVK-HPTDHEHDDNPFSSWVLPGLDNNP 213

Qy 66 KLRTHSOSHNPPLSRTSNST 85
   ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 214 KTVTSSLPHNNPADASSSS 233

RESULT 15
D86470
F21H2.9 protein - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: D86470
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chen, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A>Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: D86470
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-365 <STO>
A:Cross-references: UNIPROT:Q959Z2; GB:AE005172; NID:G5668784; PIDN:AAD46010.1; GSPDB:GN
C:Genetics:
A:Map position: 1
C:Superfamily: Arabidopsis myb-related protein M4; myb DNA-binding repeat homology

Query Match          14.4%; Score 76.5; DB 2; Length 365;
Best Local Similarity 27.5%; Pred. No. 2.8;
Matches 22; Conservative 17; Mismatches 36; Indels 5; Gaps 3;

Qy 9 LPTNRPKIAHCILFNQPHSPNSHSHNPPLKLRHSHSH--NRPRVILITILPSKL 65
   ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 263 LPSQGDPLLDH-VPFSLQTLNSEDHFDNLVK-HPTDHEHDDNPFSSWVLPGLDNNP 320

Qy 66 KLRTHSOSHNPPLSRTSNST 85
   ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 321 KTVTSSLPHNNPADASSSS 340
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Search completed: October 11, 2005, 07:01:38  
Job time : 17.1979 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 11, 2005, 06:57:07 ; Search time 58.8262 Seconds  
(without alignments)  
853.085 Million cell updates/sec

Title: US-10-092-934-6

Perfect score: 531

Sequence: 1 EAYTMLHPTTNRPKIAHC.....SRTSNSTPNSFLMTSSKPR 98

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03:\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Query Match	Score	Length	DB ID	Description
1	90.5	17.0	305	Q9YPF7	Q9YPF7 human herpe
2	88.5	16.7	145	Q8N2Q6	Q8N2Q6 homo sapien
3	88.5	16.7	1671	Q7SE26	Q7SE26 neurospora
4	88	16.6	348	Q8WV24	Q8WV24 homo sapien
5	88	16.6	400	Q15184	Q15184 homo sapien
6	87	16.4	587	Q8FR28	Q8FR28 corynebacte
7	86.5	16.3	1311	Q9VXJ5	Q9VXJ5 drosophila
8	85.5	16.1	2958	Q9VDY5	Q9VDY5 drosophila
9	85	16.0	52	Q9NZ17	Q9NZ17 homo sapien
10	85	16.0	356	Q8SY01	Q8SY01 drosophila
11	85	16.0	612	Q8AXX1	Q8AXX1 brachydanio
12	85	16.0	717	Q9VW27	Q9VW27 drosophila
13	85	16.0	891	Q8IB61	Q8IB61 plasmodium
14	84	15.8	372	Q8LC22	Q8LC22 arabidopsis
15	83.5	15.7	720	1 Z408 HUMAN	Q9H9D4 homo sapien
16	83	15.6	502	Q7S315	Q7S315 neurospora
17	83	15.6	1379	Q7RY49	Q7RY49 neurospora
18	82.5	15.5	226	Q8N850	Q8N850 homo sapien
19	82	15.4	215	Q9SN24	Q9SN24 arabidopsis
20	82	15.4	623	P90533	P90533 dictyosteli
21	81.5	15.3	1399	Q9W437	Q9W437 drosophila
22	81	15.3	261	Q62392	Q62392 mus musculu
23	81	15.3	340	1 LRPI HHV1F	P17588 human herpe
24	80.5	15.2	272	Q69079	Q69079 human herpe
25	80.5	15.2	365	1 YQ23_CABEL	Q99452 caenorhabdi
26	80.5	15.2	670	1 DOT6_YEAST	P40059 saccharomyc
27	80.5	15.2	1111	2 Q9FH74	Q9FH74 arabidopsis
28	80	15.1	233	2 Q8MP30	Q8MP30 dictyosteli
29	80	15.1	260	2 Q96NW2	Q96NW2 homo sapien
30	79.5	15.0	239	2 Q9LMP5	Q9LMP5 arabidopsis
31	79.5	15.0	329	2 Q8NIY1	Q8NIY1 neurospora

#### ALIGNMENTS

##### RESULT 1

```

ID Q9YPF7 PRELIMINARY; PRT; 305 AA.
AC Q9YPF7;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Latency associated transcript.
OS Human herpesvirus 1 (HHV-1) (Human herpes simplex virus 1).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Simplexvirus.
OX NCBI_TaxID=10298;
RN [1]
RX SEQUENCE FROM N.A.
RP MEDLINE=88155754; PubMed=2831380;
RA Wagner E.K., Devi-Rao G.B., Feldman L.T., Dobson A.T., Zhang Y.-K.,
RA Flanagan W.M., Stevens J.G.;
RT "Physical characterization of the herpes simplex virus latency-
RT associated transcript in neurons.";
RL J. Virol. 62:1194-1202 (1988).
DR EMBL; M17921; AAA45797.1; -.
SQ SEQUENCE 305 AA; 33087 MW; 994D3762BA4B82F4 CRC64;

```

Query Match 17.0%; Score 90.5; DB 2; Length 305;  
Best Local Similarity 31.6%; Pred. No. 0.54; Mismatches 7; Indels 23; Gaps 4;  
Matches 31; Conservative

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Qy 9 LPTNRPKIAHCILFNQPSRNSHSHPN-----PLKLHRRSHSHNRPRAYILIT 59
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 39 LPTPTTTHPS---HAPLPRTPTTTPHSHAPPLPRTPTTTPHSHAPPLPR-----T 90
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

Qy 60 ILPSKLRTHSOSHNPISRTSNSTPNSFLMTSSKP 97
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 91 PTP-----THPSHAPPLPRTPAIHPTQTKRYKSKP 122
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

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##### RESULT 2

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ID Q8N2Q6 PRELIMINARY; PRT; 145 AA.
AC Q8N2Q6;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein FLJ90047.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RX SEQUENCE FROM N.A.
RP TISSUE=Whole embryo;
RA Isogai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,
RA Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahari K.,

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RA Masuko Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,
RA Hattori A., Okumura K., Iwayanagi T., Ninomiya K.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK074528; BAC11041.1; -.
SQ SEQUENCE 145 AA; 16153 MW; EF44C8E658ECAC2E CRC64;

Query Match 16.7%; Score 88.5; DB 2; Length 145;
Best Local Similarity 30.7%; Pred. No. 0.37;
Matches 23; Conservative 6; Mismatches 13; Indels 33; Gaps 3;

QY 28 SPRSNSHSHNPPL-----KLHRRSHSHNRPRAYILITLPSKILKLRTHSQSHN- 76
Db 65 TPSSHPHQHHPHYTTPSPPLNLRHRRPHSHPR-----LHTHTRPHHHL 109
QY 77 -----PLSRSTNS 84
Db 110 PRVTAAPLHRPENS 124

RESULT 3
ID Q7SE26 PRELIMINARY; PRT; 1671 AA.
AC Q7SE26;
DT 01-MAR-2004 (TREMBlrel. 26, Created)
DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
DE Hypothetical protein.
GN Name=NCU02768.1;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OR748;
RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA Jaffe D., Fitzhugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,
RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA Qui D., Iankiev P., Pedersen D., Nelson M., Washburne M.,
RA Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
RA Kothe G.O., Jedd G., Mewes W., Staben C., Barrett E., Greenberg D.,
RA Roy A., Foley K., Naylor J., Thomann N., Marcotte E., Gherre S.,
RA Kamal M., Kamysellis M., Maucelli E., Bieleke C., Rudd S., Frishman D.,
RA Krystofova S., Rasmussen C., Metzenberg R.L., Perkins D.D., Kroken S.,
RA Cogoni C., Macino G., Catchside D., Li W., Pratt R.J., Osmani S.A.,
RA DeSouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,
RA Yarden O., Planann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
RA Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M.,
RA Paulsen I., Sachs M.S., Lander E.S., Nussbaum C., Birren B.;
RL "The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
RL Nature 0:0-0(2003).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AABX01000039; EAA35027.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0006350; P:transcription; IEA.
DR InterPro; IPR007219; Fungal_trans.
DR InterPro; IPR021173; PfkB.
DR Pfam; PF04082; Fungal_trans; 1.
DR PROSITE; PS00583; PFKE_KINASES_1; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 1671 AA; 182498 MW; CRCDSB90957DA706 CRC64;

Query Match 16.7%; Score 88.5; DB 2; Length 1671;
Best Local Similarity 32.0%; Pred. No. 5.7;
Matches 24; Conservative 12; Mismatches 24; Indels 15; Gaps 3;

QY 10 PTNRPKIAHCILFNQPHSPRSNSHSHNPPLKLRHSHSHNRPRAYILITLPSKILK 66
Db 1536 PPSSTPATAHI-----PIPTTHAHHPN-----SYQHHPHPRAYITTSIPSRDTLLP 1583
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QY 67 LRTHSQSHHNPLSRT 81
Db 1584 LCTVPTATHNRSR 1598

RESULT 4
Q8WV24
ID Q8WV24 PRELIMINARY; PRT; 348 AA.
AC Q8WV24;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE PHLDA1 protein (Fragment).
GN Name=PHLDA1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Uterus;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426038999;
RA Krausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skaleka U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RL "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=uterus;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC018929; AAH18929.2; -.
DR SMART; SM00233; PH; 1.
FT NON TER 1
SQ SEQUENCE 348 AA; 38924 MW; 6637BE6D821FB6A4 CRC64;

Query Match 16.6%; Score 88; DB 2; Length 348;
Best Local Similarity 34.7%; Pred. No. 1.1;
Matches 25; Conservative 6; Mismatches 25; Indels 16; Gaps 4;

QY 14 RPKIAHCILFNQPHSPRSNSHSHNPPLKLRHSHSHNRPRAYILITLPSKILKLRTHSQS 73
Db 291 QPQLHPYPHPHPH-PhSHPHSHPH-HPHPHPHQIHPHP-----PQPHSQP 335
QY 74 H-HNPLSRSTNS 84
Db 336 HGHRLLRSTNS 347

RESULT 5
Q15184
ID Q15184 PRELIMINARY; PRT; 400 AA.
AC Q15184;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
```

```
DE PO-rich protein (Apoptosis-associated nuclear protein).
GN Name=PHLDA1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Wagner F.F., Flegel W.A.;
RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Kueke M.D.A., Johnson J.P.;
RT "Assignment of the human PHLDA1 (TDAG51) gene to chromosome 12 band
RT q15 by radiation hybrid mapping.";
RL Cytogenet. Cell Genet. 0:0-0(2000).
RN [3]
RP SEQUENCE FROM N.A.
RA Gerlinger M., Johnson J.J.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z50194; CAA90576.1; -.
DR EMBL; AF239986; AAF64165.1; -.
DR PIR; S58222; S58222.
DR Genew; HGNC:8933; PHLDA1.
DR GO; GO:0005634; C:nucleus; IEA.
DR InterPro; IPR001849; PH.
DR InterPro; IPR011036; PH_related.
DR SMART; SM00233; PH; 1.
KW Nuclear protein.
SQ SEQUENCE 400 AA; 4488 MW; 941CC500C57046DD CRC64;

Query Match 16.6%; Score 88; DB 2; Length 400;
Best Local Similarity 34.7%; Pred. No. 1.3;
Matches 25; Conservative 6; Mismatches 25; Indels 16; Gaps 4;

QY 14 RPKIAHCILFNQPHSPRSHSHNPNLKLHRRSHSHNPRAYILITLPKSLKLRTHSQS 73
DB 343 QPQQLHPYPHPHPH-PSHSPHSHPHP---HPHPHPHPHPHPH-----POPHSQP 387
QY 74 H-HNPLSRSTNS 84
DB 388 HGHLRLRSTNS 399

RESULT 6
Q8FRP8 Q8FRP8 PRELIMINARY; PRT; 587 AA.
AC Q8FRP8;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Putative amino-acid permease.
GN OrderedLocusNames=CE0711;
OS Corynebacterium efficiens.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
OX NCBI_TaxID=152794;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=YS-314;
RX MEDLINE=22723752; PubMed=12840036; DOI=10.1101/gr.1285603;
RA Nishio Y., Nakamura Y., Kawarabayashi Y., Usuda Y., Ikemura E.,
RA Sugimoto S., Matsui K., Yamagishi A., Kikuchi H., Ikeyo K.,
RA Gojibori T.;
RT "Comparative complete genome sequence analysis of the amino acid
RT replacements responsible for the thermostability of Corynebacterium
RT efficiens.";
RL Genome Res. 13:1572-1579(2003).
DR EMBL; AP005216; BAC17521.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005279; F:amino acid-polyamine transporter activity; IEA.
DR GO; GO:0006865; P:amino acid transport; IEA.

DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR002293; AA:rel_permease1.
DR InterPro; IPR004841; Permease_region.
DR Pfam; PF00324; AA_permease; 1.
KW Complete proteome; Transmembrane; Transport.
SQ SEQUENCE 587 AA; 62335 MW; 226D58982B764476 CRC64;

Query Match 16.4%; Score 87; DB 2; Length 587;
Best Local Similarity 34.4%; Pred. No. 2.5;
Matches 21; Conservative 10; Mismatches 30; Indels 0; Gaps 0;

QY 29 PRGNSHSHNPNLKLHRRSHSHNPRAYILITLPKSLKLRTHSQSHNPLSRSTNSPTN 88
DB 509 PRNRAHPHPVALESPRNSHTAAAPPATMTITPDPDVTGCTGTAHAESARTSTRSTG 568
QY 89 S 89
DB 569 T 569

RESULT 7
Q9VXJ5 Q9VXJ5 PRELIMINARY; PRT; 1311 AA.
AC Q9VXJ5; Q9VXJ6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE CG32577-PA.
GN Namesdisco-T; ORFNames=CG32577;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrier S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houch J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Paclbb J.M.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
```

RT "The genome sequence of Drosophila melanogaster.";

RL [2]

RX MEDLINE=22426065; PubMed=12537568;

RA Celnikier S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,

RA Patel S., Adams M., Champagne M., Dugan S.P., Frise E., Hodgson A.,

RA George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.R.,

RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,

RA Svirkas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,

RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.,

RT "Finishing a whole-genome shotgun: Release 3 of the Drosophila

RT melanogaster euchromatic genome sequence.";

RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).

RN [3]

RX MEDLINE=22426070; PubMed=12537573;

RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirkas R.,

RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,

RA Ashburner M., Celnikier S.E.;

RT "The transposable elements of the Drosophila melanogaster euchromatin:

RT a genomics perspective.";

RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).

RN [4]

RX MEDLINE=22426069; PubMed=12537572;

RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,

RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,

RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,

RA Bettencourt B.R., Celnikier S.E., de Grey A.D., Drysdale R.A.,

RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,

RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,

RA Lewis S.E.;

RT "Annotation of the Drosophila melanogaster euchromatic genome: a

RT systematic review";

RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).

RN [5]

RX MEDLINE=22426071; PubMed=12537574;

RA FlyBase;

RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.

RN [6]

RX MEDLINE=22426065; PubMed=12537568;

RA Celnikier S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,

RA Patel S., Adams M., Champagne M., Dugan S.P., Frise E., Hodgson A.,

RA George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.R.,

RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,

RA Svirkas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,

RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.,

RT "Finishing a whole-genome shotgun: Release 3 of the Drosophila

RT melanogaster euchromatic genome sequence.";

RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).

RN [3]

RX MEDLINE=22426065; PubMed=12537568;

RA Celnikier S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,

RA Patel S., Adams M., Champagne M., Dugan S.P., Frise E., Hodgson A.,

RA George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.R.,

RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,

RA Svirkas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,

RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.,

RT "Finishing a whole-genome shotgun: Release 3 of the Drosophila

RT melanogaster euchromatic genome sequence.";

RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).

RN [3]

RX MEDLINE=22426070; PubMed=12537573;

RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirkas R.,

RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,

RA Ashburner M., Celnikier S.E.;

RT "The transposable elements of the Drosophila melanogaster euchromatin:

RT a genomics perspective.";

RT

ID Q9VDY5 PRELIMINARY; PRT; 2958 AA.

AC Q9VDY5;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE CG5237-PA.

GN ORFNames=CG5237;

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Phyllophaga; Drosophilidae; Drosophila.

OX NCBI\_TaxID=7227;

RN [1]

RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;

RA Adams M.D., Celnikier S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,

RA Abril J.F., Aghayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,

RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,

RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,

RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,

RA Flotok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwan C.,

RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,

RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,

RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,

RA Svirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

RA Wang Z.X., Wasserman D.A., Weinstein G.M., Weissenbach J.,

RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,

RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,

RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,

RA Zheng R.A., Myers E.W., Rubin G.M., Venter J.C.;

RT "The genome sequence of Drosophila melanogaster.";

RL Science 287:2185-2195(2000).

RN [2]

RX MEDLINE=22426065; PubMed=12537568;

RA Celnikier S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,

RA Patel S., Adams M., Champagne M., Dugan S.P., Frise E., Hodgson A.,

RA George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.R.,

RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,

RA Svirkas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,

RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.,

RT "Finishing a whole-genome shotgun: Release 3 of the Drosophila

RT melanogaster euchromatic genome sequence.";

RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).

RN [3]

RX MEDLINE=22426070; PubMed=12537573;

RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirkas R.,

RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,

RA Ashburner M., Celnikier S.E.;

RT "The transposable elements of the Drosophila melanogaster euchromatin:

RT a genomics perspective.";

RT



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RL  Genome Biol. 3:RESEARCH0084-RESEARCH0084 (2002).
RN  [4]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=22426069; PubMed=12537572;
RA  Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA  Hradecky P., Huang Y., Winkler J.S., Millburn G.H., Prochuk S.E.,
RA  Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA  Bettencourt B.R., Celisner S.E., de Grey A.D., Drysdale R.A.,
RA  Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA  Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA  Lewis S.E.;
RT  "Annotation of the Drosophila melanogaster euchromatic genome: a
RT  systematic review.";
RN  Genome Biol. 3:RESEARCH0083-RESEARCH0083 (2002).
RN  [5]
RP  SEQUENCE FROM N.A.
RG  FlyBase;
RL  Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN  [6]
RP  SEQUENCE FROM N.A.
RG  FlyBase;
RL  Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR  EMBL; AE003725; AAF55654.2; -.
DR  FlyBase; FBgn0038693; CG5237.
DR  InterPro; IPR000345; CytC_heme_BS.
DR  PROSITE; PS00190; CYTOCHROME_C; UNKNOWN 1.
SQ  SEQUENCE 2958 AA; 325706 MW; 86763328F59947F3 CRC64;

Query Match 16.1%; Score 85.5; DB 2; Length 2958;
Best Local Similarity 26.4%; Pred. No. 21;
Matches 23; Conservative 13; Mismatches 32; Indels 19; Gaps 3;

Qy 11 TTRPKIAHCLFNQPHS--PRNSHSHNPPLKLRHSHNRPR-----AYILITLP 62
Db 1339 SSSRPKPPCPVHQSAHTAPFYTHHHHPGHGHPYHPHPHHHPHHAGSAHVATTATT 1398

Qy 63 SKULRTHSQ-----SHNPL 78
Db 1399 SAGLVSTHSQSHQVLRHCVPSPSHSPM 1425

RESULT 9
ID Q9NZ17 PRELIMINARY; PRT; 52 AA.
AC Q9NZ17;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Apoptosis-associated nuclear protein PHLDAL (Fragment).
GN Name=PHLDAL;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20354976; PubMed=10894922;
RA Kuske M.D., Johnson J.P.;
RT "Assignment of the human PHLDAL gene to chromosome 12q15 by radiation
RT hybrid mapping.";
RL Cytogenet. Cell Genet. 89:1-1(2000).
[2]
RP SEQUENCE FROM N.A.
RA Kuske M.D., Johnson J.P.;
RT "PHRIP: a novel differentially expressed mRNA in metastatic
RT melanoma.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF220656; AAF36387.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
KW Nuclear protein.
FT NON TER 1
SQ SEQUENCE 52 AA; 5969 MW; 3E616AB55EC13BD9 CRC64;

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Query Match 16.0%; Score 85; DB 2; Length 52;
Best Local Similarity 35.9%; Pred. No. 0.26;
Matches 23; Conservative 5; Mismatches 20; Indels 16; Gaps 4;

Qy 23 FNOPH-SPRNSHSHNPPLKLRHSHNRPRAYILITLPKLRTHSQSH-HNPLSR 80
Db 2 YPHPHPHPHSHSHHPH---HHPHPHQHPHPH-----POPHSOPHGHRLRS 47
Qy 81 TSNS 84
Db 48 TSNS 51

RESULT 10
Q8SY01 PRELIMINARY; PRT; 356 AA.
AC Q8SY01;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE RE33994p.
GN ORFNames=CG8780;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkely;
RA Scapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celisner S.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY075473; AAL68285.1; -.
DR FlyBase; FBgn0036899; CG8780.
SQ SEQUENCE 356 AA; 36699 MW; 4F453F17950BD9EA CRC64;

Query Match 16.0%; Score 85; DB 2; Length 356;
Best Local Similarity 28.0%; Pred. No. 2.2;
Matches 23; Conservative 15; Mismatches 28; Indels 16; Gaps 4;

Qy 11 TTRPKI-----AHCILFNQPHSPRNSHSHNPPLKLRHSHNRPRAYILI 58
Db 209 STSNPAISTATSSVAVSMASHLAASSPHHHHPHTAHSHPHPL-AHPAHSHHHVGH--V 265
Qy 59 TILPSKLKRLT-HSQSHNPLS 79
Db 266 GAPPVSTAVTTHHMAHPHPLS 287

RESULT 11
Q8AXX1 PRELIMINARY; PRT; 612 AA.
AC Q8AXX1;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Putative gag protein.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=14963102; DOI=10.1093/molbev/msh072;
RA Goodwin T.J., Poulter R.T.;
RT "A new group of tyrosine recombinase-encoding retrotransposons.";
RL Mol. Biol. Evol. 21:746-759(2004).

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RN  [2]
RP  SEQUENCE FROM N.A.
RL  Goodwin T.J.D., Poulter R.T.M.;
DR  Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
SQ  EMBL: AY152729; AAN71720.1; -
    SEQUENCE 612 AA; 66457 MW; 9A0140DC6C3F1D8D CRC64;

Query Match      16.0%; Score 85; DB 2; Length 612;
Best Local Similarity 34.0%; Pred. No. 4.1;
Matches 33; Conservative 11; Mismatches 31; Indels 22; Gaps 7;

QY  10 PTTNRPKIAHCILFNOPHS-----PRSNSHSHNPCLKHRR--SHSHNRPAYILITIL 61
Db  213 PLANISTISHA---NOPTSLTWPPAPHSSTPSP-PLHTTAISHSHSQPP-----IPNL 264

QY  62 PSKLLKLRTHSQSHHNPLRSTNSNTP-TNSFLMTSSKP 97
Db  265 P-----RTSTQLHTTSSSHHNAQPLSNPTLSIPP 296

RESULT 12
Q9VM27 PRELIMINARY; PRT; 717 AA.
ID AC Q9VM27
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE CG8780-PA.
GN ORFNAMES=CG8780;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Ananides P.G., Scher S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.G., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Mortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Borchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Folsler C., Gabrieli A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodita C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Moberly C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodagett, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
    "The genome sequence of Drosophila melanogaster.";
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OX NCBI_TaxID=36329;
RN
RP SEQUENCE FROM N.A.
RA Seger K., Murphy L., Harris D., Berriman M., Pain A., Hall N.,
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL844507; CAD51147.1; -.
DR InterPro: IPR000884; TSP1.
DR SMART: SM00209; TSP1; 1.
DR PROSITE; PSS0092; TSP1; 1.
KW Hypothetical protein.
SQ SEQUENCE 891 AA; 107237 MW; 4765013F17B51B46 CRC64;

Query Match 16.0%; Score 85; DB 2; Length 891;
Best Local Similarity 28.9%; Pred. No. 6.3;
Matches 26; Conservative 8; Mismatches 24; Indels 32; Gaps 4;

Qy 18 AHCLIFNQPHS---PRSNSHHPNPLKLRHRRSHHNRPRAYILITLPSKLKLRTHSQS 74
Db 107 SHNSHNSHNSHNSHNSHNSHNS---HNSHSHNSHSHS-----SHNSH 150

Qy 75 HNPUSRTSNT-----PTNSFL 91
Db 151 SNHSHSSTQNSLYHDTNQANFLKPTGFFL 180

RESULT 14
O8LC22 PRELIMINARY; PRT; 372 AA.
AC O8LC22;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN
RP SEQUENCE FROM N.A.
RX Haas B.J., Volfovsky N., Town C.D., Troukhan M., Alexandrov N.,
RA Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;
RT "Full-length messenger RNA sequences greatly improve genome
RT annotation.";
RL Genome Biol. 3:RESEARCH0029-RESEARCH0029(2002).
RN
RP SEQUENCE FROM N.A.
RA Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,
RA Feldmann K.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY086310; AAM64382.1; -.
DR InterPro: IPR011541; NICO_transpt.
DR Pfam; PF03824; NICO; 1.
KW Hypothetical protein.
SQ SEQUENCE 372 AA; 39686 MW; 9FDB12077B5B3FFA CRC64;

Query Match 15.8%; Score 84; DB 2; Length 372;
Best Local Similarity 33.3%; Pred. No. 3;
Matches 30; Conservative 13; Mismatches 25; Indels 22; Gaps 6;

Qy 14 RPKIAHCILFNQPHSPRSNSHHPNPLKLRHRRSHHNRPRAYILITLPSKLKLRTHSQS 73
Db 6 QPPSSHSI-----AP-SKTQSRSPLLHL-LRHSPN-----LTFPPSSRLLESRRIS 50

Qy 74 -----HNNPLSRGS-NSTPTNSFLMTSSK 96
Db 51 SISCFFRRHNPPLDTPSPGINSQSNFLIASQ 80

RESULT 15
Z408_HUMAN
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ID AC
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Zinc finger protein 408 (PR-domain zinc finger protein 17).
GN Name=ZNF408; Synonyms=PFM14, PRDM17;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN
RP SEQUENCE FROM N.A.
RA Du Y., Huang S.;
RT "A family of novel PR-domain (PRDM) genes as candidate tumor
RT suppressors.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RN
RP SEQUENCE FROM N.A.
RX PubMed=14702039; DOI=10.1038/ng1285;
RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Sekine M., Obayashi M., Nishi T., Shibahata T., Tanaka T., Ishii S.,
RA Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y.,
RA Nagahari K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuna M.,
RA Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H.,
RA Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E.,
RA Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M.,
RA Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,
RA Fujimori K., Tanai H., Kimata M., Watanabe M., Hiraoa S., Chiba Y.,
RA Ishida S., Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T.,
RA Kusano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O.,
RA Nomura Y., Togashi S., Komai F., Hara R., Takeuchi K., Arita M.,
RA Inose N., Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA Fujimori Y., Komiyama M., Tashiro K., Tanigami A., Fujiwara T.,
RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Komatsu T.,
RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y.,
RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
RT "Complete sequencing and characterization of 21,243 full-length human
RT cDNAs.";
RL Nat. Genet. 36:40-45(2004).
RN
RP SEQUENCE FROM N.A.
RX TISSUE=Lung and Uterus;
RL PubMed=22388257; PubMed=12477932; DOI=10.1073/pnas.2426038999;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fanev J., Helton E., Kettelman M., Madan A.C., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schermer A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
```

```
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: May function as a transcription factor.
CC -!- SUBCELLULAR LOCATION: Nuclear (Potential).
CC -!- SIMILARITY: Contains 10 C2H2-type zinc fingers.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF346626; AAK29075.1; -.
DR EMBL; AK022889; BAB14295.1; -.
DR EMBL; BC013355; AAI13355.1; -.
DR EMBL; BC015708; AAI15708.1; -.
DR HSSP; P25490; IUBD.
DR IntAct; Q9H9D4; -.
DR Genew; HGNC:20041; ZNF408.
DR H-InvDB; HIX0009606; -.
DR InterPro; IPR007087; Znf_C2H2.
DR Pfam; PF00036; zf-C2H2; 10.
DR SMART; SM00355; Znf_C2H2; 10.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 10.
DR PROSITE; PS00157; ZINC_FINGER_C2H2_2; 10.
KW DNA-binding; Metal-binding; Nuclear protein; Repeat;
KW Transcription regulation; Zinc-finger.
FT ZN_FING 353 375 C2H2-type 1.
FT ZN_FING 381 403 C2H2-type 2.
FT ZN_FING 409 431 C2H2-type 3.
FT ZN_FING 437 459 C2H2-type 4.
FT ZN_FING 468 490 C2H2-type 5.
FT ZN_FING 496 518 C2H2-type 6.
FT ZN_FING 524 546 C2H2-type 7.
FT ZN_FING 551 573 C2H2-type 8.
FT ZN_FING 579 601 C2H2-type 9.
FT ZN_FING 607 629 C2H2-type 10.
SQ SEQUENCE 720 AA; 78438 MW; 0D3CDA7572D17721 CRC64;

Query Match 15.7%; Score 83.5; DB 1; Length 720;
Best Local Similarity 33.3%; Pred. No. 7;
Matches 31; Conservative 5; Mismatches 26; Indels 31; Gaps 5;

QY 7 LHLPTNRP-KIAHCI-LFNQPHSPRSNSHS-----PNTPLKLRSHS 48
Db 515 LRLTGERPYRCPHCADAFPLPELRRLISHTGEAHLCPVCGKALRDPHTLRAHERLMS 574

QY 49 HNRP-----RAYILITILPSKLRTHSQSH 74
Db 575 GERPPCPQCGRAYTLAT-----KLRRHLKSH 601

Search completed: October 11, 2005, 07:18:49
Job time : 61.8262 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 11, 2005, 06:57:07 ; Search time 72.5829 Seconds  
(without alignments)  
522.196 Million cell updates/sec

Title: US-10-092-934-6

Perfect score: 531

Sequence: 1 EAYTMLHLPTTRPKIAHC.....SRTSNSTPTNSFLMTSSKPR 98

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

- 1: Geneseq1980s:\*
- 2: Geneseq1990s:\*
- 3: Geneseq2000s:\*
- 4: Geneseq2001s:\*
- 5: Geneseq2002s:\*
- 6: Geneseq2003as:\*
- 7: Geneseq2003bs:\*
- 8: Geneseq2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	531	100.0	98	2	AAR63235
2	531	100.0	98	2	AAR95914
3	531	100.0	98	5	AAE29147
4	531	100.0	98	6	ABR63245
5	531	100.0	98	6	ABU02977
6	531	100.0	98	6	ABP59927
7	531	100.0	98	6	AAE33194
8	531	100.0	98	6	ABJ19450
9	531	100.0	98	7	ADB37524
10	531	100.0	98	7	ADL96025
11	500	94.2	147	4	AAE63838
12	117	22.0	23	6	ABP59910
13	117	22.0	23	7	ADL96056
14	89.5	16.9	185	5	ABJ03679
15	88.5	16.7	145	4	AM933210
16	88.5	16.7	145	8	ADL30575
17	88	16.6	151	4	ABG29454
18	88	16.6	259	8	ADO20034
19	88	16.6	259	8	ADP22472
20	88	16.6	259	8	ADP55210
21	88	16.6	259	8	ADP24864
22	88	16.6	400	7	ADD18728
23	88	16.6	400	7	ADF76875
24	88	16.6	400	8	ADQ18293
25	88	16.6	445	5	ADJ33773

26	86.5	16.3	682	4	ABG03784	Abg03784	Novel hum
27	86	16.2	15	6	ABP59906	Abp59906	Human neu
28	86	16.2	15	7	ADL96052	Adl96052	Human neu
29	85.5	16.1	2958	4	ABB71368	Abb71368	Drosophila
30	85	16.0	15	6	ABP59907	Abp59907	Human neu
31	85	16.0	15	7	ADL96053	Adl96053	Human neu
32	85	16.0	525	5	ABA47787	Aba47787	Protein e
33	85	16.0	525	7	ADM86624	Adm86624	Aspergill
34	85	16.0	793	4	ABB71688	Abb71688	Drosophila
35	84	15.8	15	6	ABP59905	Abp59905	Human neu
36	84	15.8	15	7	ADL96051	Adl96051	Human neu
37	84	15.8	197	3	AAG58875	Agag58875	Arabidops
38	84	15.8	207	3	AAG58874	Agag58874	Arabidops
39	84	15.8	372	3	AAG15870	Agag15870	Arabidops
40	83.5	15.7	273	6	AAU16468	Aau16468	Human nov
41	83.5	15.7	273	6	ABU55537	Abu55537	Human nov
42	83.5	15.7	316	4	AAU16083	Aau16083	Human nov
43	83.5	15.7	316	6	ABU55152	Abu55152	Human nov
44	83.5	15.7	450	5	ABB97178	Abb97178	Novel hum
45	83.5	15.7	720	4	AAB94329	Aab94329	Human pro

#### ALIGNMENTS

RESULT 1  
AAR63235  
ID AAR63235 standard; protein; 98 AA.  
AC AAR63235;  
XX  
DT 25-MAR-2003 (revised)  
DT 06-JUL-1995 (first entry)  
XX  
DE CNS neural thread protein HB4.  
XX  
KW Central nervous system; neural thread protein HB4; Alzheimer's;  
KW neuroectodermal tumours; malignant astrocytomas; glioblastomas.  
XX  
OS Homo sapiens.  
XX  
PN WO9423756-Al.  
XX  
PD 27-OCT-1994.  
XX  
PF 20-APR-1994; 94WO-US004321.  
XX  
PR 20-APR-1993; 93US-00050559.  
XX  
PA (GEHO ) GEN HOSPITAL CORP.  
XX  
PI De La Monte SM, Wands JR;  
XX  
DR WPI; 1994-341497/42.  
DR N-PSDB; AAQ77871.  
XX  
PT Detection of neural thread proteins - to detect sporadic and familial  
PT Alzheimer's disease, neuroectodermal tumours, malignant astrocytomas and  
PT glioblastomas (Eng).  
XX  
PS Example 4; Fig 11a; 158pp; English.  
XX  
CC AAQ77870 encodes AAR63235 the HB4 CNS neural thread protein (NTP). These  
CC sequences were used in the development of an antibody dependent method,  
CC for the detection of NTPs. This new method could be used to diagnose  
CC Alzheimer's disease (differentiating between sporadic and familial),  
CC neuroectodermal tumours, malignant astrocytomas and glioblastomas.  
CC (Updated on 25-MAR-2003 to correct PN field.)  
XX  
SQ Sequence 98 AA;  
Query Match 100.0%; Score 531; DB 2; Length 98;  
Best Local Similarity 100.0%; Pred. No. 1.5e-53;

Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EAYYTMLHPTTNRPKIAHCILFNQPHSPRSNSHSHNPPLKLRHRRSHSHNRPRAYILITI 60  
 Db 1 EAYYTMLHPTTNRPKIAHCILFNQPHSPRSNSHSHNPPLKLRHRRSHSHNRPRAYILITI 60  
 Qy 61 LPSKCLKRTHSQSHHNPPLSRSTNSPTNSFLMTSSKPR 98  
 Db 61 LPSKCLKRTHSQSHHNPPLSRSTNSPTNSFLMTSSKPR 98

## RESULT 2

AAR95914  
 ID AAR95914 standard; protein; 98 AA.

XX AC AAR95914;

DT 14-NOV-1996 (first entry)

XX HB4 human neural thread protein partial sequence.

XX Neural thread protein; NTP; diagnosis; detection; Alzheimer's disease;  
 KW neuroectodermal tumour; malignant astrocytoma; monoclonal antibody;  
 KW binding fragment.

XX Homo sapiens.

XX WO9615272-A1.

XX PD 23-MAY-1996.

XX PF 14-NOV-1995; 95WO-US017111.

XX PR 14-NOV-1994; 94US-00340426.

XX PA (GEHO ) GEN HOSPITAL CORP.

XX PI De La Monte S, Wands JR;

XX DR WPI; 1996-259865/26.

XX DR N-PSDB; AAT27753.

XX Detection of neural thread protein in diagnosis of Alzheimer's disease -  
 PT also NTP DNA and protein sequences used in gene and anti:sense therapy.

XX Example 4b; Fig 11A; 238pp; English.

XX A method for detecting the presence of neural thread protein (NTP) having  
 CC a molecular weight of 8, 14, 17, 21, 26 or 42 kD in a human subject  
 CC comprises (a) contacting a sample from a human subject that is suspected  
 CC of containing the NTP with at least one molecule capable of binding to  
 CC the protein; and (b) detecting any of the molecule bound to the protein.  
 CC The binding molecule is selected from an antibody free of natural  
 CC impurities, a monoclonal antibody or a binding fragment of either of  
 CC these. The method may be used for diagnosing the presence of Alzheimer's  
 CC disease, neuroectodermal tumours and a malignant astrocytoma in a human.  
 CC A number of clones of neural thread protein were isolated from healthy 17  
 CC -18 week old fetal human brain (HB) 2 year old temporal lobe neocortex  
 CC and end stage Alzheimer's disease (AD) cerebral cortex. See AAT27753-75

XX Sequence 98 AA;

Query Match 100.0%; Score 531; DB 2; Length 98;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-53;  
 Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EAYYTMLHPTTNRPKIAHCILFNQPHSPRSNSHSHNPPLKLRHRRSHSHNRPRAYILITI 60  
 Db 1 EAYYTMLHPTTNRPKIAHCILFNQPHSPRSNSHSHNPPLKLRHRRSHSHNRPRAYILITI 60  
 Qy 61 LPSKCLKRTHSQSHHNPPLSRSTNSPTNSFLMTSSKPR 98  
 Db 61 LPSKCLKRTHSQSHHNPPLSRSTNSPTNSFLMTSSKPR 98

## RESULT 3

AAE29147

XX AAE29147 standard; protein; 98 AA.

AC AAE29147;

DT 27-JAN-2003 (first entry)

XX Neural thread protein (NTP) #5.

XX Neural thread protein; NTP; hyperplasia; hypertrophy; arteriosclerosis;  
 KW haemorrhoid; gene therapy; tumour; vascular disease; atherosclerosis;  
 KW inflammatory disease; nutritional deficiency disease; genetic disease;  
 KW autoimmune disease; metabolic disease; traumatic disease; intoxication;  
 KW infectious disease; congenital malformation; enzyme deficiency disease;  
 KW amyloid disease; fibrosis disease; storage disease; radiation disease;  
 KW poisoning; environmental disease; endocrine disease; protein therapy;  
 KW degenerative disease; mechanical disease.

XX Unidentified.

XX WO200274323-A2.

XX PD 26-SEP-2002.

XX PF 08-MAR-2002; 2002WO-1B001959.

XX PR 08-MAR-2001; 2001US-0273957P.

XX PA (AVER/) AVERBACK P.

XX PI Averbach P;

XX WPI; 2002-759864/82.

XX Treating a condition in a patient requiring removal or destruction of  
 PT cells, such as a benign or malignant tumor of a tissue or an inflammatory  
 PT disease, comprises administering a neural thread protein (NTP) or a NTP  
 PT gene to a mammal.

XX Claim 23; Fig 6; 70pp; English.

XX The invention relates to a method for treating a condition in a patient  
 CC requiring removal or destruction of cells. The method involves  
 CC administering to a mammal a neural thread protein (NTP), or administering  
 CC to a tumour or other target cell a NTP gene, where the expression of the  
 CC NTP gene is induced resulting in expression of the NTP protein. The  
 CC method and NTP are useful for treating a condition in a patient requiring  
 CC removal or destruction of cells, such as a benign or malignant tumour of  
 CC a tissue, a hyperplasia, hypertrophy, or overgrowth of a tissue,  
 CC preferably tonsillar hypertrophy or prostatic hyperplasia, a virally,  
 CC bacterially, or parasitically altered tissue, or a malformation of a  
 CC tissue. Other conditions include a cosmetic modification to a tissue,  
 CC such as removal of unwanted facial hair, warts or unwanted fatty tissue,  
 CC a vascular disease, particularly atherosclerosis or arteriosclerosis,  
 CC haemorrhoids, or varicose veins, an inflammatory disease, autoimmune  
 CC disease, metabolic disease, hereditary/genetic disease, traumatic disease  
 CC or physical injury, nutritional deficiency disease, infectious disease,  
 CC congenital malformation, amyloid disease, fibrosis disease, storage  
 CC disease, enzyme deficiency disease, poisoning, intoxication, degenerative  
 CC disease, radiation disease, environmental disease, endocrine disease or  
 CC mechanical disease. The invention is useful in protein therapy and gene  
 CC therapy. The present sequence is NTP protein

XX Sequence 98 AA;

Query Match 100.0%; Score 531; DB 5; Length 98;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-53;  
 Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EAYYTMLHPTTNRPKIAHCILFNQPHSPRSNSHSHNPPLKLRHRRSHSHNRPRAYILITI 60

```
Db 1 EAYTMLHLPTTNRPKIAHCLIFNQPHSPRSNSHSHNPPLKLRHRSNRPAYILITI 60
Qy 61 LPSKLLRTHSQSHHNPFLSRTSNSTPTNSFLMTSSKPR 98
Db 61 LPSKLLRTHSQSHHNPFLSRTSNSTPTNSFLMTSSKPR 98

RESULT 4
ID ABR63245 standard; protein; 98 AA.
AC ABR63245;
XX
DT 28-AUG-2003 (first entry)
DE 98 amino acid neural thread protein.
XX
KW Cytostatic; Antibacterial; Immunosuppressive; Antiinflammatory;
KW neural thread protein; NTP; tumour.
XX
OS Unidentified.
XX
PN WO2003008443-A2.
XX
PD 30-JAN-2003.
XX
PF 19-JUL-2002; 2002WO-CA001105.
XX
PR 19-JUL-2001; 2001US-0306150P.
PR 19-JUL-2001; 2001US-0306161P.
PR 16-NOV-2001; 2001US-0331477P.
XX
PA (NYMO-) NYMOX CORP.
XX
PI Averbach PA;
XX
WPI; 2003-247995/24.
XX
PT Novel neural thread protein peptide, referred as cell death peptide,
PT useful for treating prostatic hyperplasia, psoriasis, eczema, dermatosis,
PT atherosclerosis, cosmetic modification to skin, throat, mouth, muscle.
XX
PS Disclosure; Fig 6; 77pp; English.
XX
CC The present invention relates to a neural thread protein (NTP) peptide
CC referred to as cell death peptide. Thought to be cytostatic.
CC antibacterial, immunosuppressive and antiinflammatory. It is useful for
CC treating a condition in a patient requiring removal or destruction of
CC cells, for treating a condition such as benign or malignant tumor.
CC inflammatory disease, autoimmune disease and infectious disease. The
CC peptide useful for treatment is derived from the amino acid sequence for
CC a pancreatic thread protein. The peptide is conjugated, linked or bound
CC to a molecule chosen from antibody or its fragment, antibody-like binding
CC molecule, where the molecule has a higher affinity for binding to a tumor
CC or other target than binding to other cells. Treatment using NTP peptides
CC can remove benign tumors with less risk and fewer of the undesirable side
CC effects of surgery. The present sequence is an NTP amino acid sequence
XX
SQ Sequence 98 AA;
Query Match 100.0%; Score 531; DB 6; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.5e-53;
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EAYTMLHLPTTNRPKIAHCLIFNQPHSPRSNSHSHNPPLKLRHRSNRPAYILITI 60
Db 1 EAYTMLHLPTTNRPKIAHCLIFNQPHSPRSNSHSHNPPLKLRHRSNRPAYILITI 60
Qy 61 LPSKLLRTHSQSHHNPFLSRTSNSTPTNSFLMTSSKPR 98
Db 61 LPSKLLRTHSQSHHNPFLSRTSNSTPTNSFLMTSSKPR 98
```

```
RESULT 5
ABU02977
ID ABU02977 standard; protein; 98 AA.
XX
AC ABU02977;
XX
DT 20-JAN-2003 (first entry)
DE Human neural thread protein AD7C-NTP, protein fragment #5.
XX
KW Neural thread protein; NTP-peptide; AD7C-NTP; surgical excision;
KW transplantation; grafting; chemotherapy; immunotherapy; vaccination;
KW ablation; cryotherapy; laser therapy; phototherapy; gene therapy;
KW radiation; tumour; hyperplasia; hypertrophy; overgrowth of tissue;
KW malformation of tissue; tonsillary hypertrophy; prostatic hyperplasia;
KW cosmetic modification; vascular disease; atherosclerosis;
KW arteriosclerosis; haemorrhoid; varicose vein; inflammatory disease;
KW autoimmune disease; metabolic disease; traumatic disease;
KW physical injury; nutritional deficiency disease; infectious disease;
KW amyloid disease; fibrosis disease; storage disease;
KW congenital malformation; enzyme deficiency disease; poisoning;
KW intoxication; environmental disease; radiation disease;
KW endocrine disease; degenerative disease; mechanical disease.
XX
OS Homo sapiens.
XX
PN WO200297030-A2.
XX
PD 05-DEC-2002.
XX
PF 24-MAY-2002; 2002WO-CA000759.
XX
PR 25-MAY-2001; 2001US-0293156P.
XX
PA (NYMO-) NYMOX CORP.
XX
PI Averbach PA;
XX
WPI; 2003-041406/03.
XX
PT Novel peptides similar in amino acid sequence to neural thread proteins
PT (NTP), useful for treating unwanted cellular proliferations such as
PT malignant tumors and prostatic hyperplasia.
XX
PS Disclosure; Fig 6; 78pp; English.
XX
CC The invention describes an NTP-peptide (I) comprising at least one amino
CC acid sequence corresponding to part of the amino acid sequence of a
CC neural thread protein, AD7C-NTP. The invention provides a method of
CC treating a condition requiring removal or destruction of cells of a
CC mammal comprising administering to a mammal, a therapeutic amount of (I).
CC The treatment is administered to the mammal before, during or after
CC surgical excision, transplantation, grafting, chemotherapy,
CC immunotherapy, vaccination, thermal or electrical ablation, cryotherapy,
CC laser therapy, phototherapy, gene therapy and/or radiation. The method is
CC useful for treatment of benign or malignant tumour; hyperplasia,
CC hypertrophy or overgrowth of tissue; virally, bacterially or
CC parasitically altered tissue; malformation of tissue selected from lung,
CC sinus, colon, stomach, pancreas, prostate, bladder, bone, ovary, skin, kidney,
CC gland, blood, brain and its coverings, spinal cord, muscle, connective
CC tissue, reproductive organs, liver, hair, gall bladder, eye, ear, nose, throat,
CC tonsils, mouth and lymph nodes and lymphoid system; tonsillary
CC hypertrophy; prostatic hyperplasia; cosmetic modification to a tissue;
CC vascular disease (atherosclerosis or arteriosclerosis); haemorrhoids;
CC varicose veins; inflammatory disease; autoimmune disease; metabolic
CC disease; hereditary/genetic disease; traumatic disease; physical injury;
CC nutritional deficiency disease; infectious disease; amyloid disease;
CC fibrosis disease; storage disease; congenital malformation; enzyme
CC deficiency disease; poisoning; intoxication; environmental disease;
CC radiation disease; endocrine disease; degenerative disease and mechanical
```

CC disease. This is the amino acid sequence of a human neural thread protein  
 CC AD7C-NTP protein fragment  
 XX  
 SQ Sequence 98 AA;

Query Match 100.0%; Score 531; DB 6; Length 98;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-53;  
 Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EAYTLMHLPTTNRPKIAHCILFNQPHSPRSNSHSHPNPLKLRHRRSHSHNRPRAYILITI 60  
 DB 1 EAYTLMHLPTTNRPKIAHCILFNQPHSPRSNSHSHPNPLKLRHRRSHSHNRPRAYILITI 60

OY 61 LPSKLRTHSQSHHNPPLSRSTNSPTNSFLMTSSKPR 98  
 DB 61 LPSKLRTHSQSHHNPPLSRSTNSPTNSFLMTSSKPR 98

RESULT 6  
 ABP59927  
 ID ABP59927 standard; protein; 98 AA.  
 XX  
 AC ABP59927;  
 XX  
 DT 08-SEP-2003 (first entry)  
 XX  
 DE Human 98 amino acid neural thread protein.  
 XX  
 KW Human; tumour; cancer; neural thread protein; NTP; cell removal;  
 KW cell destruction; antipsoriatic; antimicrobial; immunosuppressive;  
 KW antiinflammatory; dermatological; antiarteriosclerotic; vasotropic;  
 KW gene therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003044053-A2.  
 XX  
 PD 30-MAY-2003.  
 XX  
 PF 18-NOV-2002; 2002WO-CA001757.  
 XX  
 PR 16-NOV-2001; 2001US-0331477P.  
 XX  
 PA (NYMO-) NYMOX CORP.  
 XX  
 PI Averbach P, Gemmell J;  
 XX  
 PS WPI; 2003-457592/43.  
 XX  
 CC New neural thread protein (NTP), useful for preparing a composition for  
 PT treating or preventing a condition in a mammal requiring removal or  
 PT destruction of cells, e.g. psoriasis, eczema, atherosclerosis or  
 PT inflammatory disease.  
 XX  
 PS Disclosure; Fig 4; 98pp; English.  
 XX  
 CC The present invention relates to peptides derived from the human neural  
 CC thread protein (NTP). The peptides are useful for preparing a composition  
 CC for treating or preventing a condition in a mammal requiring removal or  
 CC destruction of cells, comprising tonsillary hypertrophy, prostatic  
 CC hyperplasia, psoriasis, eczema, dermatosis, cosmetic modification to a  
 CC breast, connective, skin, eye, ear, nose, throat, mouth or muscle tissue,  
 CC varicose veins, atherosclerosis, inflammatory, metabolic, infectious,  
 CC fibrosis, endocrine or autoimmune disease, or stenosis, restenosis,  
 CC occlusion or blockage of an artery or of a stent placed or implanted in  
 CC an artery. The present sequence is an NTP protein used to produce  
 CC peptides of the invention  
 XX  
 SQ Sequence 98 AA;

Query Match 100.0%; Score 531; DB 6; Length 98;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-53;  
 Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EAYTLMHLPTTNRPKIAHCILFNQPHSPRSNSHSHPNPLKLRHRRSHSHNRPRAYILITI 60  
 DB 1 EAYTLMHLPTTNRPKIAHCILFNQPHSPRSNSHSHPNPLKLRHRRSHSHNRPRAYILITI 60

OY 61 LPSKLRTHSQSHHNPPLSRSTNSPTNSFLMTSSKPR 98  
 DB 61 LPSKLRTHSQSHHNPPLSRSTNSPTNSFLMTSSKPR 98

RESULT 7  
 AAE33194  
 ID AAE33194 standard; protein; 98 AA.  
 XX  
 AC AAE33194;  
 XX  
 DT 16-APR-2003 (first entry)  
 XX  
 DE Neural thread protein (NTP) #5.  
 XX  
 KW Cell death; tissue necrosis; neural thread protein; NTP; amyloidosis;  
 KW stroke; brain tumour; Pick's disease; Parkinson's disease; glaucoma;  
 KW Alzheimer's disease; gene therapy.  
 XX  
 OS Unidentified.  
 XX  
 PN WO200289841-A2.  
 XX  
 PD 14-NOV-2002.  
 XX  
 PF 06-MAY-2002; 2002WO-CA000691.  
 XX  
 PR 04-MAY-2001; 2001US-0288463P.  
 XX  
 PA (NYMO-) NYMOX CORP.  
 XX  
 PI Averbach PA;  
 XX  
 DR WPI; 2003-120506/11.  
 XX  
 CC Preventing, controlling, modulating, ameliorating and/or treating cell  
 CC death or tissue necrosis using antibodies to neural thread proteins,  
 CC useful in disorders such as stroke, brain tumor, glaucoma and Alzheimer's  
 CC disease.  
 XX  
 PS Disclosure; Fig 9; 60pp; English.  
 XX  
 CC The invention relates to a method of preventing, and/or inhibiting cell  
 CC death and/or tissue necrosis in live tissue containing neural thread  
 CC proteins (NTP). The method involves contacting the live tissue with at  
 CC least one antibody, fragment or derivative that recognises NTP, where the  
 CC antibody, fragment or derivative is present to prevent, control,  
 CC ameliorate and/or inhibit cell death and/or tissue necrosis caused by the  
 CC presence of NTP. Methods and compositions of the invention are useful for  
 CC preventing, modulating, controlling and/or treating disorders associated  
 CC with cell death and/or tissue necrosis such as stroke, brain tumour,  
 CC Pick's disease, Parkinson's disease, amyloidosis, glaucoma and  
 CC Alzheimer's disease. The invention is useful in gene therapy. The present  
 CC sequence is NTP protein  
 XX  
 SQ Sequence 98 AA;

Query Match 100.0%; Score 531; DB 6; Length 98;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-53;  
 Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EAYTLMHLPTTNRPKIAHCILFNQPHSPRSNSHSHPNPLKLRHRRSHSHNRPRAYILITI 60  
 DB 1 EAYTLMHLPTTNRPKIAHCILFNQPHSPRSNSHSHPNPLKLRHRRSHSHNRPRAYILITI 60

OY 61 LPSKLRTHSQSHHNPPLSRSTNSPTNSFLMTSSKPR 98  
 DB 61 LPSKLRTHSQSHHNPPLSRSTNSPTNSFLMTSSKPR 98



RESULT 8  
 ABJ19450  
 ID ABJ19450 standard; protein; 98 AA.  
 XX AC  
 XX ABJ19450;  
 XX DT 27-MAR-2003 (first entry)  
 XX DE  
 XX DE 98-mer neural thread protein.  
 XX KW Nootropic; neuroprotective; cell death; tissue necrosis; NTP;  
 KW neural thread protein; neurodegenerative disorder; Alzheimer's disease.  
 XX OS Unidentified.  
 XX PN WO200292115-A2.  
 XX PD 21-NOV-2002.  
 XX PF 16-MAY-2002; 2002WO-CA000712.  
 XX PR 16-MAY-2001; 2001US-0290971P.  
 XX PA (NYMO-) NYMOX CORP.  
 XX PI Averbach PA;  
 XX DR WPI; 2003-129234/12.  
 XX PT Preventing and/or inhibiting cell death and/or tissue necrosis in a  
 PT tissue for treating a neurodegenerative disorder, e.g. Alzheimer's  
 PT disease, by contacting the live tissue with at least one segment of  
 PT neural thread proteins (NTP).  
 XX PS Disclosure; Fig 6; 60pp; English.  
 XX CC The invention relates to a novel method for preventing and/or inhibiting  
 CC cell death and/or tissue necrosis in a tissue comprising contacting the  
 CC live tissue with at least one segment of neural thread proteins (NTP).  
 CC The methods are composition are useful for treating a neurodegenerative  
 CC disorder, such as Alzheimer's disease. This sequence represents an NTP  
 CC protein of the invention  
 XX SQ Sequence 98 AA;  
 Query Match 100.0%; Score 531; DB 6; Length 98;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-53;  
 Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 EAYYTMHLPTTNRPKIAHCILFNQPHSPRNSHSHNPPLKLRSHSHNRPAYILITI 60  
 Db 1 EAYYTMHLPTTNRPKIAHCILFNQPHSPRNSHSHNPPLKLRSHSHNRPAYILITI 60  
 Qy 61 LPSKLLRTHSQSHHNPFLSRTNSTPTNSFLMTSSKPR 98  
 Db 61 LPSKLLRTHSQSHHNPFLSRTNSTPTNSFLMTSSKPR 98  
 RESULT 9  
 ADB37524  
 ID ADB37524 standard; protein; 98 AA.  
 XX AC  
 XX ADB37524;  
 XX DT 04-DEC-2003 (first entry)  
 XX DE Neural thread protein #3.  
 XX KW Cytostatic; Antitumour; Antipsoriatic; Dermatological;  
 KW Antiatherosclerotic; Antiarteriosclerotic; Vasotropic; Antiinflammatory;  
 KW Immunosuppressive; Tranquillizer; Antiemetic; Virucide; AD7c-NTP;

KW neural thread protein; neuritic sprouting.  
 XX Unidentified.  
 XX PN WO2003008444-A2.  
 XX PD 30-JAN-2003.  
 XX PF 19-JUL-2002; 2002WO-CA001106.  
 XX PR 19-JUL-2001; 2001US-0306150P.  
 XX PR 19-JUL-2001; 2001US-0306161P.  
 XX PR 16-NOV-2001; 2001US-0331477P.  
 XX PA (NYMO-) NYMOX CORP.  
 XX PI Averbach PA, Gemmell J;  
 XX DR WPI; 2003-248000/24.  
 XX PT Novel Related peptide or AD7c-neural thread peptide, useful for treating  
 PT unwanted cellular proliferations, glandular hyperplasia, unwanted facial  
 PT hair, warts and unwanted fatty tissue.  
 XX PS Disclosure; Fig 6; 109pp; English.  
 XX CC The present invention relates to AD7c-neural thread protein (NTP) and  
 CC related proteins and peptides (I; ADB37528-ADB37641). The sequences are  
 CC useful for treating a condition in a patient requiring removal or  
 CC destruction of cells. The condition can be selected from benign or  
 CC malignant tumour of a tissue, hyperplasia, hypertrophy or overgrowth of a  
 CC tissue, virally, bacterially or parasitically altered tissue, or  
 CC malformation of a tissue, where the tissue is selected from lung, breast,  
 CC stomach, pancreas, prostate, bladder, bone, ovary, skin, kidney, sinus,  
 CC colon, intestine, stomach, rectum, oesophagus, heart, spleen, salivary  
 CC gland, blood, brain and its coverings, spinal cord and its coverings,  
 CC muscle, connective tissue, adrenal, parathyroid, thyroid, uterus, testis,  
 CC pituitary, reproductive organs, liver, gall bladder, eye, ear, nose,  
 CC throat, tonsils, mouth, lymph nodes and lymphoid tissue. The condition is  
 CC preferably tonsillary hypertrophy, prostatic hyperplasia, psoriasis,  
 CC eczema, dermatosis, cosmetic modification to a tissue (skin, eye, ear,  
 CC nose, throat, mouth, muscle, connective, hair or breast tissue), vascular  
 CC disease (atherosclerosis or arteriosclerosis), haemorrhoids, varicose  
 CC veins, inflammatory disease, autoimmune disease, metabolic disease,  
 CC hereditary/genetic disease, traumatic disease or physical injury,  
 CC nutritional deficiency disease, infectious disease, amyloid disease,  
 CC fibrosis disease, storage disease, congenital malformation, enzyme  
 CC deficiency disease, poisoning, intoxication, environmental disease  
 CC radiation disease, endocrine disease, degenerative disease and mechanical  
 CC disease. The peptides are useful for treating unwanted cellular  
 CC proliferations, glandular (e.g. prostate) hyperplasia, unwanted facial  
 CC hair, warts and unwanted fatty tissue, or for preparing antibodies that  
 CC recognize and/or bind to Related proteins, Related peptides or NTP  
 CC peptides. The present sequence was used to illustrate the invention.  
 XX SQ Sequence 98 AA;  
 Query Match 100.0%; Score 531; DB 7; Length 98;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-53;  
 Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 EAYYTMHLPTTNRPKIAHCILFNQPHSPRNSHSHNPPLKLRSHSHNRPAYILITI 60  
 Db 1 EAYYTMHLPTTNRPKIAHCILFNQPHSPRNSHSHNPPLKLRSHSHNRPAYILITI 60  
 Qy 61 LPSKLLRTHSQSHHNPFLSRTNSTPTNSFLMTSSKPR 98  
 Db 61 LPSKLLRTHSQSHHNPFLSRTNSTPTNSFLMTSSKPR 98  
 RESULT 10  
 ADL96025  
 ID ADL96025 standard; protein; 98 AA.

XX AC ADL96025;  
 XX DT 20-MAY-2004 (first entry)  
 XX DE Human neural thread protein, NTP98.  
 XX DE  
 XX KW Human; neural thread protein; NTP122; NTP112; NTP106; NTP98; NTP75;  
 KW NTP68; NTP61; stenosis; stent; tumour; prostatic hyperplasia; psoriasis;  
 KW eczema; haemorrhoid; atherosclerosis; inflammatory disease;  
 KW autoimmune disease; metabolic disease; hereditary disease;  
 KW genetic disease; traumatic disease; physical injury;  
 KW nutritional deficiency disease; infectious disease; amyloid disease;  
 KW Alzheimer's disease; storage disease; congenital malformation;  
 KW enzyme deficiency disease; poisoning; intoxication;  
 KW environmental disease; radiation disease; endocrine disease;  
 KW degenerative disease; mechanical disease.  
 XX OS Homo sapiens.  
 XX PN US200316569-A1.  
 XX PD 04-SEP-2003.  
 XX PF 15-NOV-2002; 2002US-00294891.  
 XX PR 16-NOV-2001; 2001US-0331477P.  
 XX PA (AVER/) AVERBACK P.  
 XX PA (GEMM/) GEMMELL J.  
 XX PI Averbach P, Gemmell J;  
 XX DR WPI; 2003-898099/82.  
 XX PT New neural thread protein or its variants, useful for treating tumors and  
 PT other conditions requiring the removal or destruction of cells (e.g.  
 PT prostatic hyperplasia, psoriasis, eczema, hemorrhoids or  
 PT atherosclerosis).  
 XX PS Disclosure; SEQ ID NO 4; 32pp; English.  
 XX CC The invention relates to a peptide, or its homologue, derivative,  
 CC fragment, variant or mimetic, comprising at least one neural thread  
 CC protein (NTP) peptide appearing as ADL96029-ADL96069, derived from  
 CC NTP122, 112, 106, 98, 75, 68 or 61. Also included are a nucleic acid  
 CC encoding an amino acid sequence corresponding to the above peptide, a  
 CC composition comprising one or more peptides or nucleic acids cited above  
 CC and a carrier, a method of treating a condition in a mammal requiring  
 CC removal or destruction of cells (comprising administering to the mammal  
 CC an amount of the peptide cited above) and a method of preventing or  
 CC inhibiting the stenosis, occlusion or blockage of a stent, comprising  
 CC coating the stent with an amount of the above peptide. The peptide  
 CC further comprises an amino acid in a reverse-D order based on the above  
 CC amino acid sequences. The composition and methods are useful in treating  
 CC tumours and other conditions requiring the removal or destruction of  
 CC cells (e.g. prostatic hyperplasia, psoriasis, eczema, haemorrhoids or  
 CC atherosclerosis). These may also be used in treating inflammatory  
 CC diseases, autoimmune diseases, metabolic diseases, hereditary/genetic  
 CC diseases, traumatic diseases or physical injuries, nutritional deficiency  
 CC diseases, infectious diseases, amyloid diseases e.g. Alzheimer's disease,  
 CC storage diseases, congenital malformation, enzyme deficiency diseases,  
 CC poisoning, intoxication, environmental diseases, radiation diseases,  
 CC endocrine diseases, degenerative diseases or mechanical diseases. The  
 CC present sequence is a human NTP protein from which the peptides of the  
 CC invention are derived.  
 XX SQ Sequence 98 AA;  
 XX Query Match 100.0%; Score 531; DB 7; Length 98;  
 XX Best Local Similarity 100.0%; Pred. No. 1.5e-53;  
 XX Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EAYYTMHLPTTNRPKIAHCILFNQPHSPRSNSHSHPNPLKLRHRRSHSHNRPRAYILITI 60  
 DB 1 EAYYTMHLPTTNRPKIAHCILFNQPHSPRSNSHSHPNPLKLRHRRSHSHNRPRAYILITI 60  
 QY 61 LPSKLLRTHSQSHHNPRLSRTNSTPTNSFLMTSSKPR 98  
 DB 61 LPSKLLRTHSQSHHNPRLSRTNSTPTNSFLMTSSKPR 98  
 RESULT 11  
 AAB63838  
 ID AAB63838 standard; protein; 147 AA.  
 XX AAB63838;  
 XX AC  
 XX DT 26-MAR-2001 (first entry)  
 XX DE Human prostate cancer associated antigen protein sequence SEQ ID NO:1200.  
 XX KW Human; breast cancer; gastric cancer; prostate cancer; diagnosis;  
 KW cancer associated antigen; cytostatic; cancer vaccine.  
 XX OS Homo sapiens.  
 XX PN WO200073801-A2.  
 XX PD 07-DEC-2000.  
 XX PF 26-MAY-2000; 2000WO-US014749.  
 XX PR 28-MAY-1999; 99US-0136526P.  
 XX PR 10-SEP-1999; 99US-0153454P.  
 XX PA (LUDW-) LUDWIG INST CANCER RES.  
 XX PI Obata Y;  
 XX WPI; 2001-025274/03.  
 XX DR  
 XX PT Nucleic acids encoding breast, gastric and prostate cancer associated  
 PT antigen precursors, useful for diagnosing and treating a condition  
 PT characterized by expression of an abnormal amount of a protein, e.g.  
 PT cancer.  
 XX PS Example 1; Page 740-741; 799pp; English.  
 XX CC AAF22422 to AAF22626, AAF22627 to AAF22773 and AAF22774 to AAF23014  
 CC represent nucleotide sequences encoding human breast, gastric and  
 CC prostate cancer associated antigen precursors (CAAP) respectively.  
 CC AAB63232 to AAB63467, AAB63468 to AAB63721 and AAB63722 to AAB63970  
 CC represent human breast, gastric and prostate CAAP protein sequence  
 CC respectively, CAAPs have cytostatic activity and can be used in the  
 CC production of cancer vaccines. The human CAAP proteins, peptides, nucleic  
 CC acids or anti-CAAP antibodies are useful for diagnosing and treating a  
 CC condition characterised by expression of an abnormal amount of a protein,  
 CC e.g. cancer  
 XX SQ Sequence 147 AA;  
 XX Query Match 94.2%; Score 500; DB 4; Length 147;  
 XX Best Local Similarity 96.8%; Pred. No. 9.9e-50;  
 XX Matches 92; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 4 YTMHLPTTNRPKIAHCILFNQPHSPRSNSHSHPNPLKLRHRRSHSHNRPRAYILITILPS 63  
 DB 53 YNKLHLPTTNRPKIAHCILFNQPHSPRSNSHSHPNPLKLRHRRSHSHNRPRAYILITILPS 112  
 QY 64 KKLRLTHSQSHHNPRLSRTNSTPTNSFLMTSSKPR 98  
 DB 113 KKLRLTHSQSHHNPRLSRTNSTPTNSFLMTSSKPR 147  
 RESULT 12

ABP59910  
ID ABP59910 standard; peptide; 23 AA.  
XX  
AC ABP59910;  
XX  
XX 28-AUG-2003 (first entry)  
DT  
XX Human neural thread protein NTP(98) peptide #6.  
DE  
XX Human; tumour; cancer; neural thread protein; NTP; cell removal;  
KW cell destruction; antipsoriatic; antimicrobial; immunosuppressive;  
KW antiinflammatory; dermatological; antiarteriosclerotic; vasotropic;  
KW gene therapy.  
XX  
XX Homo sapiens.  
OS  
XX WO2003044053-A2.  
PN  
XX 30-MAY-2003.  
PD  
XX 18-NOV-2002; 2002WO-CA001757.  
PF  
XX 16-NOV-2001; 2001US-0331477P.  
PR  
XX (NYMO-) NYMOX CORP.  
PA  
XX Averbach P, Gemmell J;  
PI  
XX WPI; 2003-457592/43.  
DR  
XX New neural thread protein (NTP), useful for preparing a composition for  
PT treating or preventing a condition in a mammal requiring removal or  
PT destruction of cells, e.g. psoriasis, eczema, atherosclerosis or  
PT inflammatory disease.  
XX  
XX Claim 1; Page 37; 98pp; English.  
PS  
XX The present invention relates to peptides derived from the human neural  
CC thread protein (NTP). The peptides are useful for preparing a composition  
CC for treating or preventing a condition in a mammal requiring removal or  
CC destruction of cells, comprising tonsillary hypertrophy, prostatic  
CC hyperplasia, psoriasis, eczema, dermatosis, cosmetic modification to a  
CC breast, connective, skin, eye, ear, nose, throat, mouth or muscle tissue,  
CC varicose veins, atherosclerosis, inflammatory, metabolic, infectious,  
CC fibrosis, endocrine or autoimmune disease, or stenosis, restenosis,  
CC occlusion or blockage of an artery or of a stent placed or implanted in  
CC an artery. The present sequence is a peptide of the invention  
XX  
XX Sequence 23 AA;  
Query Match 22.0%; Score 117; DB 6; Length 23;  
Best Local Similarity 100.0%; Pred. No. 2.3e-06;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 76 NPLSRTSNSTPTNSFLMTSSKPR 98  
DB 1 NPLSRTSNSTPTNSFLMTSSKPR 23  
RESULT 13  
ADL96056  
ID ADL96056 standard; peptide; 23 AA.  
XX  
XX ADL96056;  
AC  
XX 20-MAY-2004 (first entry)  
DT  
XX Human neural thread protein, NTP98, peptide #6.  
DE  
XX Human; neural thread protein; NTP122; NTP106; NTP98; NTP75;  
KW NTP68; NTP61; stenosis; stent; tumour; prostatic hyperplasia; psoriasis;  
KW eczema; haemorrhoid; atherosclerosis; inflammatory disease;  
KW autoimmune disease; metabolic disease; hereditary disease;

genetic disease; traumatic disease; physical injury;  
KW nutritional deficiency disease; infectious disease; amyloid disease;  
KW Alzheimer's disease; storage disease; congenital malformation;  
KW enzyme deficiency disease; poisoning; intoxication;  
KW environmental disease; radiation disease; endocrine disease;  
KW degenerative disease; mechanical disease.  
XX  
XX Homo sapiens.  
OS  
XX US2003166569-A1.  
PN  
XX 04-SEP-2003.  
PD  
XX 15-NOV-2002; 2002US-00294891.  
PF  
XX 16-NOV-2001; 2001US-0331477P.  
PR  
XX (AVER/) AVERBACK P.  
PA (GEMM/) GEMMELL J.  
PI Averbach P, Gemmell J;  
XX WPI; 2003-898099/82.  
DR  
XX New neural thread protein or its variants, useful for treating tumors and  
XX other conditions requiring the removal or destruction of cells (e.g.  
PT prostatic hyperplasia, psoriasis, eczema, hemorrhoids or  
PT atherosclerosis).  
PT  
XX Claim 1; SEQ ID NO 35; 32pp; English.  
PS  
XX The invention relates to a peptide, or its homologue, derivative,  
CC fragment, variant or mimetic, comprising at least one neural thread  
CC protein (NTP) peptide appearing as ADL96029-ADL96069, derived from  
CC NTP122, 112, 106, 98, 75, 68 or 61. Also included are a nucleic acid  
CC encoding an amino acid sequence corresponding to the above peptide, a  
CC composition comprising one or more peptides or nucleic acids cited above  
CC and a carrier, a method of treating a condition in a mammal requiring  
CC removal or destruction of cells (comprising administering to the mammal  
CC an amount of the peptide cited above) and a method of preventing or  
CC inhibiting the stenosis, occlusion or blockage of a stent, comprising  
CC coating the stent with an amount of the above peptide. The peptide  
CC further comprises an amino acid in a reverse-D order based on the above  
CC amino acid sequences. The composition and methods are useful in treating  
CC tumours and other conditions requiring the removal or destruction of  
CC cells (e.g. prostatic hyperplasia, psoriasis, eczema, haemorrhoids or  
CC atherosclerosis). These may also be used in treating inflammatory  
CC diseases, autoimmune diseases, metabolic diseases, hereditary/genetic  
CC diseases, traumatic diseases or physical injuries, nutritional deficiency  
CC diseases, infectious diseases, amyloid diseases e.g. Alzheimer's disease,  
CC storage diseases, congenital malformation, enzyme deficiency diseases,  
CC poisoning, intoxication, environmental diseases, radiation diseases,  
CC endocrine diseases, degenerative diseases or mechanical diseases. The  
CC present sequence is a NTP peptide of the invention.  
XX  
XX Sequence 23 AA;  
Query Match 22.0%; Score 117; DB 7; Length 23;  
Best Local Similarity 100.0%; Pred. No. 2.3e-06;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 76 NPLSRTSNSTPTNSFLMTSSKPR 98  
DB 1 NPLSRTSNSTPTNSFLMTSSKPR 23  
RESULT 14  
ABJ03679  
ID ABJ03679 standard; protein; 185 AA.  
XX  
XX ABJ03679;  
AC  
XX 25-SEP-2002 (first entry)  
DT

```
XX DE Human ovary specific protein SEQ ID NO: 121.
XX KW Human; ovary; ovarian cancer; ovarian disease; gene therapy; cytostatic.
XX OS Homo sapiens.
XX PN WO200240720-A2.
XX PD 23-MAY-2002.
XX PF 20-NOV-2001; 2001WO-US045010.
XX PR 20-NOV-2000; 2000US-0249997P.
XX PA (DIAD-) DIADEXUS INC.
XX PI Salceda S, Macina RA, Recipon H, Cafferkey R, Sun Y, Liu C;
XX DR WPI; 2002-547588/58.
XX PT New ovary polypeptides useful for detecting, diagnosing, monitoring,
XX PT treating, staging and imaging cancers in humans having cancer and non-
XX PT cancerous ovary disease.
XX PS Claim 11; Page 233-234; 296pp; English.
XX CC The present invention provides human proteins and coding sequences
XX CC specifically found in ovary cells. These can be used in the diagnosis and
XX CC treatment of ovarian diseases, including cancer. The present sequence is
XX CC a protein of the invention
XX SQ Sequence 185 AA;

Query Match 16.9%; Score 89.5; DB 5; Length 185;
Best Local Similarity 33.0%; Pred. No. 0.046;
Matches 30; Conservative 15; Mismatches 33; Indels 13; Gaps 6;

QY 4 YTMHLPTTNRPKIAICILNQPHSPR--SNSHSHNPPLKLRH-SHSHNRPRAYILITI 60
Db 100 HTSPFHPTYNH--LSHIFLNPQPHHRLDSSPTHP-PLHIHKOINHTSAPHNTHTRSTL 156

QY 61 LPSKCLKLRTHSQSHHNPPLSRSTNSPTNSPL 91
Db 157 TTPPTL--HSHSHSPL-----TTPHHLL 180

RESULT 15
AAM93210
ID AAM93210 standard; protein; 145 AA.
XX AC AAM93210;
XX DT 06-NOV-2001 (first entry)
XX DE Human polypeptide, SEQ ID NO: 2508.
XX KW Human; full length cDNA; cDNA synthesis; oligo-capping.
XX OS Homo sapiens.
XX PN EP1130094-A2.
XX PD 05-SEP-2001.
XX PF 07-JUL-2000; 2000EP-00114089.
XX PR 08-JUL-1999; 99JP-00194486.
XX PR 11-JAN-2000; 2000JP-00118774.
XX PR 02-MAY-2000; 2000JP-00183765.
XX PA (HELI-) HELIX RES INST.
XX PA
XX ^

PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
XX WPI; 2001-524355/58.
XX N-PSDB; AAK94119.
XX PT 830 Primers useful for synthesizing full length cDNA clones and their use
XX PT in genetic manipulation.
XX PS Claim 8; SEQ ID NO 2608; 1380pp + Sequence Listing; English.
XX CC The invention relates to primers for synthesising full length cDNA
XX CC clones. 830 cDNA molecules encoding a human protein have been isolated
XX CC and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have
XX CC been determined. Primers for synthesising the full length cDNA are useful
XX CC for clarifying the function of the protein encoded by the cDNA. The full
XX CC length clones were obtained by construction of full length enriched cDNA
XX CC libraries that were synthesised by the oligo-capping method. The primers
XX CC enable the production of the full length cDNA easily without any special
XX CC methods. The present sequence is a polypeptide encoded by a full length
XX CC human cDNA of the invention. Note: The sequence data for this patent did
XX CC not form part of the printed specification, but was obtained in CD-ROM
XX CC format directly from EPO
XX SQ Sequence 145 AA;

Query Match 16.7%; Score 88.5; DB 4; Length 145;
Best Local Similarity 30.7%; Pred. No. 0.045;
Matches 23; Conservative 6; Mismatches 13; Indels 33; Gaps 3;

QY 28 SPRSNSHSHPNPL-----KLHRRSHSHNRPRAYILITILPSKCLKLRTHSQSHHN- 76
Db 65 TPSSHPHQHHHTYITPPSTPLNLHRRPHSHPR-----LHTTRPHHL 109

QY 77 -----PLSRTSNS 84
Db 110 PRVRTAAPLHRPENS 124

Search completed: October 11, 2005, 07:11:09
Job time : 74.5829 secs
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OM protein - protein search, using sw model

Run on: October 11, 2005, 06:57:16 ; Search time 164.294 Seconds  
(without alignments)  
248.149 Million cell updates/sec

Title: US-10-092-934-6

Perfect score: 531

Sequence: 1 EAYTLMHLPTNRPKIAHC.....SRTSNSTPTNSFLMTSSKPR 98

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1854112 seqs, 416015017 residues

Total number of hits satisfying chosen parameters: 1854112

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*  
1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*  
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14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep.\*  
15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep.\*  
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18: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*  
19: /cgn2\_6/ptodata/2/pubpaa/US11A\_PUBCOMB.pep.\*  
20: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep.\*  
21: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*  
22: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	531	100.0	98	14	US-10-138-516-5
2	531	100.0	98	14	US-10-146-130-7
3	531	100.0	98	14	US-10-092-934-6
4	531	100.0	98	14	US-10-153-334-6
5	531	100.0	98	14	US-10-198-069-6
6	531	100.0	98	14	US-10-198-070-6
7	531	100.0	98	14	US-10-294-891-4
8	531	100.0	98	17	US-10-920-313-4
9	117	22.0	23	14	US-10-294-891-35
10	117	22.0	23	17	US-10-920-313-35
11	99.5	18.7	123	16	US-10-425-115-365713

12	90.5	17.0	117	16	US-10-437-963-165665	Sequence 165665,
13	90	16.9	136	15	US-10-424-599-177792	Sequence 177792,
14	89.5	16.9	185	13	US-10-001-833-121	Sequence 121, App
15	88	16.6	151	18	US-10-450-763-59813	Sequence 59813, A
16	88	16.6	400	14	US-10-301-822-155	Sequence 155, App
17	88	16.6	400	16	US-10-723-860-1111	Sequence 1111, Ap
18	88	16.6	400	16	US-10-370-7158-550	Sequence 550, App
19	88	16.6	400	18	US-10-970-698A-28	Sequence 28, Appl
20	86.5	16.3	682	18	US-10-450-763-34143	Sequence 34143, A
21	86	16.2	15	14	US-10-294-891-31	Sequence 31, Appl
22	86	16.2	15	17	US-10-920-313-31	Sequence 31, Appl
23	85.5	16.1	2958	20	US-11-097-143-40896	Sequence 40896, A
24	85	16.0	15	14	US-10-294-891-32	Sequence 32, Appl
25	85	16.0	15	17	US-10-920-313-32	Sequence 32, Appl
26	85	16.0	793	20	US-11-097-143-41856	Sequence 41856, A
27	84	15.8	15	14	US-10-294-891-30	Sequence 30, Appl
28	84	15.8	15	17	US-10-920-313-30	Sequence 30, Appl
29	83.5	15.7	273	9	US-09-764-864-1421	Sequence 1421, Ap
30	83.5	15.7	316	9	US-09-764-864-1036	Sequence 1036, Ap
31	83.5	15.7	720	15	US-10-200-012-18	Sequence 18, Appl
32	83	15.6	708	20	US-11-097-143-10932	Sequence 10932, A
33	82.5	15.5	207	15	US-10-424-599-283755	Sequence 283755,
34	82.5	15.5	226	15	US-10-108-260A-4030	Sequence 4030, Ap
35	81.5	15.3	657	17	US-10-794-514A-324	Sequence 324, App
36	81.5	15.3	1399	20	US-11-097-143-34929	Sequence 34929, A
37	81	15.3	261	14	US-10-280-953-17	Sequence 17, Appl
38	80	15.1	15	14	US-10-294-891-34	Sequence 34, Appl
39	80	15.1	15	17	US-10-920-313-34	Sequence 34, Appl
40	80	15.1	260	15	US-10-094-749-1890	Sequence 1890, Ap
41	79.5	15.0	67	16	US-10-425-115-310747	Sequence 310747,
42	79.5	15.0	1113	16	US-10-739-930-5799	Sequence 5799, Ap
43	79.5	15.0	3972	14	US-10-156-761-8476	Sequence 8476, Ap
44	79.5	15.0	3972	16	US-10-204-862A-4	Sequence 4, Appl
45	79.5	15.0	3972	16	US-10-204-862A-8	Sequence 8, Appl

#### ALIGNMENTS

##### RESULT 1

US-10-138-516-5  
; Sequence 5, Application US/10138516  
; Publication No. US20030003445A1  
; GENERAL INFORMATION:  
; APPLICANT: AVERBACK, PAUL  
; TITLE OF INVENTION: METHOD OF PREVENTING CELL DEATH USING ANTIBODIES TO  
; TITLE OF INVENTION: NEURAL THREAD PROTEINS  
; FILE REFERENCE: 59003.000004  
; CURRENT APPLICATION NUMBER: US/10/138,516  
; CURRENT FILING DATE: 2002-07-23  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 98  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-138-516-5

Query Match 100.0%; Score 531; DB 14; Length 98;  
Best Local Similarity 100.0%; Pred. No. 8.7e-49;  
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy	61	LPSKCLKRTHSQSHHNPFLSRTNSTPTNSFLMTSSKPR	98
Db	61	LPSKCLKRTHSQSHHNPFLSRTNSTPTNSFLMTSSKPR	98

RESULT 2  
US-10-146-130-7

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; Sequence 7, Application US/10146130
; Publication No. US20030004107A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; TITLE OF INVENTION: METHOD OF PREVENTING CELL DEATH USING SEGMENTS OF
; FILE REFERENCE: 59003.000007
; CURRENT APPLICATION NUMBER: US/10/146,130
; CURRENT FILING DATE: 2002-08-06
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-146-130-7

Query Match      100.0%; Score 531; DB 14; Length 98;
Best Local Similarity 100.0%; Pred. No. 8.7e-49;
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EAYTMLHLPTTNRPKIAHCILFNQPHSPRSNSHSHPNPLKLRHSHSHNRPRAYILITI 60
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   |||||||

QY 61 LPSKLLRTHSQSHHNPPLSRSTNSPTNSFLMTSSKPR 98
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Db 61 LPSKLLRTHSQSHHNPPLSRSTNSPTNSFLMTSSKPR 98
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RESULT 3
US-10-092-934-6
; Sequence 6, Application US/10092934
; Publication No. US20030054990A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; TITLE OF INVENTION: METHODS OF USING NEURAL THREAD PROTEINS TO TREAT TUMORS
; TITLE OF INVENTION: AND CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF
; FILE REFERENCE: 018792-0199
; CURRENT APPLICATION NUMBER: US/10/092,934
; CURRENT FILING DATE: 2002-06-05
; PRIOR APPLICATION NUMBER: 60/273,957
; PRIOR FILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Neural thread
US-10-092-934-6

Query Match      100.0%; Score 531; DB 14; Length 98;
Best Local Similarity 100.0%; Pred. No. 8.7e-49;
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EAYTMLHLPTTNRPKIAHCILFNQPHSPRSNSHSHPNPLKLRHSHSHNRPRAYILITI 60
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QY 61 LPSKLLRTHSQSHHNPPLSRSTNSPTNSFLMTSSKPR 98
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US-10-153-334-6
; Sequence 6, Application US/10153334
; Publication No. US20030096350A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 59003-000006
; CURRENT APPLICATION NUMBER: US/10/153,334
; CURRENT FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: 60/293,156
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-153-334-6

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Best Local Similarity 100.0%; Pred. No. 8.7e-49;
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 LPSKLLRTHSQSHHNPPLSRSTNSPTNSFLMTSSKPR 98
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Db 61 LPSKLLRTHSQSHHNPPLSRSTNSPTNSFLMTSSKPR 98
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RESULT 5
US-10-198-069-6
; Sequence 6, Application US/10198069
; Publication No. US20030096756A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 59003.000009
; CURRENT APPLICATION NUMBER: US/10/198,069
; CURRENT FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/306,161
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/306,150
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/331,477
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Unknown NTP
US-10-198-069-6

Query Match      100.0%; Score 531; DB 14; Length 98;
Best Local Similarity 100.0%; Pred. No. 8.7e-49;
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 EAYTMLHLPTTNRPKIAHCILFNQPHSPRSNSHSHPNPLKLRHSHSHNRPRAYILITI 60
   |||||||

QY 61 LPSKLLRTHSQSHHNPPLSRSTNSPTNSFLMTSSKPR 98
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RESULT 6
US-10-198-069-6
; Sequence 6, Application US/10198069
; Publication No. US20030096756A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 59003.000009
; CURRENT APPLICATION NUMBER: US/10/198,069
; CURRENT FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/306,161
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/306,150
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/331,477
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Unknown NTP
US-10-198-069-6

Query Match      100.0%; Score 531; DB 14; Length 98;
Best Local Similarity 100.0%; Pred. No. 8.7e-49;
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EAYTMLHLPTTNRPKIAHCILFNQPHSPRSNSHSHPNPLKLRHSHSHNRPRAYILITI 60
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QY 61 LPSKLLRTHSQSHHNPPLSRSTNSPTNSFLMTSSKPR 98
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Db 61 LPSKLLRTHSQSHHNPPLSRSTNSPTNSFLMTSSKPR 98
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US-10-198-070-6
; Sequence 6, Application US/10198070
; Publication No. US20030109437A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; APPLICANT: GEMMEL, JACK
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 59003.000008
; CURRENT APPLICATION NUMBER: US/10/198,070
; CURRENT FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/306,161
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/306,150
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/331,477
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 6
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Unknown NTP
; OTHER INFORMATION: peptide
US-10-198-070-6
Query Match 100.0%; Score 531; DB 14; Length 98;
Best Local Similarity 100.0%; Pred. No. 8.7e-49;
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 EAYTMLHLPTTNRPKIAHCILFNQPHSPRSNSHSHNPPLKLRHRRSHNRPRAYILITI 60
Db 1 EAYTMLHLPTTNRPKIAHCILFNQPHSPRSNSHSHNPPLKLRHRRSHNRPRAYILITI 60
Qy 61 LPSKLLRTHSQSHHNPPLSRSTNSPTNSFLMTSSKPR 98
Db 61 LPSKLLRTHSQSHHNPPLSRSTNSPTNSFLMTSSKPR 98
RESULT 7
US-10-294-891-4
; Sequence 4, Application US/10294891
; Publication No. US20030166569A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; APPLICANT: GEMMEL, JACK
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF CELLS
; FILE REFERENCE: 59003.000010
; CURRENT APPLICATION NUMBER: US/10/294,891
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: 60/331,447
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-294-891-4
Query Match 100.0%; Score 531; DB 14; Length 98;
Best Local Similarity 100.0%; Pred. No. 8.7e-49;
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 EAYTMLHLPTTNRPKIAHCILFNQPHSPRSNSHSHNPPLKLRHRRSHNRPRAYILITI 60
Db 1 EAYTMLHLPTTNRPKIAHCILFNQPHSPRSNSHSHNPPLKLRHRRSHNRPRAYILITI 60
Qy 61 LPSKLLRTHSQSHHNPPLSRSTNSPTNSFLMTSSKPR 98
Db 61 LPSKLLRTHSQSHHNPPLSRSTNSPTNSFLMTSSKPR 98
RESULT 8
US-10-920-313-4
; Sequence 4, Application US/10920313
; Publication No. US20050032704A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; APPLICANT: GEMMEL, JACK
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF CELLS
; FILE REFERENCE: 59003.000010
; CURRENT APPLICATION NUMBER: US/10/920,313
; CURRENT FILING DATE: 2004-08-18
; PRIOR APPLICATION NUMBER: 60/331,447
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-920-313-4
Query Match 100.0%; Score 531; DB 17; Length 98;
Best Local Similarity 100.0%; Pred. No. 8.7e-49;
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 EAYTMLHLPTTNRPKIAHCILFNQPHSPRSNSHSHNPPLKLRHRRSHNRPRAYILITI 60
Db 1 EAYTMLHLPTTNRPKIAHCILFNQPHSPRSNSHSHNPPLKLRHRRSHNRPRAYILITI 60
Qy 61 LPSKLLRTHSQSHHNPPLSRSTNSPTNSFLMTSSKPR 98
Db 61 LPSKLLRTHSQSHHNPPLSRSTNSPTNSFLMTSSKPR 98
RESULT 9
US-10-294-891-35
; Sequence 35, Application US/10294891
; Publication No. US20030166569A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; APPLICANT: GEMMEL, JACK
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF CELLS
; FILE REFERENCE: 59003.000010
; CURRENT APPLICATION NUMBER: US/10/294,891
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: 60/331,447
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 35
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-294-891-35
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Best Local Similarity 100.0%; Pred. No. 1.9e-05;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 76 NPLSRSTNSPTNSFLMTSSKPR 98
Db 1 NPLSRSTNSPTNSFLMTSSKPR 23
RESULT 10
US-10-920-313-35
; Sequence 35, Application US/10920313
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; Publication No. US20050032704A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; APPLICANT: GEMMEL, JACK
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF CELLS
; FILE REFERENCE: 59003.000010
; CURRENT APPLICATION NUMBER: US/10/920,313
; CURRENT FILING DATE: 2004-08-18
; PRIOR APPLICATION NUMBER: 60/331,447
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 35
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-920-313-35

Query Match      22.0%; Score 117; DB 17; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.9e-05;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      76 NPLSRTSNSTPTNSFLMTSSKPR 98
Db      1 NPLSRTSNSTPTNSFLMTSSKPR 23

RESULT 11
US-10-425-115-365713
; Sequence 365713, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 365713
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(123)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_96695C.1.pap
US-10-425-115-365713

Query Match      18.7%; Score 99.5; DB 16; Length 123;
Best Local Similarity 31.2%; Pred. No. 0.0096;
Matches 35; Conservative 13; Mismatches 43; Indels 21; Gaps 8;

QY      3 YVTMLH-LPTTRPKIAHCILFNQPHSPRSNSHSHPNPLKLH--RRSHSHN-----RPR 53
Db      4 YVTLLHTTLPXHX-KSNH--TXSQHHXAHXSHHXXHXTKXHHSHXTHKHNLHXXHPH 60

QY      54 AYILITILPSKLRTHSQSHHN-PLSR-----TSNSTPTNSFLMTSSKP 97
Db      61 YXXLI-YHPXLPIRHTQPSHHQFPLSHYVYXHHSSISSTTILSYILYTPP 111

RESULT 12
US-10-437-963-165665
; Sequence 165665, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
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; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 165665
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_6444C.1.pap
US-10-437-963-165665

Query Match      17.0%; Score 90.5; DB 16; Length 117;
Best Local Similarity 27.6%; Pred. No. 0.082;
Matches 32; Conservative 10; Mismatches 51; Indels 23; Gaps 3;

QY      3 YVTMLHLPTRPKIAHCILFNQPHSPRSNSHSHPNPLKL-----HRRSHS-----HNR 51
Db      2 YHTQTHTHTHTHHTTTLFNVYVHTNSLSLTHSTNSLSLTHTHQTQHSLSLTHTH 61

QY      52 PRAYLITILPSKLRTHSQSHHNPLS-----RTSNSTPTNSFLMTSS 95
Db      62 THNFTLTLLKKMHTKSLSTHTHTNPLSLSLSLSHSTHTQTQTHTHTHTNNTHTST 117

RESULT 13
US-10-424-599-177792
; Sequence 177792, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 177792
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(136)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_131562C.1.pap
US-10-424-599-177792

Query Match      16.9%; Score 90; DB 15; Length 136;
Best Local Similarity 28.0%; Pred. No. 0.11;
Matches 26; Conservative 9; Mismatches 30; Indels 28; Gaps 5;

QY      5 TMLHLPTRPKIAHCILFNQPHS-----PRNSHSHPNPLK-----LHRRSHSHNRPR 53
Db      43 TLIHVP-----PHSTTIFHTNMHTHTPTSTTHHPPPLHHHPAPCILHHHHT--- 92

QY      54 AYILITILPSKLRTHSQSHHNPLSRSTNSSTP 86
Db      93 -----YYXTPANPTTHHHHHPP--APANATP 118
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Db 78 APRSHH-RPRR-----PTATWATHANSQPSHTKGTGAGFLTLSFLQFRSGP 126

Search completed: October 11, 2005, 07:39:45  
Job time : 164.294 secs

RESULT 14  
US-10-001-835-121  
; Sequence 121, Application US/10001835  
; Publication No. US20020160387A1  
; GENERAL INFORMATION:  
; APPLICANT: Salceda, Susana  
; APPLICANT: Macina, Roberto  
; APPLICANT: Recipon, Herve  
; APPLICANT: Caferkey, Robert  
; APPLICANT: Sun, Yongming  
; APPLICANT: Liu, Chenghua  
; TITLE OF INVENTION: Compositions and Methods Relating to Ovary Specific Genes and Pro  
; FILE REFERENCE: DEX-0277  
; CURRENT APPLICATION NUMBER: US/10/001,835  
; CURRENT FILING DATE: 2001-11-20  
; PRIOR APPLICATION NUMBER: 60/249,997  
; PRIOR FILING DATE: 2000-11-20  
; NUMBER OF SEQ ID NOS: 228  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 121  
; LENGTH: 185  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-10-001-835-121

Query Match 16.9%; Score 89.5; DB 13; Length 185;  
Best Local Similarity 33.0%; Pred. No. 0.18;  
Matches 30; Conservative 15; Mismatches 33; Indels 13; Gaps 6;  
Qy 4 YTMHLHTTRPKTAHCILFNQPHSPR--SNSHSHNPPLKLRHRR-SHSHNRPRAYILITI 60  
Db 100 HTSPHSPTYNH--LSHPLNQPPHHRLDSSPTHP-PLHIKQINHTSAPHNTHTRSTL 156  
Qy 61 LPSKLRTHSQSHHNPRLSRSTNSPTNSFL 91  
Db 157 TPPPTL--HSHSHSPL-----TTPHHLL 180

RESULT 15  
US-10-450-763-59813  
; Sequence 59813, Application US/10450763  
; Publication No. US20050198754A1  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc  
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES  
; FILE REFERENCE: 790CIE3/US  
; CURRENT APPLICATION NUMBER: US/10/450,763  
; CURRENT FILING DATE: 2003-06-11  
; PRIOR APPLICATION NUMBER: PCT/US01/08631  
; PRIOR FILING DATE: 2001-03-30  
; PRIOR APPLICATION NUMBER: 09/540,217  
; PRIOR FILING DATE: 2000-03-31  
; PRIOR APPLICATION NUMBER: 09/649,167  
; PRIOR FILING DATE: 2000-08-23  
; NUMBER OF SEQ ID NOS: 60736  
; SOFTWARE: Custom  
; SEQ ID NO 59813  
; LENGTH: 151  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-450-763-59813

Query Match 16.6%; Score 88; DB 18; Length 151;  
Best Local Similarity 31.6%; Pred. No. 0.2;  
Matches 37; Conservative 9; Mismatches 37; Indels 34; Gaps 8;  
Qy 4 YTMHL-----PTTRPK--IAHCILFNQPHSPRNS-----HSHNPPL---KL 42  
Db 21 HTVLTHAKSHIHFGTRSPNHTVTCG---PHPTQGRSSRTHTPPSAHSHKRPDLHPES 77  
Qy 43 HRRSHSHNRPRAYILITILPSKLRTHSQSHHNPRLS--RTSNSTPTNSFLMTSSKP 97

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 11, 2005, 06:57:19 ; Search time 22.4037 Seconds  
(without alignments)  
326.535 Million cell updates/sec

Title: US-10-092-934-6

Perfect score: 531

Sequence: 1 EAYVTMLHLPTTNRPKIAHC.....SRTSNSTPTNSFLMTSSKPR 98

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.\*

- 1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep.\*
- 2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*
- 3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*
- 4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*
- 5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep.\*
- 6: /cgn2\_6/ptodata/1/iaa/backfiles.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	531	100.0	98	2	US-08-454-557C-30
2	531	100.0	98	2	US-08-340-426D-30
3	531	100.0	98	2	US-08-450-673C-30
4	531	100.0	98	5	PCT-US95-17111A-30
5	81	15.3	261	4	US-09-602-565-34
6	80.5	15.2	651	1	US-08-431-080-24
7	80.5	15.2	651	2	US-08-938-534-24
8	80.5	15.2	651	3	US-09-345-294-24
9	75.5	14.2	379	4	US-09-270-767-57074
10	75.5	14.2	1557	4	US-09-410-551B-27
11	75.5	14.2	1557	4	US-09-940-316B-27
12	75.5	14.2	1574	4	US-09-410-551B-25
13	75.5	14.2	1574	4	US-09-940-316B-25
14	75.5	14.2	1578	4	US-09-410-551B-31
15	75.5	14.2	1578	4	US-09-940-316B-31
16	75.5	14.2	1588	4	US-09-410-551B-29
17	75.5	14.2	1588	4	US-09-940-316B-29
18	75.5	14.2	1605	4	US-09-410-551B-33
19	75.5	14.2	1605	4	US-09-940-316B-33
20	75	14.1	165	4	US-08-252-931A-25261
21	75	14.1	170	4	US-09-270-767-44218
22	75	14.1	639	4	US-09-949-016-6812
23	75	14.1	652	4	US-09-949-016-7323
24	74.5	14.0	423	4	US-09-270-767-41561
25	74	13.9	254	4	US-09-248-796A-19089
26	74	13.9	834	2	US-08-861-464-4
27	74	13.9	834	2	US-08-396-001-4

28	74	13.9	834	3	US-09-323-433A-4	Sequence 4, Appli
29	74	13.9	834	4	US-09-826-752-4	Sequence 4, Appli
30	73.5	13.8	410	4	US-09-270-767-43824	Sequence 43824, A
31	73	13.7	1013	4	US-09-612-402B-15	Sequence 15, Appl
32	73	13.7	1013	4	US-09-612-402B-16	Sequence 16, Appl
33	73	13.6	544	4	US-09-532-594B-18	Sequence 18, Appl
34	72	13.6	598	4	US-09-532-594B-16	Sequence 16, Appl
35	72	13.6	734	4	US-09-532-594B-4	Sequence 4, Appli
36	71.5	13.5	1007	4	US-10-144-198-36	Sequence 36, Appl
37	71.5	13.5	1041	4	US-10-144-198-14	Sequence 14, Appl
38	71	13.4	668	1	US-08-468-036-5	Sequence 5, Appli
39	71	13.4	668	2	US-08-376-843-5	Sequence 5, Appli
40	71	13.4	668	4	US-09-538-092-19	Sequence 19, Appl
41	71	13.4	1482	4	US-09-410-551B-21	Sequence 21, Appl
42	71	13.4	1482	4	US-09-940-316B-21	Sequence 21, Appl
43	71	13.4	1488	4	US-09-410-551B-17	Sequence 17, Appl
44	71	13.4	1488	4	US-09-940-316B-17	Sequence 17, Appl
45	71	13.4	1509	4	US-09-410-551B-23	Sequence 23, Appl

ALIGNMENTS

RESULT 1  
US-08-454-557C-30  
; Sequence 30, Application US/08454557C  
; Patent No. 5830670  
; GENERAL INFORMATION:  
; APPLICANT: de la Monte, Suzanne  
; APPLICANT: Wands, Jack R.  
; TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection  
; TITLE OF INVENTION: of Alzheimer's Disease  
; NUMBER OF SEQUENCES: 121  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.  
; STREET: 1100 New York Avenue, Suite 600  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/454,557C  
; FILING DATE: 30-MAY-1995  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ludwig, Steven R.  
; REGISTRATION NUMBER: 36,203  
; REFERENCE/DOCKET NUMBER: 0609.3840003  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 371-2600  
; TELEFAX: (202) 371-2540  
; INFORMATION FOR SEQ ID NO: 30:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 98 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
US-08-454-557C-30

Query Match	100.0%;	Score 531;	DB 2;	Length 98;
Best Local Similarity	100.0%;	Pred. No. 2e-55;		
Matches	98;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
Qy	1	EAYVTMLHLPTTNRPKIAHCILFNQPHSPRSNSHSHNPPLKLRHRSNHNPRAYILITI	60	
Db	1	EAYVTMLHLPTTNRPKIAHCILFNQPHSPRSNSHSHNPPLKLRHRSNHNPRAYILITI	60	
Qy	61	LPSKLRTHSQSHNPLSRSTNSPTNSFLMTSSKPR	98	



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; LENGTH: 98 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
PCT-US95-17111A-30

Query Match 100.0%; Score 531; DB 5; Length 98;
Best Local Similarity 100.0%; Pred. No. 2e-55;
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EAYTMLHLPTTNRPKIAHCILFNQPHSPRSNSHSHNPPLKLRSHSHNRPRAYILITI 60
Db 1 EAYTMLHLPTTNRPKIAHCILFNQPHSPRSNSHSHNPPLKLRSHSHNRPRAYILITI 60

Qy 61 LPSKLRTHSQSHHNPFLSTNSPTNSFLMTSSKPR 98
Db 61 LPSKLRTHSQSHHNPFLSTNSPTNSFLMTSSKPR 98

RESULT 5
US-09-602-565-34
; Sequence 34, Application US/09602565
; Patent No. 6500642
; GENERAL INFORMATION:
; APPLICANT: Yue, Henry
; APPLICANT: Patterson, Chandra
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; TITLE OF INVENTION: MOLECULE ASSOCIATED WITH APOPTOSIS
; FILE REFERENCE: PC-0018 US
; CURRENT APPLICATION NUMBER: US/09/602,565
; CURRENT FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 09/106,120
; PRIOR FILING DATE: 1998-06-29
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PERL Program
; SEQ ID NO 34
; LENGTH: 261
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6500642 g1469400
US-09-602-565-34

Query Match 15.3%; Score 81; DB 4; Length 261;
Best Local Similarity 34.7%; Pred. No. 0.12;
Matches 25; Conservative 4; Mismatches 33; Indels 10; Gaps 4;

Qy 14 RPKIAHCILFNQPHSPRSNSHSHNPPLKLRSHSHNRPRAYILITIPLSKLRTHSQS 73
Db 198 QPQLHSYPPHPH-PYSHPHQHPH---HPHPHPHPHPYQL-----QHAHQPLHSQP 248

Qy 74 H-HNPLSRSTNS 84
Db 249 QGHRLLRSTNS 260

RESULT 6
US-08-431-080-24
; Sequence 24, Application US/08431080
; Patent No. 5698686
; GENERAL INFORMATION:
; APPLICANT: Gottschling, Daniel E.
; APPLICANT: Singer, Miriam S.
; TITLE OF INVENTION: Telomerase Compositions and Methods
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TEXAS
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 77210

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/431,080
FILING DATE: Concurrently Herewith
CLASSIFICATION: 514
PRIOR APPLICATION NUMBER: SN 08/326,781
FILING DATE: October 20, 1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Parker, David L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: ARCD:155/PAR
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (713) 789-2679
TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 651 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-431-080-24

Query Match 15.2%; Score 80.5; DB 1; Length 651;
Best Local Similarity 29.1%; Pred. No. 0.43;
Matches 25; Conservative 14; Mismatches 34; Indels 13; Gaps 2;

Qy 26 PHSPRSNSHSHNPPLKLRSHSHNRPRAYILITILPS-----KLRTHSQSHH 75
Db 206 PHHPQHLLHHHPHKTLPKPSNSHSTNSLNQDPVRSNDEEKYGFIPKVFVRSRSFA 265

Qy 76 NPLS---RTSNSTPTNSFLMTSSKPR 98
Db 266 YPQQVAITTTSPSPNSHVLSSKSR 291

RESULT 7
US-08-938-534-24
; Sequence 24, Application US/08938534
; Patent No. 5916752
; GENERAL INFORMATION:
; APPLICANT: Gottschling, Daniel E.
; APPLICANT: Singer, Miriam S.
; TITLE OF INVENTION: Telomerase Compositions and Methods
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TEXAS
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 77210

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/938,534
FILING DATE: 26-SEP-1997
CLASSIFICATION: 536
PRIOR APPLICATION NUMBER: 08/431,080
FILING DATE:
APPLICATION NUMBER: SN 08/326,781
FILING DATE: October 20, 1994
ATTORNEY/AGENT INFORMATION:
```

```
/ NAME: Parker, David L.
/ REGISTRATION NUMBER: 32,165
/ REFERENCE/DOCKET NUMBER: ARCD:155/PAR
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (512) 418-3000
/ TELEFAX: (713) 789-2679
/ TELEX: 79-0924
/ INFORMATION FOR SEQ ID NO: 24:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 651 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/
US-08-938-534-24

Query Match      15.2%; Score 80.5; DB 2; Length 651;
Best Local Similarity 29.1%; Pred. No. 0.43;
Matches 25; Conservative 14; Mismatches 34; Indels 13; Gaps 2;

QY 26 PHSPRNSHSHNPPLKLRSHSHNRPRAYILITILPS-----KLLRTHSQSHH 75
Db 206 PHHPQHLLHHPHHKTLPKPSNSHSFTNSLNQDPVIRSNDDEKYGFIPKVFVRSRSSFA 265
QY 76 NPLS---RTSNSTPTNSFLMTSSKPR 98
Db 266 YPQQVAITTPSPSPNSHVLSSKSR 291

RESULT 8
US-09-345-294-24
/ Sequence 24, Application US/09345294
/ Patent No. 6387619
/ GENERAL INFORMATION:
/ APPLICANT: Gottschling, Daniel E.
/
/ TITLE OF INVENTION: Telomerase Compositions and Methods
/ NUMBER OF SEQUENCES: 32
/ CORRESPONDENCE ADDRESS:
/ ADDRESSES: Arnold, White & Durkee
/ STREET: P.O. Box 4433
/ CITY: Houston
/ STATE: TEXAS
/ COUNTRY: UNITED STATES OF AMERICA
/ ZIP: 77210
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
/ SOFTWARE: Patent In Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/345,294
/ FILING DATE: 30-Jun-1999
/ CLASSIFICATION: <Unknown>
/ PRIORITY APPLICATION DATA:
/ APPLICATION NUMBER: 08/431,080
/ FILING DATE: <Unknown>
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Parker, David L.
/ REGISTRATION NUMBER: 32,165
/ REFERENCE/DOCKET NUMBER: ARCD:155/PAR
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (512) 418-3000
/ TELEFAX: (713) 789-2679
/ TELEX: 79-0924
/ INFORMATION FOR SEQ ID NO: 24:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 651 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/
/ SEQUENCE DESCRIPTION: SEQ ID NO: 24:
/
US-09-345-294-24
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Query Match      15.2%; Score 80.5; DB 3; Length 651;
Best Local Similarity 29.1%; Pred. No. 0.43;
Matches 25; Conservative 14; Mismatches 34; Indels 13; Gaps 2;

QY 26 PHSPRNSHSHNPPLKLRSHSHNRPRAYILITILPS-----KLLRTHSQSHH 75
Db 206 PHHPQHLLHHPHHKTLPKPSNSHSFTNSLNQDPVIRSNDDEKYGFIPKVFVRSRSSFA 265
QY 76 NPLS---RTSNSTPTNSFLMTSSKPR 98
Db 266 YPQQVAITTPSPSPNSHVLSSKSR 291

RESULT 9
US-09-270-767-57074
/ Sequence 57074, Application US/09270767
/ Patent No. 6703491
/ GENERAL INFORMATION:
/ APPLICANT: Homburger et al.
/ TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
/ FILE REFERENCE: File Reference: 7326-094
/ CURRENT APPLICATION NUMBER: US/09/270,767
/ CURRENT FILING DATE: 1999-03-17
/ NUMBER OF SEQ ID NOS: 62517
/ SOFTWARE: Patent In Ver. 2.0
/ SEQ ID NO 57074
/ LENGTH: 379
/ TYPE: PRT
/ ORGANISM: Drosophila melanogaster
/ FEATURE:
/ OTHER INFORMATION: Xaa means any amino acid
/
US-09-270-767-57074

Query Match      14.2%; Score 75.5; DB 4; Length 379;
Best Local Similarity 32.8%; Pred. No. 0.83;
Matches 22; Conservative 10; Mismatches 26; Indels 9; Gaps 3;

QY 19 HCILFNQPHSPRSNSHSHNPPLKLRSHSHNRPRAYILITILPSKLLRTHSQSHHNP 78
Db 100 HCLTFEXIRN-RSQSHSP-----HLHLHLRPP---VIVVIIRSQLLNIVLVIVNHAM 150
QY 79 SRTSNST 85
Db 151 OCTCAST 157

RESULT 10
US-09-410-551B-27
/ Sequence 27, Application US/09410551B
/ Patent No. 6503737
/ GENERAL INFORMATION:
/ APPLICANT: KOSAN BIOSCIENCES, Inc.
/ APPLICANT: REEVES, CHRISTOPHER
/ APPLICANT: CHU, DANIEL
/ APPLICANT: KHOSLA, CHAITAN
/ APPLICANT: SANTI, DANIEL
/ APPLICANT: WU, KAI
/ TITLE OF INVENTION: POLYKETIDE SYNTHASE ENZYMES AND RECOMBINANT DNA
/ TITLE OF INVENTION: CONSTRUCTS THEREFOR
/ FILE REFERENCE: 30062-20026.00
/ CURRENT APPLICATION NUMBER: US/09/410,551B
/ CURRENT FILING DATE: 1999-10-01
/ PRIOR APPLICATION NUMBER: US 60/139,650
/ PRIOR FILING DATE: 1999-06-17
/ PRIOR APPLICATION NUMBER: US 60/123,810
/ PRIOR FILING DATE: 1999-03-11
/ PRIOR APPLICATION NUMBER: US 60/102,748
/ PRIOR FILING DATE: 1998-10-02
/ NUMBER OF SEQ ID NOS: 72
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 27
/ LENGTH: 1557
/ TYPE: PRT
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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic PKS
; OTHER INFORMATION: synthase fragment
US-09-410-551B-27

Query Match      14.2%; Score 75.5; DB 4; Length 1557;
Best Local Similarity 26.3%; Pred. No. 5;
Matches 25; Conservative 12; Mismatches 43; Indels 15; Gaps 3;

Qy 8 HLPITNRPKIAHCILFNQPHS-----PRSNHSHPNPKLHRRSHSHNRPRAYILITILP 62
Db 1271 HLITTNHTLVHTTT-DPPGAAVGTGLRTAQNEHPGRIHLIETHHPHTPLPLTQLTTLHQ 1329

Qy 63 SKLKLRTHS-----QSHHNPLSRSTNSPTN 88
Db 1330 PHLRLTNTLHTPLHTPIITTHNTTTTTPTPPLN 1364

RESULT 11
US-09-940-316B-27
; Sequence 27, Application US/09940316B
; Patent No. 6759536
; GENERAL INFORMATION:
; APPLICANT: KOSAN BIOSCIENCES, Inc.
; APPLICANT: REEVES, CHRISTOPHER
; APPLICANT: CHU, DANIEL
; APPLICANT: KHOSLA, CHAITAN
; APPLICANT: SANTI, DANIEL
; APPLICANT: WU, KAI
; TITLE OF INVENTION: POLYKETIDES ENCODING THE FKBA GENE OF THE FK-520 POLYKETIDE SYNTH
; FILE REFERENCE: 30062-20026.11
; CURRENT APPLICATION NUMBER: US/09/940,316B
; CURRENT FILING DATE: 2001-08-27
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: US 60/139,650
; PRIOR FILING DATE: 1999-06-17
; PRIOR APPLICATION NUMBER: US 60/123,810
; PRIOR FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: US 60/102,748
; PRIOR FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 1557
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic PKS
; OTHER INFORMATION: synthase fragment
US-09-940-316B-27

Query Match      14.2%; Score 75.5; DB 4; Length 1557;
Best Local Similarity 26.3%; Pred. No. 5;
Matches 25; Conservative 12; Mismatches 43; Indels 15; Gaps 3;

Qy 8 HLPITNRPKIAHCILFNQPHS-----PRSNHSHPNPKLHRRSHSHNRPRAYILITILP 62
Db 1271 HLITTNHTLVHTTT-DPPGAAVGTGLRTAQNEHPGRIHLIETHHPHTPLPLTQLTTLHQ 1329

Qy 63 SKLKLRTHS-----QSHHNPLSRSTNSPTN 88
Db 1330 PHLRLTNTLHTPLHTPIITTHNTTTTTPTPPLN 1364

RESULT 12
US-09-410-551B-25
; Sequence 25, Application US/09410551B
; Patent No. 6503737
; GENERAL INFORMATION:
; APPLICANT: KOSAN BIOSCIENCES, Inc.
; APPLICANT: REEVES, CHRISTOPHER
; APPLICANT: CHU, DANIEL
; APPLICANT: KHOSLA, CHAITAN
; APPLICANT: SANTI, DANIEL
; APPLICANT: WU, KAI
; TITLE OF INVENTION: POLYKETIDES ENCODING THE FKBA GENE OF THE FK-520 POLYKETIDE SYNTH
; FILE REFERENCE: 30062-20026.11
; CURRENT APPLICATION NUMBER: US/09/940,316B
; CURRENT FILING DATE: 2001-08-27
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: US 60/139,650
; PRIOR FILING DATE: 1999-06-17
; PRIOR APPLICATION NUMBER: US 60/123,810
; PRIOR FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: US 60/102,748
; PRIOR FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 1557
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic PKS
; OTHER INFORMATION: synthase fragment
US-09-940-316B-27

Query Match      14.2%; Score 75.5; DB 4; Length 1557;
Best Local Similarity 26.3%; Pred. No. 5;
Matches 25; Conservative 12; Mismatches 43; Indels 15; Gaps 3;

Qy 8 HLPITNRPKIAHCILFNQPHS-----PRSNHSHPNPKLHRRSHSHNRPRAYILITILP 62
Db 1271 HLITTNHTLVHTTT-DPPGAAVGTGLRTAQNEHPGRIHLIETHHPHTPLPLTQLTTLHQ 1329

Qy 63 SKLKLRTHS-----QSHHNPLSRSTNSPTN 88
Db 1330 PHLRLTNTLHTPLHTPIITTHNTTTTTPTPPLN 1364

RESULT 13
US-09-940-316B-25
; Sequence 25, Application US/09940316B
; Patent No. 6759536
; GENERAL INFORMATION:
; APPLICANT: KOSAN BIOSCIENCES, Inc.
; APPLICANT: REEVES, CHRISTOPHER
; APPLICANT: CHU, DANIEL
; APPLICANT: KHOSLA, CHAITAN
; APPLICANT: SANTI, DANIEL
; APPLICANT: WU, KAI
; TITLE OF INVENTION: POLYKETIDES ENCODING THE FKBA GENE OF THE FK-520 POLYKETIDE SYNTH
; FILE REFERENCE: 30062-20026.11
; CURRENT APPLICATION NUMBER: US/09/940,316B
; CURRENT FILING DATE: 2001-08-27
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: US 60/139,650
; PRIOR FILING DATE: 1999-06-17
; PRIOR APPLICATION NUMBER: US 60/123,810
; PRIOR FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: US 60/102,748
; PRIOR FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 1574
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic PKS
; OTHER INFORMATION: synthase fragment
US-09-410-551B-25

Query Match      14.2%; Score 75.5; DB 4; Length 1574;
Best Local Similarity 26.3%; Pred. No. 5.1;
Matches 25; Conservative 12; Mismatches 43; Indels 15; Gaps 3;

Qy 8 HLPITNRPKIAHCILFNQPHS-----PRSNHSHPNPKLHRRSHSHNRPRAYILITILP 62
Db 1288 HLITTNHTLVHTTT-DPPGAAVGTGLRTAQNEHPGRIHLIETHHPHTPLPLTQLTTLHQ 1346

Qy 63 SKLKLRTHS-----QSHHNPLSRSTNSPTN 88
Db 1347 PHLRLTNTLHTPLHTPIITTHNTTTTTPTPPLN 1381
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 11, 2005, 06:57:07 ; Search time 11.631 Seconds  
(without alignments)  
620.432 Million cell updates/sec

Title: US-10-092-934-7  
Perfect score: 409  
Sequence: 1 SSSLGPKCWDYRHELLSLA.....CPVKALLTNGHCTWLPAS 75

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	73	17.8	252	2 PC4259	ferritin associate
2	73	17.8	627	4 A40201	artifact-warning s
3	68	16.6	613	4 C40201	artifact-warning s
4	65	15.9	597	4 E40201	artifact-warning s
5	62.5	15.3	191	1 W6WLK1	E6 protein - rhesu
6	62.5	15.3	346	2 T47411	hypothetical prote
7	60.5	14.8	2946	2 T15840	hypothetical prote
8	60	14.7	1808	2 T47792	hypothetical prote
9	59	14.4	569	2 B84470	Mutator-like trans
10	59	14.4	951	2 T00017	gene ADAMTS-1 prot
11	58	14.2	301	4 B40201	artifact-warning s
12	58	14.2	1628	2 T43682	nucleoporin - fiss
13	57	13.9	442	2 T42955	hypothetical prote
14	57	13.9	734	2 T02196	hypothetical prote
15	57	13.9	882	2 T01168	hypothetical prote
16	56.5	13.8	118	2 G90129	hypothetical prote
17	56.5	13.8	139	2 G97240	amino acid transpo
18	56.5	13.8	185	1 J02394	phospholipase A2 i
19	56.5	13.8	355	2 T42397	opsin, green-sensi
20	56.5	13.8	498	1 HJBE11	helicase (EC 3.6.1
21	56.5	13.8	727	2 T41069	hypothetical prote
22	56	13.7	276	2 T49123	hypothetical prote
23	56	13.7	535	2 S48268	probable membrane
24	56	13.7	564	2 T41168	hypothetical prote
25	56	13.7	682	2 T41680	hypothetical prote
26	55.5	13.6	151	2 E43584	15K cysteine-rich
27	55.5	13.6	349	2 B45229	opsin, green-sensi
28	55	13.4	150	2 C71515	probable 15kda cys
29	55	13.4	152	2 F43584	15K cysteine-rich

30 55 13.4 316 2 T21039  
31 55 13.4 354 2 J04152  
32 55 13.4 354 2 S34378  
33 55 13.4 490 2 T46162  
34 55 13.4 521 2 T46250  
35 55 13.4 673 4 F40201  
36 55 13.4 843 2 H82362  
37 54.5 13.3 220 2 T28503  
38 54.5 13.3 220 2 S33080  
39 54.5 13.3 220 2 G72158  
40 54.5 13.3 259 2 T23849  
41 54.5 13.3 428 2 B84964  
42 54.5 13.3 458 2 A29361  
43 54.5 13.3 519 2 AH0064  
44 54.5 13.3 639 2 T31983  
45 54.5 13.3 822 1 TVHUFE

hypothetical prote  
wnt-11 protein pre  
wnt-11 protein - m  
glucosyltransferas  
hypothetical prote  
artifact-warning s  
adenylate cyclase  
hypothetical prote  
G2R protein - vari  
I3R protein - vari  
adenosylmethionine  
adenosylmethionine  
DG17 protein - sli  
thiamin transport  
hypothetical prote  
protein-tyrosine k

ALIGNMENTS

RESULT 1

PC4259  
ferritin associated protein - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 11-Apr-1997 #sequence\_revision 09-May-1997 #text\_change 09-Jul-2004  
C/Accession: PC4259  
R/Kedar, V.; Moss, D.; Halliday, J.; Powell, L.  
Biochem. Biophys. Res. Commun. 228, 683-689, 1996  
A/Title: Molecular cloning of a partial cDNA of a novel gene in iron metabolism.  
A/Reference number: PC4259; MUID:97096315; PMID:8941339  
A/Accession: PC4259  
A/Molecule type: mRNA  
A/Residues: 1-252 <RED>  
A/Cross-references: UNIPROT:P78394; GB:U63542; NID:g1890646; PIDN:AAC51145.1; PID:g18906  
A/Experimental source: T lymphoid cell  
C/Comment: This protein plays roles in normal cellular iron metabolism and in iron overl.

Query Match 17.8%; Score 73; DB 2; Length 252;  
Best Local Similarity 40.4%; Pred. No. 0.21;  
Matches 19; Conservative 2; Mismatches 14; Indels 12; Gaps 2;

Qy 1 SSSLGPKCWDYR-----HELLSLALMINFR-VMACTFKQH 35  
Db 20 SSSLGLPKCWDYRGDPPRPVLEDCSESLEYLSSNNLKEVLACRGLSH 66

RESULT 2

A40201  
artifact-warning sequence (translated ALU class A) - human  
C/Species: Homo sapiens (man)  
C/Date: 31-Mar-1992 #sequence\_revision 11-Aug-1995 #text\_change 19-May-2000  
C/Accession: A40201  
R/Claverie, J.M.  
Personal communication, 1992  
A/Reference number: A40201  
A/Accession: A40201  
A/Molecule type: DNA  
A/Residues: 1-627 <CLA>  
R/Claverie, J.M.  
Genomics 12, 838-841, 1992  
A/Title: Identifying coding exons by similarity search: Alu-derived and other potential  
A/Reference number: A40200; MUID:92241891; PMID:1572661  
A/Contents: annotation  
C/Comment: This "warning" entry is a conceptual translation in all 6 reading frames of o  
in-frame stop codons are shown as 'X'.  
C/Comment: Any significant similarity of a predicted protein sequence to a portion of th

Query Match 17.8%; Score 73; DB 4; Length 627;  
Best Local Similarity 80.0%; Pred. No. 0.5;  
Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;





C;Accession: T43682  
R;Whalen, W.A.; Yoon, J.H.; Shen, R.; Dhar, R.  
Genetics 152, 827-838, 1999  
A;Title: Regulation of mRNA export by nutritional status in fission yeast.  
A;Reference number: 222629; MUID:99318821; PMID:10388805  
A;Accession: T43682  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-1628 <WHA>  
A;Cross-references: EMBL:AF055035; NID:G5478223; PIDN:AAD43830.1; PID:G5478224  
A;Experimental source: strain 972  
C;Genetics:  
A;Gene: nup184  
A;Introns: 6/2

Query Match 14.2%; Score 58; DB 2; Length 1628;  
Best Local Similarity 23.9%; Pred. No. 86;  
Matches 22; Conservative 10; Mismatches 20; Indels 40; Gaps 3;

QY 12 YRHLSLALMINF-----RVMA-----CTFKQHIELROKISI----- 44  
Db 815 YLHPLLSVMDLINLLTYDFTSISSPRAKAKWMLSSFCAMKTLICLRGFLNLKPSELE 874  
QY 45 -----VPRKLCMGVPCVPVKIALL 63  
Db 875 RELFSRSPDLFNCLPRLCCIAPIQLLSALI 906

RESULT 13  
T42955  
hypothetical protein 40 - ateline herpesvirus 3 (strain 73)  
C;Species: ateline herpesvirus 3  
A;Variety: strain 73  
C;Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 09-Jul-2004  
C;Accession: T42955  
R;Albrecht, J.C.; Fleckenstein, B.  
submitted to the EMBL Data Library, August 1998  
A;Description: Primary structure of the herpesvirus ateles genome.  
A;Reference number: 222274  
A;Accession: T42955  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-442 <ALB>  
A;Cross-references: UNIPROT:Q9YTM5; EMBL:AF083424; PIDN:AAC95566.1  
A;Experimental source: strain 73  
C;Superfamily: ateline herpesvirus 3 hypothetical protein 40

Query Match 13.9%; Score 57; DB 2; Length 442;  
Best Local Similarity 28.9%; Pred. No. 34;  
Matches 22; Conservative 6; Mismatches 26; Indels 22; Gaps 3;

QY 3 SLGLPKCWDYRHLLSLALMIN----FRVMACTF---KQHIELROKISIVPRKLCMGVPV 55  
Db 174 SEGLYRCSATREPPLKKTQOINIEDLFKINCFSVVAKHINVRTIPI----- 222  
QY 56 CPVKIALLLINGHCTW 71  
Db 223 -----FHLWVNVCKW 234

RESULT 14  
T02196  
hypothetical protein At2g46910 [imported] - Arabidopsis thaliana  
N;Alternate names: hypothetical protein F14M4.26  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 05-Mar-1999 #sequence\_revision 05-Mar-1999 #text\_change 09-Jul-2004  
C;Accession: T02196; G84908  
R;Rounsley, S.D.; Lin, X.; Kaul, S.; Shea, T.P.; Fujii, C.Y.; Mason, T.M.; Shen, M.; Ron  
submitted to the EMBL Data Library, September 1998  
A;Description: Arabidopsis thaliana chromosome II BAC F14M4 genomic sequence.  
A;Reference number: Z14609  
A;Accession: T02196  
A;Status: translated from GB/EMBL/DBJ

A;Molecule type: DNA  
A;Residues: 1-734 <ROU>  
A;Cross-references: UNIPROT:O80733; EMBL:AC004411; NID:G3522932; PID:G3522947  
A;Experimental source: cultivar Columbia  
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M  
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.  
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.  
Nature 402, 761-768, 1999  
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
A;Reference number: A84420; MUID:20083487; PMID:10617197  
A;Accession: G84908  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-734 <STO>  
A;Cross-references: GB:AE002093; NID:G3522947; PIDN:AAC34229.1; GSPDB:GN00139  
C;Genetics:  
A;Gene: F14M4.26; At2g46910  
A;Map position: 2  
A;Introns: 138/2; 167/3; 214/2; 259/3; 369/2; 406/3; 467/2; 513/3; 535/3; 547/3; 560/1; 5  
C;Superfamily: Arabidopsis thaliana hypothetical protein F14M4.26

Query Match 13.9%; Score 57; DB 2; Length 734;  
Best Local Similarity 27.2%; Pred. No. 55;  
Matches 22; Conservative 18; Mismatches 27; Indels 14; Gaps 5;

QY 4 LGLPKCWDYRHLLSLALMIN--FRVMACTFKQHIELROKISI----VPRKLCMGVPCP 57  
Db 503 LGYKQTWD-RYQNMYSKGVGDRCFRMYDTFKIKVEMRVEKAISTLTVP-KACCYRDTIG 560

QY 58 VKIAL-----LTINGHCTWL 72  
Db 561 LEMSVEVLQDSMELSDCFWL 581

RESULT 15  
T01168  
hypothetical protein F7N22.13 - Arabidopsis thaliana  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 12-Feb-1999 #sequence\_revision 12-Feb-1999 #text\_change 09-Jul-2004  
C;Accession: T01168  
R;Dante, M.  
submitted to the EMBL Data Library, April 1998  
A;Description: The sequence of A. thaliana F7N22.  
A;Reference number: Z14250  
A;Accession: T01168  
A;Status: translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-882 <DAN>  
A;Cross-references: UNIPROT:O65231; EMBL:AF058825; NID:G3047060; PID:G3047071  
A;Experimental source: cultivar Columbia  
C;Genetics:  
A;Map position: 4  
A;Introns: 60/1; 230/1; 852/3  
A;Note: F7N22.13  
C;Superfamily: Arabidopsis thaliana hypothetical protein F26C24.7

Query Match 13.9%; Score 57; DB 2; Length 882;  
Best Local Similarity 23.5%; Pred. No. 65;  
Matches 16; Conservative 11; Mismatches 23; Indels 18; Gaps 3;

QY 22 MINFRV-----MACTFKQHIELROKISIVPRKLC-C--MGVPCVPVKIALL 63  
Db 289 LLNFRADTQAEISTTCETLFGVSGFKRKVLQOTMSLQPIKQCFCKQPKSCPCTLKMV 348  
QY 64 TTINGHCTW 71  
Db 349 CVDETCPW 356

Search completed: October 11, 2005, 07:01:39  
Job time : 12.631 secs



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RC TISSUE=Cerebellum;
RA Nishi T., Nakagawa S., Senoh A., Mizuguchi H., Inagaki H., Suzuki Y.,
RA Hata H., Nakagawa K., Mizuno S., Morinaga M., Kawamura M.,
RA Sugiyama T., Irie R., Otsuki T., Sato H., Nishikawa T., Sugiyama A.,
RA Kawakami B., Nagai K., Isogai T., Sugano S.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK057815; BAB71388.1; -.
SQ SEQUENCE 160 AA; 18242 MW; 702C9970AA279A11 CRC64;

Query Match      21.3%; Score 87; DB 2; Length 160;
Best Local Similarity 50.0%; Pred. No. 0.0081;
Matches 15; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 1 SSSGLGPKCDYRHEHLLSLALMINFRVMAC 30
   | : |||||:||||| :||| : :|||
Db 3 SPHYLPKCNWRHEPLCLAVCFHFQLSLC 32

RESULT 3
Q9PLI7 PRELIMINARY; PRT; 477 AA.
ID O9P1V7
AC O9P1V7
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE KIAA1541 protein (Fragment).
GN Name=KIAA1541;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=20277482; PubMed=10819331;
RA Nagase T., Kikuno R., Ishikawa K., Hirose M., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. XVII.
RT The complete sequences of 100 new cDNA clones from brain which code
RT for large proteins in vitro.";
RL DNA Res. 7:143-150(2000).
CC -1- SIMILARITY: Contains 5 WD repeats.
DR EMBL; AB040974; BAA96065.1; -.
DR Genbank; HGNC:23732; PP2R2D.
DR GO; GO:000159; C:protein phosphatase type 2A complex; IEA.
DR GO; GO:0008601; F:protein phosphatase type 2A regulator activity; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR000009; Pp2A_PR55.
DR InterPro; IPR001680; WD40.
DR InterPro; IPR011046; WD40_like.
DR Pfam; PF00400; WD40; 5.
DR PRINTS; PR00600; PP2APR55.
DR SMART; SM00320; WD40; 7.
DR PROSITE; PS01024; PR55_1; 1.
DR PROSITE; PS01025; PR55_2; 1.
KW Repeat; WD repeat.
FT NON TER
FT NON TER
SQ SEQUENCE 477 AA; 55544 MW; B20AB833C65DFC9 CRC64;

Query Match      21.0%; Score 86; DB 2; Length 477;
Best Local Similarity 29.08%; Pred. No. 0.033;
Matches 20; Conservative 13; Mismatches 24; Indels 12; Gaps 2;

QY 1 SSSGLGPKCDYRHEHLLSLALMINFRVMACFKQHIEL-----RQKISIVPRKLCMGVPV 55
   ||| |||||:|:|:| :||| : :|||
Db 1 SSHLGLPKCWYKHEPHWVAATCLFSLRVYNWRSYRELGPLLSHTRAHLTPGH-----53

QY 56 CPVKIALLT 64
   ||:|:|:|
Db 54 CPLKSDIIS 62

RESULT 4
Q6ZVL2 PRELIMINARY; PRT; 138 AA.
ID Q6ZVL2

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AC Q6ZVL2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein FLJ42427.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Bladder;
RA Tanigami A., Fujiwara T., Shibahara T., Goto Y., Hirao M., Shimizu F.,
RA Wakebe H., Ono T., Hishigaki H., Watanabe T., Ozaki K., Sugiyama T.,
RA Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J.,
RA Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K.,
RA Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,
RA Wagatsuma M., Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A.,
RA Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahari K.,
RA Masuho Y., Nagai K., Isogai T.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK124418; BAC85849.1; -.
DR InterPro; IPR006209; EGF_like.
DR PROSITE; PS00022; EGF_1; UNKNOWN 1.
SQ SEQUENCE 138 AA; 15713 MW; C3A176B6CBACB51B CRC64;

Query Match      19.7%; Score 80.5; DB 2; Length 138;
Best Local Similarity 41.7%; Pred. No. 0.046;
Matches 25; Conservative 6; Mismatches 24; Indels 5; Gaps 3;

QY 2 SSSGLGPKCDYRHE--LLSLALMINFRVMACTFK--QHIELRQKISIVPRKLCMGVPVCP 57
   ||||| ||||| :||| : :|||
Db 43 SCGLGPKHWDYRHEPLPGCLMFLTGLLNSFNLSLPLAPVSLPRELLC-PPLFP 101

RESULT 5
Q6ZSB5 PRELIMINARY; PRT; 143 AA.
ID Q6ZSB5
AC Q6ZSB5;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein FLJ45662.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Tongue;
RA Tashiro H., Yamazaki M., Watanabe K., Kumagai A., Itakura S.,
RA Fukuzumi Y., Fujimori Y., Komiyama M., Sugiyama T., Irie R.,
RA Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M.,
RA Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A.,
RA Kawakami B., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K.,
RA Isogai T.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK127569; BAC87039.1; -.
SQ SEQUENCE 143 AA; 15821 MW; BE877B3E7AD73D52 CRC64;

Query Match      19.7%; Score 80.5; DB 2; Length 143;
Best Local Similarity 34.2%; Pred. No. 0.048;
Matches 26; Conservative 6; Mismatches 21; Indels 23; Gaps 4;

QY 1 SSSGLGPKCDYRHEHLLSLALMINFRVMACFKQHIELRQKISIVPRKLCMGVPVVKI 60
   ||| :|:|:|:|:| :||| : :|||
Db 55 SSHLSFPGWYRHPHTHPVNVNF-----FLRQSLTSPR-LECSG-----95

QY 61 ALLTINGHCTW-LPAS 75
   ||:|:|:|
Db 96 ---TISAHCKRLPGS 108

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RESULT 6
Q6ZN97 Q6ZN97 PRELIMINARY; PRT; 134 AA.
AC Q6ZN97; 2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein FJ16303.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP TISSUE=Prostate;
RC TISSUE=Testis;
RA Tanai H., Watanabe S., Ishida S., Ono Y., Hotuta T., Watanabe M.,
RA Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S.,
RA Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T.,
RA Kimura K., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,
RA Wagatsuma M., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B.,
RA Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK131315; BAD18478.1; -.
SQ SEQUENCE 134 AA; 15299 MW; A49A2899FB14AE2F CRC64;

Query Match 19.3%; Score 79; DB 2; Length 134;
Best Local Similarity 51.7%; Pred. No. 0.069;
Matches 15; Conservative 6; Mismatches 6; Indels 2; Gaps 1;

Oy 4 LGLPKCDWYRHEHLSLA--LMINFRVNVAC 30
Db 100 LGLPKCDWYRCEPLHQLTQFVILNLLSC 128

RESULT 7
Q8NED3 Q8NED3 PRELIMINARY; PRT; 94 AA.
AC Q8NED3; 2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP TISSUE=Testis;
RC TISSUE=Testis;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Schenker C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
```

```

RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
KW EMBL; BC032019; AAH32019.1; -.
KW Hypothetical protein.
SQ SEQUENCE 94 AA; 11243 MW; DC87F1464046578C CRC64;

Query Match 19.1%; Score 78; DB 2; Length 94;
Best Local Similarity 66.7%; Pred. No. 0.064;
Matches 14; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Oy 1 SSSIGLPKCDWYRHEHLSLA 21
Db 74 SACLGFPCWDYRSEPLRLAI 94

RESULT 8
ALU7_HUMAN
ID ALU7_HUMAN STANDARD; PRT; 593 AA.
AC P39194;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Alu subfamily SQ sequence contamination warning entry.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95021756; PubMed=7935834; DOI=10.1038/371752a0;
RA Claverie J.-M., Makalowski W.;
RT "Alu alert.";
RL Nature 371:752-752(1994).
RN [2]
RP CONCEPT.
RX MEDLINE=92241891; PubMed=1572661;
RA Claverie J.-M.;
RT "Identifying coding exons by similarity search: alu-derived and other
RT potentially misleading protein sequences.";
RL Genomics 12:838-841(1992).
RN [3]
RP ALU FAMILIES CLASSIFICATION.
RX MEDLINE=88333009; PubMed=3138422;
RA Quentin Y.;
RT "The Alu family developed through successive waves of fixation closely
RT connected with primate lineage history.";
RL J. Mol. Evol. 27:194-202(1988).
RN [4]
RP ALU FAMILIES CLASSIFICATION.
RX MEDLINE=91178815; PubMed=1706781;
RA Jurka J., Milosavljevic A.;
RT "Reconstruction and analysis of human Alu genes.";
RL J. Mol. Evol. 32:105-121(1991).
CC -1- MISCELLANEOUS: Various analyses indicate that Alu repeats fall
CC into 8 subfamilies (Ref.3 and Ref.4). Therefore, 8 Alu warning
CC consensus sequences have been constituted that contain all six
CC frames conceptual translations of each of these classes of Alu
CC repeats.
CC -1- MISCELLANEOUS: Isolated 'X' indicates the presence of a stop
CC codon, 'XXX' is used to separate the various translation phases.
CC -1- CAUTION: This Alu entry is provided in order to avoid the further
CC pollution of protein sequence databases with Alu-derived amino
CC acid sequences.
CC -1- CAUTION: Alu repetitive sequences are interspersed in human and
CC primate genomes with an average spacing of 4 kb. Some of them are
CC actively transcribed by pol III. Normal transcripts may contain
CC Alu-derived sequences in 5' or 3' untranslated regions. However,
CC cDNA libraries also contain partial and/or rearranged cDNAs
CC ligated with Alu-derived sequence in any orientation. Although Alu
CC elements (especially situated on the complementary strand) have a
```







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RL Nature 371:752-752(1994).
RN [2]
RP CONCEPT.
RX MEDLINE=92241891; PubMed=1572661;
RA Claverie J.-M.;
RT "Identifying coding exons by similarity search: alu-derived and other
RT potentially misleading protein sequences.";
RL Genomics 12:838-841(1992).
RN [3]
RP ALU FAMILIES CLASSIFICATION.
RX MEDLINE=88333009; PubMed=3138422;
RA Quentin Y.;
RT "The Alu family developed through successive waves of fixation closely
RT connected with primate lineage history.";
RL J. Mol. Evol. 27:194-202(1988).
RN [4]
RP ALU FAMILIES CLASSIFICATION.
RX MEDLINE=91178815; PubMed=1706781;
RA Jurka J., Milosavljevic A.;
RT "Reconstruction and analysis of human Alu genes.";
RL J. Mol. Evol. 32:105-121(1991).
CC -!- MISCELLANEOUS: Various analyses indicate that Alu repeats fall
CC into 8 subfamilies (Ref.3 and Ref.4). Therefore, 8 Alu warning
CC consensus sequences have been constituted that contain all six
CC frames conceptual translations of each of these classes of Alu
CC repeats.
CC -!- MISCELLANEOUS: Isolated 'X' indicates the presence of a stop
CC codon, 'XXX' is used to separate the various translation phases.
CC -!- CAUTION: This Alu entry is provided in order to avoid the further
CC pollution of protein sequence databases with Alu-derived amino
CC acid sequences.
CC -!- CAUTION: Alu repetitive sequences are interspersed in human and
CC primate genomes with an average spacing of 4 kb. Some of them are
CC actively transcribed by pol III. Normal transcripts may contain
CC Alu-derived sequences in 5' or 3' untranslated regions. However,
CC cDNA libraries also contain partial and/or rearranged cDNAs
CC ligated with Alu-derived sequence in any orientation. Although Alu
CC elements (especially situated on the complementary strand) have a
CC great potential to create additional/alternative exons,
CC consideration should be given to the possibility that the presence
CC of an Alu in an open reading frame may have resulted from a
CC cloning artifact or may be due to misinterpretation of sequencing
CC data. This point has been overlooked on several occasions, with
CC the consequence of erroneous Alu-derived amino acid sequences
CC being reported.
CC -!- CAUTION: Any significant similarity of a putative protein sequence
CC with an Alu-translated entry must be taken as a warning that a
CC part of Alu repeat may have been artifactually included in the
CC coding nucleotide sequence.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U14571; -; NOT_ANNOTATED_CDS.
KW Hypothetical protein.
FT DOMAIN 1 95 Frame-1.
FT DOMAIN 99 193 Frame-2.
FT DOMAIN 197 291 Frame-3.
FT DOMAIN 295 389 Frame-4.
FT DOMAIN 393 487 Frame-5.
FT DOMAIN 491 585 Frame-6.
SQ SEQUENCE 585 AA; 63957 MW; 46EB8C4F493650A7 CRC64;
Query Match 17.8%; Score 73; DB 1; Length 585;
Best Local Similarity 80.0%; Pred. No. 1.8;
Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 SSSLGLPKCWDYRHE 15

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Db 566 SARLGLPKCWDYRRE 580
|: ||||| |
ALU2_HUMAN STANDARD; PRT; 587 AA.
ID ALU2_HUMAN
AC P39189;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Alu subfamily SB sequence contamination warning entry.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95021758; PubMed=7935834; DOI=10.1038/371752a0;
RA Claverie J.-M., Makalowski W.;
RT "Alu alert.";
RL Nature 371:752-752(1994).
RN [2]
RP CONCEPT.
RX MEDLINE=92241891; PubMed=1572661;
RA Claverie J.-M.;
RT "Identifying coding exons by similarity search: alu-derived and other
RT potentially misleading protein sequences.";
RL Genomics 12:838-841(1992).
RN [3]
RP ALU FAMILIES CLASSIFICATION.
RX MEDLINE=88333009; PubMed=3138422;
RA Quentin Y.;
RT "The Alu family developed through successive waves of fixation closely
RT connected with primate lineage history.";
RL J. Mol. Evol. 27:194-202(1988).
RN [4]
RP ALU FAMILIES CLASSIFICATION.
RX MEDLINE=91178815; PubMed=1706781;
RA Jurka J., Milosavljevic A.;
RT "Reconstruction and analysis of human Alu genes.";
RL J. Mol. Evol. 32:105-121(1991).
CC -!- MISCELLANEOUS: Various analyses indicate that Alu repeats fall
CC into 8 subfamilies (Ref.3 and Ref.4). Therefore, 8 Alu warning
CC consensus sequences have been constituted that contain all six
CC frames conceptual translations of each of these classes of Alu
CC repeats.
CC -!- MISCELLANEOUS: Isolated 'X' indicates the presence of a stop
CC codon, 'XXX' is used to separate the various translation phases.
CC -!- CAUTION: This Alu entry is provided in order to avoid the further
CC pollution of protein sequence databases with Alu-derived amino
CC acid sequences.
CC -!- CAUTION: Alu repetitive sequences are interspersed in human and
CC primate genomes with an average spacing of 4 kb. Some of them are
CC actively transcribed by pol III. Normal transcripts may contain
CC Alu-derived sequences in 5' or 3' untranslated regions. However,
CC cDNA libraries also contain partial and/or rearranged cDNAs
CC ligated with Alu-derived sequence in any orientation. Although Alu
CC elements (especially situated on the complementary strand) have a
CC great potential to create additional/alternative exons,
CC consideration should be given to the possibility that the presence
CC of an Alu in an open reading frame may have resulted from a
CC cloning artifact or may be due to misinterpretation of sequencing
CC data. This point has been overlooked on several occasions, with
CC the consequence of erroneous Alu-derived amino acid sequences
CC being reported.
CC -!- CAUTION: Any significant similarity of a putative protein sequence
CC with an Alu-translated entry must be taken as a warning that a
CC part of Alu repeat may have been artifactually included in the
CC coding nucleotide sequence.
CC -----
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC -----  
 CC EMBL; U14568; -; NOT\_ANNOTATED\_CDS.

CC Hypothetical protein\_96  
 CC FT DOMAIN 1 96 Frame-1.  
 CC FT DOMAIN 100 194 Frame-2.  
 CC FT DOMAIN 198 292 Frame-3.  
 CC FT DOMAIN 296 391 Frame-4.  
 CC FT DOMAIN 395 489 Frame-5.  
 CC FT DOMAIN 493 587 Frame-6.  
 CC SQ SEQUENCE 587 AA; 63703 MW; 3FAAB3E3E3929203 CRC64;

Query Match 17.8%; Score 73; DB 1; Length 587;  
 Best Local Similarity 80.0%; Pred. No. 1.8;  
 Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 SSSLGPKCWDYRHE 15  
 Db 372 SARGLPKCWDYRRE 386

# RESULT 15

ALU3\_HUMAN STANDARD; PRT; 587 AA.  
 AC P39190;  
 DT 01-FEB-1995 (Rel. 31, Created)  
 DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Alu subfamily SBI sequence contamination warning entry.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=95021759; PubMed=7935834; DOI=10.1038/371752a0;  
 RA Claverie J.-M., Makalowski W.;  
 RT "Alu alert."  
 RL Nature 371:752-752 (1994).  
 RN [2]  
 RP CONCEPT.  
 RX MEDLINE=92241891; PubMed=1572661;  
 RA Claverie J.-M.;  
 RT "Identifying coding exons by similarity search: alu-derived and other  
 RT potentially misleading protein sequences."  
 RL Genomics 12:838-841 (1992).  
 RN [3]  
 RP ALU FAMILIES CLASSIFICATION.  
 RX MEDLINE=88333009; PubMed=3138422;  
 RA Quentin Y.;  
 RT "The Alu family developed through successive waves of fixation closely  
 RT connected with primate lineage history."  
 RL J. Mol. Evol. 27:194-202 (1988).  
 RN [4]  
 RP ALU FAMILIES CLASSIFICATION.  
 RX MEDLINE=9117815; PubMed=1706781;  
 RA Jurka J., Milosavljevic A.;  
 RT "Reconstruction and analysis of human Alu genes."  
 RL J. Mol. Evol. 32:105-121 (1991).  
 CC -1- MISCELLANEOUS: Various analyses indicate that Alu repeats fall  
 CC into 8 subfamilies (Ref. 3 and Ref. 4). Therefore, 8 Alu warning  
 CC consensus sequences have been constituted that contain all six  
 CC frames conceptual translations of each of these classes of Alu  
 CC repeats.  
 CC -1- MISCELLANEOUS: Isolated 'x' indicates the presence of a stop  
 CC codon, 'xxx' is used to separate the various translation phases.  
 CC -1- CAUTION: This Alu entry is provided in order to avoid the further  
 CC pollution of protein sequence databases with Alu-derived amino  
 CC acid sequences.

CC -1- CAUTION: Alu repetitive sequences are interspersed in human and  
 CC primate genomes with an average spacing of 4 kb. Some of them are  
 CC actively transcribed by pol III. Normal transcripts may contain  
 CC Alu-derived sequences in 5' or 3' untranslated regions. However,  
 CC cDNA libraries also contain partial and/or rearranged cDNAs  
 CC ligated with Alu-derived sequence in any orientation. Although Alu  
 CC elements (especially situated on the complementary strand) have a  
 CC great potential to create additional/alternative exons,  
 CC consideration should be given to the possibility that the presence  
 CC of an Alu in an open reading frame may have resulted from a  
 CC cloning artifact or may be due to misinterpretation of sequencing  
 CC data. This point has been overlooked on several occasions, with  
 CC the consequence of erroneous Alu-derived amino acid sequences  
 CC being reported.  
 CC -1- CAUTION: Any significant similarity of a putative protein sequence  
 CC with an Alu-translated entry must be taken as a warning that a  
 CC part of Alu repeat may have been artifactually included in the  
 CC coding nucleotide sequence.

CC -----  
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 CC entities requires a license agreement (See <http://www.isb-sib.ch/announcement/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC EMBL; U14569; -; NOT\_ANNOTATED\_CDS.

CC Hypothetical protein.  
 CC KW DOMAIN 1 96 Frame-1.  
 CC FT DOMAIN 100 194 Frame-2.  
 CC FT DOMAIN 198 292 Frame-3.  
 CC FT DOMAIN 296 391 Frame-4.  
 CC FT DOMAIN 395 489 Frame-5.  
 CC FT DOMAIN 493 587 Frame-6.  
 CC SQ SEQUENCE 587 AA; 63573 MW; 85C4155726DEF235 CRC64;

Query Match 17.8%; Score 73; DB 1; Length 587;

Best Local Similarity 80.0%; Pred. No. 1.8;  
 Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 SSSLGPKCWDYRHE 15  
 Db 372 SARGLPKCWDYRRE 386

Search completed: October 11, 2005, 07:18:51  
 Job time : 47.0201 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 11, 2005, 06:57:07 ; Search time 55.5481 Seconds  
(without alignments)  
522.196 Million cell updates/sec

Title: US-10-092-934-7

Perfect score: 409

Sequence: 1 SSSLSGLPKWCWYRHELLSLA.....CPVKIALLTINGHCTWLPAS 75

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*  
1: Geneseqp1980s:\*  
2: Geneseqp1990s:\*  
3: Geneseqp2000s:\*  
4: Geneseqp2001s:\*  
5: Geneseqp2002s:\*  
6: Geneseqp2003as:\*  
7: Geneseqp2003bs:\*  
8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	409	100.0	75	2	AAR63238 Neural th
2	409	100.0	75	2	AAR95917 AD 16C-T7
3	409	100.0	75	5	AAR29148 Neural th
4	409	100.0	75	6	ABR63246 75 amino
5	409	100.0	75	6	ABU02978 Human neu
6	409	100.0	75	6	ABP59928 Human 75
7	409	100.0	75	6	AAE33195 Neural th
8	409	100.0	75	6	ABJ19451 75-mer ne
9	409	100.0	75	7	ADB37525 Neural th
10	409	100.0	75	7	ADL96026 Human neu
11	98	24.0	59	4	AAO02982 Human pol
12	98	24.0	109	4	AAO06037 Human pol
13	97	23.7	138	4	AAU31559 Novel hum
14	93	22.7	64	4	AAO03740 Human pol
15	92	22.5	62	4	AAO00751 Human pol
16	92	22.5	86	4	AAU22283 Human car
17	92	22.5	86	7	ADE46251 Human car
18	92	22.5	86	8	ADJ07669 Human car
19	91	22.2	74	4	AAAM86645 Human imm
20	91	22.2	77	4	AAO07835 Human pol
21	91	22.2	104	4	AAO04575 Human pol
22	90	22.0	15	6	ABP59914 Human neu
23	90	22.0	15	7	ADL96060 Human neu
24	90	22.0	37	4	AAO09372 Human pol
25	89.5	21.9	112	4	AAO04265 Human pol

26	89	21.8	15	6	ABP59911	Human neu
27	89	21.8	15	7	ADL96057	Human neu
28	89	21.8	47	3	AAAB25722	Human sec
29	89	21.8	202	8	ADRO9020	Human pro
30	88.5	21.6	47	4	AAU20869	Human nov
31	88	21.5	107	4	AAO04057	Human pol
32	87	21.3	44	4	AAAM82609	Human imm
33	87	21.3	45	4	AAO04635	Human pol
34	87	21.3	70	4	AAO02710	Human pol
35	86.5	21.1	104	4	ABG07702	Novel hum
36	86	21.0	72	2	AAO02926	Fragment
37	86	21.0	72	7	ADA07757	Human sec
38	86	21.0	72	8	ADN41484	Novel hum
39	86	21.0	87	5	ADK34159	Novel hum
40	85.5	20.9	109	4	AAO02394	Human pol
41	85	20.8	15	6	ABP59915	Human neu
42	85	20.8	15	7	ADL96061	Human neu
43	85	20.8	58	4	AAO03818	Human pol
44	85	20.8	82	4	AAAG73475	Human gen
45	85	20.8	104	4	AAAM89847	Human imm

ALIGNMENTS

RESULT 1  
AAR63238  
ID AAR63238 standard; protein; 75 AA.  
XX  
AC AAR63238;  
XX  
DT 25-MAR-2003 (revised)  
DT 06-JUL-1995 (first entry)  
XX  
DE Neural thread protein AD16C T7.  
XX  
KW Neural thread protein AD16C T7; Alzheimer's; neuroectodermal tumours;  
KW malignant astrocytomas; glioblastomas.  
XX  
OS Rattus rattus.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 1..75  
FT /note= "corresponding codons 1..184, AAQ77882"  
XX  
PN WO9423756-A1.  
XX  
PD 27-OCT-1994.  
XX  
PF 20-APR-1994; 94WO-US004321.  
XX  
PR 20-APR-1993; 93US-00050559.  
XX  
PA (GEO ) GEN HOSPITAL CORP.  
XX  
PI De La Monte SM, Wands JR;  
XX  
DR WPI; 1994-341497/42.  
DR N-PSDB; AAQ77882.  
XX  
PS Detection of neural thread proteins - to detect sporadic and familial  
PT Alzheimer's disease, neuroectodermal tumours, malignant astrocytomas and  
PT glioblastomas (Eng).  
XX  
PS Example 4; Fig 160; 158pp; English.  
XX  
CC AAQ77882 encodes AAR63237 the AD16C T7 neural thread protein (NTP). These  
CC sequences were used in the development of an antibody dependent method,  
CC for the detection of NTPs. This new method could be used to diagnose  
CC Alzheimer's disease (differentiating between sporadic and familial),  
CC neuroectodermal tumours, malignant astrocytomas and glioblastomas.  
CC (Updated on 25-MAR-2003 to correct PN field.)  
XX

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SQ Sequence 75 AA;
Query Match 100.0%; Score 409; DB 2; Length 75;
Best Local Similarity 100.0%; Pred. No. 9e-44;
Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSSGLPKCWDYRHELLSLALMINFRVMACTFKHIELRQKISIVPRKLCMGFVCPVKI 60
Db 1 SSSGLPKCWDYRHELLSLALMINFRVMACTFKHIELRQKISIVPRKLCMGFVCPVKI 60

QY 61 ALLTINGHCTWLPAS 75
Db 61 ALLTINGHCTWLPAS 75

RESULT 2
AAR95917
ID AAR95917 standard; protein; 75 AA.
XX
AC AAR95917;
XX
DT 14-NOV-1996 (first entry)
XX
DE AD 16c-T7 human neural thread protein clone (partial sequence).
XX
KW Neural thread protein; NTP; diagnosis; detection; Alzheimer's disease;
KW neuroectodermal tumour; malignant astrocytoma; monoclonal antibody;
KW binding fragment.
XX
OS Homo sapiens.
XX
PN WO9615272-A1.
XX
PD 23-MAY-1996.
XX
PF 14-NOV-1995; 95WO-US017111.
XX
PR 14-NOV-1994; 94US-00340426.
XX
PA (GEO ) GEN HOSPITAL CORP.
XX
PI De La Monte S, Wands JR;
XX
DR WPI; 1996-259865/26.
XX
PT Detection of neural thread protein in diagnosis of Alzheimer's disease -
PT also NTP DNA and protein sequences used in gene and anti-sense therapy.
PS Example 4c; Fig 160; 238pp; English.
XX
CC A method for detecting the presence of neural thread protein (NTP) having
CC a molecular weight of 8, 14, 17, 21, 26 or 42 kD in a human subject
CC comprises (a) contacting a sample from a human subject that is suspected
CC of containing the NTP with at least one molecule capable of binding to
CC the protein; and (b) detecting any of the molecule bound to the protein.
CC The binding molecule is selected from an antibody free of natural
CC impurities, a monoclonal antibody or a binding fragment of either of
CC these. The method may be used for diagnosing the presence of Alzheimer's
CC disease, neuroectodermal tumours and a malignant astrocytoma in a human.
CC A number of clones of neural thread protein were isolated from healthy 17
CC -18 week old foetal human brain (HB) 2 year old temporal lobe neocortex
CC and end stage Alzheimer's disease (AD) cerebral cortex. See AAT27753-75
XX
SQ Sequence 75 AA;
Query Match 100.0%; Score 409; DB 2; Length 75;
Best Local Similarity 100.0%; Pred. No. 9e-44;
Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSSGLPKCWDYRHELLSLALMINFRVMACTFKHIELRQKISIVPRKLCMGFVCPVKI 60
Db 1 SSSGLPKCWDYRHELLSLALMINFRVMACTFKHIELRQKISIVPRKLCMGFVCPVKI 60
```

```
QY 61 ALLTINGHCTWLPAS 75
Db 61 ALLTINGHCTWLPAS 75

RESULT 3
AAE29148
ID AAE29148 standard; protein; 75 AA.
XX
AC AAE29148;
XX
DT 27-JAN-2003 (first entry)
XX
DE Neural thread protein (NTP) #6.
XX
KW Neural thread protein; NTP; hyperplasia; hypertrophy; arteriosclerosis;
KW haemorrhoid; gene therapy; tumour; vascular disease; atherosclerosis;
KW inflammatory disease; nutritional deficiency disease; genetic disease;
KW autoimmune disease; metabolic disease; traumatic disease; intoxication;
KW infectious disease; congenital malformation; enzyme deficiency disease;
KW amyloid disease; fibrosis disease; storage disease; radiation disease;
KW poisoning; environmental disease; endocrine disease; protein therapy;
KW degenerative disease; mechanical disease.
XX
OS Unidentified.
XX
PN WO200274323-A2.
XX
PD 26-SEP-2002.
XX
PF 08-MAR-2002; 2002WO-IB001959.
XX
PR 08-MAR-2001; 2001US-0273957P.
XX
PA (AVER/) AVERBACK P.
XX
PI Avertack P;
XX
DR WPI; 2002-759864/82.
XX
PT Treating a condition in a patient requiring removal or destruction of
PT cells, such as a benign or malignant tumor of a tissue or an inflammatory
PT disease, comprises administering a neural thread protein (NTP) or a NTP
PT gene to a mammal.
XX
PS Claim 23; Fig 7; 70pp; English.
XX
CC The invention relates to a method for treating a condition in a patient
CC requiring removal or destruction of cells. The method involves
CC administering to a mammal a neural thread protein (NTP), or administering
CC to a tumour or other target cell a NTP gene, where the expression of the
CC NTP gene is induced resulting in expression of the NTP protein. The
CC method and NTP are useful for treating a condition in a patient requiring
CC removal or destruction of cells, such as a benign or malignant tumour of
CC a tissue, a hyperplasia, hypertrophy, or overgrowth of a tissue,
CC preferably tonsillar hypertrophy or prostatic hyperplasia, a virally,
CC bacterially, or parasitically altered tissue, or a malformation of a
CC tissue. Other conditions include a cosmetic modification to a tissue,
CC such as removal of unwanted facial hair, warts or unwanted fatty tissue,
CC a vascular disease, particularly atherosclerosis or arteriosclerosis,
CC haemorrhoids, or varicose veins, an inflammatory disease, autoimmune
CC disease, metabolic disease, hereditary/genetic disease, traumatic disease
CC or physical injury, nutritional deficiency disease, infectious disease,
CC congenital malformation, amyloid disease, fibrosis disease, storage
CC disease, enzyme deficiency disease, poisoning, intoxication, degenerative
CC disease, radiation disease, environmental disease, endocrine disease or
CC mechanical disease. The invention is useful in protein therapy and gene
CC therapy. The present sequence is NTP protein
XX
SQ Sequence 75 AA;
Query Match 100.0%; Score 409; DB 5; Length 75;
Best Local Similarity 100.0%; Pred. No. 9e-44;
```

Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSSGLPKCWDYRHELLSLALMINFRVWACTFKQHIELRQKISIVPRKLCMGVPCVKI 60  
DB 1 SSSGLPKCWDYRHELLSLALMINFRVWACTFKQHIELRQKISIVPRKLCMGVPCVKI 60

QY 61 ALLTINGHCTWLPAS 75  
DB 61 ALLTINGHCTWLPAS 75

RESULT 4  
ABR63246  
ID ABR63246 standard; protein; 75 AA.  
XX ABR63246;  
AC  
XX  
DT 28-AUG-2003 (first entry)  
XX  
DE 75 amino acid neural thread protein.  
XX  
KW Cytostatic; Antibacterial; Immunosuppressive; Antiinflammatory;  
KW neural thread protein; NTP; tumour.  
XX  
OS Unidentified.  
XX  
PN WO2003008443-A2.  
XX  
XX 30-JAN-2003.  
XX  
XX 19-JUL-2002; 2002WO-CA001105.  
XX  
PR 19-JUL-2001; 2001US-0306150P.  
PR 19-JUL-2001; 2001US-0306161P.  
PR 16-NOV-2001; 2001US-0331477P.  
XX  
PA (NYMO-) NYMOX CORP.  
XX  
PI Averbach PA;  
XX  
XX WPI; 2003-247999/24.  
XX  
PT Novel neural thread protein peptide, referred as cell death peptide,  
PT useful for treating prostatic hyperplasia, psoriasis, eczema, dermatosis,  
PT atherosclerosis, cosmetic modification to skin, throat, mouth, muscle.  
XX  
PS Disclosure; Fig 7; 77pp; English.  
XX  
XX The present invention relates to a neural thread protein (NTP) peptide  
XX referred to as cell death peptide. Thought to be cytostatic,  
XX antibacterial, immunosuppressive and antiinflammatory. It is useful for  
XX treating a condition in a patient requiring removal or destruction of  
XX cells, for treating a condition such as benign or malignant tumor.  
XX inflammatory disease, autoimmune disease and infectious disease. The  
XX peptide useful for treatment is derived from the amino acid sequence for  
XX a pancreatic thread protein. The peptide is conjugated, linked or bound  
XX to a molecule chosen from antibody or its fragment, antibody-like binding  
XX molecule, where the molecule has a higher affinity for binding to a tumor  
XX or other target than binding to other cells. Treatment using NTP peptides  
XX can remove benign tumors with less risk and fewer of the undesirable side  
XX effects of surgery. The present sequence is an NTP amino acid sequence  
XX  
SQ Sequence 75 AA;  
Query Match 100.0%; Score 409; DB 6; Length 75;  
Best Local Similarity 100.0%; Pred. No. 9e-44;  
Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSSGLPKCWDYRHELLSLALMINFRVWACTFKQHIELRQKISIVPRKLCMGVPCVKI 60  
DB 1 SSSGLPKCWDYRHELLSLALMINFRVWACTFKQHIELRQKISIVPRKLCMGVPCVKI 60

QY 61 ALLTINGHCTWLPAS 75

DB 61 ALLTINGHCTWLPAS 75

RESULT 5  
ABU02978  
ID ABU02978 standard; protein; 75 AA.  
XX  
XX ABU02978;  
AC  
XX  
DT 20-JAN-2003 (first entry)  
XX  
DE Human neural thread protein AD7C-NTP, protein fragment #6.  
XX  
KW Neural thread protein; NTP-peptide; AD7C-NTP; surgical excision;  
KW transplantation; grafting; chemotherapy; immunotherapy; vaccination;  
KW ablation; cryotherapy; laser therapy; phototherapy; gene therapy;  
KW radiation; tumour; hyperplasia; hypertrophy; overgrowth of tissue;  
KW malformation of tissue; tonsillary hypertrophy; prostatic hyperplasia;  
KW cosmetic modification; vascular disease; atherosclerosis;  
KW arteriosclerosis; haemorrhoid; varicose vein; inflammatory disease;  
KW autoimmune disease; metabolic disease; traumatic disease;  
KW physical injury; nutritional deficiency disease; infectious disease;  
KW amyloid disease; fibrosis disease; storage disease;  
KW congenital malformation; enzyme deficiency disease; poisoning;  
KW intoxication; environmental disease; radiation disease;  
KW endocrine disease; degenerative disease; mechanical disease.  
XX  
OS Homo sapiens.  
XX  
XX WO200297030-A2.  
XX  
XX 05-DEC-2002.  
XX  
XX 24-MAY-2002; 2002WO-CA000759.  
XX  
XX 25-MAY-2001; 2001US-0293156P.  
XX  
XX (NYMO-) NYMOX CORP.  
XX  
XX Averbach PA;  
XX  
XX WPI; 2003-041406/03.  
XX  
XX Novel peptides similar in amino acid sequence to neural thread proteins  
XX (NTP), useful for treating unwanted cellular proliferations such as  
XX malignant tumors and prostatic hyperplasia.  
XX  
XX Disclosure; Fig 7; 78pp; English.  
XX  
XX The invention describes an NTP-peptide (I) comprising at least one amino  
XX acid sequence corresponding to part of the amino acid sequence of a  
XX neural thread protein, AD7C-NTP. The invention provides a method of  
XX treating a condition requiring removal or destruction of cells of a  
XX mammal comprising administering to a mammal, a therapeutic amount of (I).  
XX The treatment is administered to the mammal before, during or after  
XX surgical excision, transplantation, grafting, chemotherapy,  
XX immunotherapy, vaccination, thermal or electrical ablation, cryotherapy,  
XX laser therapy, phototherapy, gene therapy and/or radiation. The method is  
XX useful for treatment of benign or malignant tumour; hyperplasia,  
XX hypertrophy or overgrowth of tissue; virally, bacterially or  
XX parasitically altered tissue; malformation of tissue selected from lung,  
XX breast, stomach, pancreas, prostate, bladder, bone, ovary, skin, kidney,  
XX sinus, colon, intestine, rectum, esophagus, heart, spleen, salivary  
XX gland, blood, brain and its coverings, spinal cord, muscle, connective  
XX tissue, adrenal, parathyroid, thyroid, uterus, testis, pituitary,  
XX reproductive organs, liver, hair, gall bladder, eye, ear, nose, throat,  
XX tonsils, mouth and lymph nodes and lymphoid system; tonsillary  
XX hypertrophy; prostatic hyperplasia; cosmetic modification to a tissue;  
XX vascular disease (atherosclerosis or arteriosclerosis); haemorrhoids;  
XX varicose veins; inflammatory disease; autoimmune disease; metabolic  
XX disease; hereditary/genetic disease; traumatic disease; physical injury;  
XX nutritional deficiency disease; infectious disease; amyloid disease;

CC fibrosis disease; storage disease; congenital malformation; enzyme  
CC deficiency disease; poisoning; intoxication; environmental disease;  
CC radiation disease; endocrine disease; degenerative disease and mechanical  
CC disease. This is the amino acid sequence of a human neural thread protein  
CC AD7C-NTP protein fragment  
XX  
SQ Sequence 75 AA;

Query Match 100.0%; Score 409; DB 6; Length 75;  
Best Local Similarity 100.0%; Pred. No. 9e-44;  
Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSSLGLPKWDYRHELLSLALMINFRVMACFTKQHIELRQKISIVPRKLCMGFVCPVKI 60  
Db |||||  
1 SSSLGLPKWDYRHELLSLALMINFRVMACFTKQHIELRQKISIVPRKLCMGFVCPVKI 60

QY 61 ALLTINGHCTWLPAS 75  
Db |||||  
61 ALLTINGHCTWLPAS 75

RESULT 6  
ABP59928  
ID ABP59928 standard; protein; 75 AA.  
XX  
AC ABP59928;  
XX

DT 08-SEP-2003 (first entry)

DE Human 75 amino acid neural thread protein.

XX Human; tumour; cancer; neural thread protein; NTP; cell removal;  
KW cell destruction; antipsoriatic; antimicrobial; immunosuppressive;  
KW antiinflammatory; dermatological; antiarteriosclerotic; vasotropic;  
KW gene therapy.

XX Homo sapiens.

OS WO2003044053-A2.

PN 30-MAY-2003.

PD 18-NOV-2002; 2002WO-CA001757.

PF 16-NOV-2001; 2001US-0331477P.

PR (NYMO-) NYMOX CORP.

PA Averbach P, Gemmell J;

XX WPI; 2003-457592/43.

DR New neural thread protein (NTP); useful for preparing a composition for  
XX treating or preventing a condition in a mammal requiring removal or  
PT destruction of cells, e.g. psoriasis, eczema, atherosclerosis or  
PT inflammatory disease.

XX Disclosure; Fig 5; 98pp; English.

PS The present invention relates to peptides derived from the human neural  
XX thread protein (NTP). The peptides are useful for preparing a composition  
CC for treating or preventing a condition in a mammal requiring removal or  
CC destruction of cells, comprising tonsillary hypertrophy, prostatic  
CC hyperplasia, psoriasis, eczema, dermatosis, cosmetic modification to a  
CC breast, connective, skin, eye, ear, nose, throat, mouth or muscle tissue,  
CC varicose veins, atherosclerosis, inflammatory, metabolic, infectious,  
CC fibrosis, endocrine or autoimmune disease, or stenosis, restenosis,  
CC occlusion or blockage of an artery or of a stent placed or implanted in  
CC an artery. The present sequence is an NTP protein used to produce  
CC peptides of the invention

XX Sequence 75 AA;

Query Match 100.0%; Score 409; DB 6; Length 75;  
Best Local Similarity 100.0%; Pred. No. 9e-44;  
Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSSLGLPKWDYRHELLSLALMINFRVMACFTKQHIELRQKISIVPRKLCMGFVCPVKI 60  
Db |||||  
1 SSSLGLPKWDYRHELLSLALMINFRVMACFTKQHIELRQKISIVPRKLCMGFVCPVKI 60

QY 61 ALLTINGHCTWLPAS 75  
Db |||||  
61 ALLTINGHCTWLPAS 75

RESULT 7  
AAE33195  
ID AAE33195 standard; protein; 75 AA.

XX AAE33195;  
AC

XX 16-APR-2003 (first entry)

DE Neural thread protein (NTP) #6.

XX Cell death; tissue necrosis; neural thread protein; NTP; amyloidosis;  
KW stroke; brain tumour; Pick's disease; Parkinson's disease; glaucoma;  
KW Alzheimer's disease; gene therapy.

OS Unidentified.

XX WO200289841-A2.

PN 14-NOV-2002.

PD 06-MAY-2002; 2002WO-CA000681.

PF 04-MAY-2001; 2001US-0288463P.

PR (NYMO-) NYMOX CORP.

PA Averbach PA;

XX WPI; 2003-120506/11.

XX Preventing, controlling, modulating, ameliorating and/or treating cell  
PT death or tissue necrosis using antibodies to neural thread proteins  
PT useful in disorders such as stroke, brain tumor, glaucoma and Alzheimer's  
PT disease.

PS Disclosure; Fig 10; 60pp; English.

CC The invention relates to a method of preventing, and/or inhibiting cell  
CC death and/or tissue necrosis in live tissue containing neural thread  
CC proteins (NTP). The method involves contacting the live tissue with at  
CC least one antibody, fragment or derivative that recognises NTP, where the  
CC antibody, fragment or derivative is present to prevent, control,  
CC ameliorate and/or inhibit cell death and/or tissue necrosis caused by the  
CC presence of NTP. Methods and compositions of the invention are useful for  
CC preventing, modulating, controlling and/or treating disorders associated  
CC with cell death and/or tissue necrosis such as stroke, brain tumour,  
CC Pick's disease, Parkinson's disease, amyloidosis, glaucoma and  
CC Alzheimer's disease. The invention is useful in gene therapy. The present  
CC sequence is NTP protein

XX Sequence 75 AA;

Query Match 100.0%; Score 409; DB 6; Length 75;  
Best Local Similarity 100.0%; Pred. No. 9e-44;  
Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSSLGLPKWDYRHELLSLALMINFRVMACFTKQHIELRQKISIVPRKLCMGFVCPVKI 60  
Db |||||  
1 SSSLGLPKWDYRHELLSLALMINFRVMACFTKQHIELRQKISIVPRKLCMGFVCPVKI 60



QY 61 ALLTINGHCTWLPAS 75  
 Db 61 ALLTINGHCTWLPAS 75

RESULT 8  
 ABJ19451  
 ID ABJ19451 standard; protein; 75 AA.  
 AC ABJ19451;  
 DT 27-MAR-2003 (first entry)  
 DE 75-mer neural thread protein.  
 KW Nootropic; neuroprotective; cell death; tissue necrosis; NTP;  
 KW neural thread protein; neurodegenerative disorder; Alzheimer's disease.  
 OS Unidentified.  
 PN WO200292115-A2.  
 XX 21-NOV-2002.  
 XX 16-MAY-2002; 2002WO-CA000712.  
 XX 16-MAY-2001; 2001US-0290971P.  
 PA (NYMO-) NYMOX CORP.  
 PI Averbach PA;  
 DR WPI; 2003-129234/12.  
 XX Preventing and/or inhibiting cell death and/or tissue necrosis in a  
 PT tissue for treating a neurodegenerative disorder, e.g. Alzheimer's  
 PT disease, by contacting the live tissue with at least one segment of  
 PT neural thread proteins (NTP).  
 XX Disclosure; Fig 7; 60pp; English.

CC The invention relates to a novel method for preventing and/or inhibiting  
 CC cell death and/or tissue necrosis in a tissue comprising contacting the  
 CC live tissue with at least one segment of neural thread proteins (NTP).  
 CC The methods are composition are useful for treating a neurodegenerative  
 CC disorder, such as Alzheimer's disease. This sequence represents an NTP  
 CC protein of the invention  
 XX Sequence 75 AA;  
 SQ

Query Match 100.0%; Score 409; DB 6; Length 75;  
 Best Local Similarity 100.0%; Pred. No. 9e-44;  
 Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSSGLPKCWDYRHEHLSLALMINFRVWACTFKQHIELRQKISIVPRKLCMGPVCPVKI 60  
 Db 1 SSSGLPKCWDYRHEHLSLALMINFRVWACTFKQHIELRQKISIVPRKLCMGPVCPVKI 60

QY 61 ALLTINGHCTWLPAS 75  
 Db 61 ALLTINGHCTWLPAS 75

RESULT 9  
 ADB37525  
 ID ADB37525 standard; protein; 75 AA.  
 AC ADB37525;  
 XX  
 DT 04-DEC-2003 (first entry)  
 DE Neural thread protein #4.  
 XX

KW Cytostatic; Antitumour; Antipsoriatic; Dermatological;  
 KW Antiatherosclerotic; Antiarteriosclerotic; Vasotropic; Antiinflammatory;  
 KW Immunosuppressive; Tranquillizer; Antileptic; Virucide; AD7c-NTP;  
 KW neural thread protein; neuritic sprouting.  
 OS Unidentified.  
 XX WO2003008444-A2.  
 XX 30-JAN-2003.  
 XX 19-JUL-2002; 2002WO-CA001106.  
 XX 19-JUL-2001; 2001US-0306150P.  
 PR 19-JUL-2001; 2001US-0306161P.  
 PR 16-NOV-2001; 2001US-0331477P.  
 XX (NYMO-) NYMOX CORP.  
 XX Averbach PA, Gemmell J;  
 XX WPI; 2003-248000/24.  
 XX Novel Related peptide or AD7c-neural thread peptide, useful for treating  
 PT unwanted cellular proliferations, glandular hyperplasia, unwanted facial  
 PT hair, warts and unwanted fatty tissue.  
 XX Disclosure; Fig 7; 109pp; English.

CC The present invention relates to AD7c-neural thread protein (NTP) and  
 CC related proteins and peptides (I; ADB37528-ADB37641). The sequences are  
 CC useful for treating a condition in a patient requiring removal or  
 CC destruction of cells. The condition can be selected from benign or  
 CC malignant tumour of a tissue, hyperplasia, hypertrophy or overgrowth of a  
 CC tissue, virally, bacterially or parasitically altered tissue, or  
 CC malformation of a tissue, where the tissue is selected from lung, breast,  
 CC stomach, pancreas, prostate, bladder, bone, ovary, skin, kidney, sinus,  
 CC colon, intestine, stomach, rectum, oesophagus, heart, spleen, salivary  
 CC gland, blood, brain and its coverings, spinal cord and its coverings,  
 CC muscle, connective tissue, adrenal, parathyroid, thyroid, uterus, testis,  
 CC pituitary, reproductive organs, liver, gall bladder, eye, ear, nose,  
 CC throat, tonsils, mouth, lymph nodes and lymphoid tissue. The condition is  
 CC preferably tonsillar hypertrophy, prostatic hyperplasia, psoriasis,  
 CC eczema, dermatosis, cosmetic modification to a tissue (skin, eye, ear,  
 CC nose, throat, mouth, muscle, connective, hair or breast tissue), vascular  
 CC disease (atherosclerosis or arteriosclerosis), haemorrhoids, varicose  
 CC veins, inflammatory disease, autoimmune disease, metabolic disease,  
 CC hereditary/genetic disease, traumatic disease or physical injury,  
 CC nutritional deficiency disease, infectious disease, amyloid disease,  
 CC fibrosis disease, storage disease, congenital malformation, enzyme  
 CC deficiency disease, poisoning, intoxication, environmental disease,  
 CC radiation disease, endocrine disease, degenerative disease and mechanical  
 CC disease. The peptides are useful for treating unwanted cellular  
 CC proliferations, glandular (e.g. prostate) hyperplasia, unwanted facial  
 CC hair, warts and unwanted fatty tissue, or for preparing antibodies that  
 CC recognize and/or bind to Related proteins, Related peptides or NTP  
 CC peptides. The present sequence was used to illustrate the invention.

QY Sequence 75 AA;  
 SQ

Query Match 100.0%; Score 409; DB 7; Length 75;  
 Best Local Similarity 100.0%; Pred. No. 9e-44;  
 Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSSGLPKCWDYRHEHLSLALMINFRVWACTFKQHIELRQKISIVPRKLCMGPVCPVKI 60  
 Db 1 SSSGLPKCWDYRHEHLSLALMINFRVWACTFKQHIELRQKISIVPRKLCMGPVCPVKI 60

QY 61 ALLTINGHCTWLPAS 75  
 Db 61 ALLTINGHCTWLPAS 75

```

RESULT 10
ADL96026
ID ADL96026 standard; protein; 75 AA.
XX AC
XX AC
XX ADL96026;
XX DT 20-MAY-2004 (first entry)
XX XX
XX Human neural thread protein, NTP75.
XX KW
XX Human; neural thread protein; NTP122; NTP112; NTP106; NTP98; NTP75;
XX KW NTP68; NTP61; stenosis; stent; tumour; prostatic hyperplasia; psoriasis;
XX KW eczema; haemorrhoid; atherosclerosis; inflammatory disease;
XX KW autoimmune disease; metabolic disease; hereditary disease;
XX KW genetic disease; traumatic disease; physical injury;
XX KW nutritional deficiency disease; infectious disease; amyloid disease;
XX KW Alzheimer's disease; storage disease; congenital malformation;
XX KW enzyme deficiency disease; poisoning; intoxication;
XX KW environmental disease; radiation disease; endocrine disease;
XX KW degenerative disease; mechanical disease.
XX OS
XX Homo sapiens.
XX XX
XX US2003166569-A1.
XX PN
XX 04-SEP-2003.
XX PD
XX 15-NOV-2002; 2002US-00294891.
XX PF
XX 16-NOV-2001; 2001US-0331477P.
XX PR
XX (AVER/) AVERBACK P.
XX PA (GEMM/) GEMMELL J.
XX PI
XX Averbach P, Gemmell J;
XX DR WPI; 2003-898099/82.
XX XX
XX New neural thread protein or its variants, useful for treating tumors and
XX PT other conditions requiring the removal or destruction of cells (e.g.
XX PT prostatic hyperplasia, psoriasis, eczema, hemorrhoids or
XX PT atherosclerosis).
XX XX
XX Disclosure; SEQ ID NO 5; 32pp; English.
XX XX
XX The invention relates to a peptide, or its homologue, derivative,
XX CC fragment, variant or mimic, comprising at least one neural thread
XX CC protein (NTP) peptide appearing as ADL96029-ADL96069, derived from
XX CC NTP122, 112, 106, 98, 75, 68 or 61. Also included are a nucleic acid
XX CC encoding an amino acid sequence corresponding to the above peptide, a
XX CC composition comprising one or more peptides or nucleic acids cited above
XX CC and a carrier, a method of treating a condition in a mammal requiring
XX CC removal or destruction of cells (comprising administering to the mammal
XX CC an amount of the peptide cited above) and a method of preventing or
XX CC inhibiting the stenosis, occlusion or blockage of a stent, comprising
XX CC coating the stent with an amount of the above peptide. The peptide
XX CC further comprises an amino acid in a reverse-D order based on the above
XX CC amino acid sequences. The composition and methods are useful in treating
XX CC tumours and other conditions requiring the removal or destruction of
XX CC cells (e.g. prostatic hyperplasia, psoriasis, eczema, haemorrhoids or
XX CC atherosclerosis). These may also be used in treating inflammatory
XX CC diseases, autoimmune diseases, metabolic diseases, hereditary/genetic
XX CC diseases, traumatic diseases or physical injuries, nutritional deficiency
XX CC diseases, infectious diseases, amyloid diseases e.g. Alzheimer's disease,
XX CC storage diseases, congenital malformation, enzyme deficiency diseases,
XX CC poisoning, intoxication, environmental diseases, radiation diseases,
XX CC endocrine diseases, degenerative diseases or mechanical diseases. The
XX CC present sequence is a human NTP protein from which the peptides of the
XX CC invention are derived.
XX XX
XX Sequence 75 AA;
XX SQ
Query Match 100.0%; Score 409; DB 7; Length 75;

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Best Local Similarity 100.0%; Pred. No. 9e-44;
Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSSLGLPKCWDYRHELLSLALMINFRVMACTFKQHIELROKISIVPRKLCMGPVCPVKI 60
Db 1 SSSLGLPKCWDYRHELLSLALMINFRVMACTFKQHIELROKISIVPRKLCMGPVCPVKI 60

Qy 61 ALLTINGHCTWLPAS 75
Db 61 ALLTINGHCTWLPAS 75

RESULT 11
AAO02982
ID AAO02982 standard; protein; 59 AA.
XX AC
XX AAO02982;
XX DT 06-NOV-2001 (first entry)
XX DE Human polypeptide SEQ ID NO 16874.
XX KW
XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
XX KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
XX KW tissue growth factor; immunomodulatory; cancer; leukaemia;
XX KW nervous system disorders; arthritis; inflammation.
XX OS
XX Homo sapiens.
XX XX
XX WO200164835-A2.
XX PN
XX 07-SEP-2001.
XX PD
XX 26-FEB-2001; 2001WO-US004927.
XX PF
XX 28-FEB-2000; 2000US-00515126.
XX PR 18-MAY-2000; 2000US-00577409.
XX XX
XX (HYSE-) HYSEQ INC.
XX PA
XX Tang YT, Liu C, Drmanac RT;
XX PI WPI; 2001-514838/56.
XX DR N-PSDB; AAI82913.
XX XX
XX Isolated nucleic acids and polypeptides, useful for preventing diagnosing
XX PT and treating e.g. leukemia, inflammation and immune disorders.
XX XX
XX Claim 20; SEQ ID NO 16874; 1399pp + Sequence Listing; English.
XX XX
XX The invention relates to human polynucleotides (AAI79941-AAI93841) and
XX CC the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to
XX CC cytokine, cell proliferation or cell differentiation or which may induce
XX CC production of other cytokines in other cell populations. The
XX CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
XX CC peptide therapy. The polypeptides have various cytokine-like activities,
XX CC e.g. stem cell growth factor activity, haematopoiesis regulating
XX CC activity, tissue growth factor activity, immunomodulatory activity and
XX CC activin/inhibin activity and may be useful in the diagnosis and/or
XX CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
XX CC inflammation. Note: The sequence data for this patent did not form part
XX CC of the printed specification, but was obtained in electronic format
XX CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX XX
XX Sequence 59 AA;
XX SQ
Query Match 24.0%; Score 98; DB 4; Length 59;
Best Local Similarity 51.1%; Pred. No. 0.00014;
Matches 24; Conservative 3; Mismatches 8; Indels 12; Gaps 3;

Qy 1 SSSLGLPKCWDYRHELLSLALMI-----NFRVM---ACTFKQHIIE 37
Db 13 SACLGLPKCWDYRREPLCPALVILLTAKFTNFRYRVKNVCTF--HVE 57

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OM protein - protein search, using sw model

Run on: October 11, 2005, 06:57:16 ; Search time 125.735 Seconds  
(without alignments)  
248.149 Million cell updates/sec

Title: US-10-092-934-7  
Perfect score: 409  
Sequence: 1 SSSGLPKCDYRHELLSLA.....CPVKIALTTINGHCTWLPAS 75

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1854112 seqs, 416015017 residues

Total number of hits satisfying chosen parameters: 1854112

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	409	100.0	75	14	US-10-138-516-6
2	409	100.0	75	14	US-10-146-130-8
3	409	100.0	75	14	US-10-092-934-7
4	409	100.0	75	14	US-10-153-334-7
5	409	100.0	75	14	US-10-198-069-7
6	409	100.0	75	14	US-10-198-070-7
7	409	100.0	75	14	US-10-294-891-5
8	409	100.0	75	17	US-10-920-313-5
9	92	22.5	86	9	US-09-764-869-1057
10	92	22.5	86	14	US-10-091-504-1057
11	92	22.5	86	15	US-10-227-577-1057

12	90	22.0	15	14	US-10-294-891-39	Sequence 39, Appl
13	90	22.0	15	17	US-10-920-313-39	Sequence 39, Appl
14	89	21.8	15	14	US-10-294-891-36	Sequence 36, Appl
15	89	21.8	15	17	US-10-920-313-36	Sequence 36, Appl
16	89	21.8	47	11	US-09-985-153-111	Sequence 111, App
17	86.5	21.1	104	18	US-10-450-763-38061	Sequence 38061, A
18	86	21.0	72	10	US-09-983-802-578	Sequence 578, App
19	86	21.0	72	10	US-09-984-490-578	Sequence 578, App
20	86	21.0	72	11	US-09-973-278-606	Sequence 606, App
21	85	20.8	15	14	US-10-294-891-40	Sequence 40, Appl
22	85	20.8	15	17	US-10-920-313-40	Sequence 40, Appl
23	84.5	20.7	214	18	US-10-450-763-38139	Sequence 38139, A
24	84	20.5	70	9	US-09-764-877-2048	Sequence 2048, Ap
25	84	20.5	70	15	US-10-242-515-2048	Sequence 2048, Ap
26	83	20.3	43	9	US-09-764-860-344	Sequence 344, App
27	83	20.3	43	14	US-10-074-095-344	Sequence 344, App
28	83	20.3	43	15	US-10-212-872-344	Sequence 344, App
29	81	19.8	34	14	US-10-106-698-4417	Sequence 4417, Ap
30	81	19.8	102	15	US-10-104-047-3864	Sequence 3864, Ap
31	81	19.8	119	10	US-09-892-877-400	Sequence 400, App
32	81	19.8	119	10	US-09-948-783-400	Sequence 400, App
33	80	19.6	154	18	US-10-450-763-54264	Sequence 54264, A
34	77.5	18.9	72	18	US-10-820-474A-69	Sequence 69, Appl
35	77	18.8	241	15	US-10-276-774-1834	Sequence 1834, Ap
36	76	18.6	35	16	US-10-332-765-47	Sequence 47, Appl
37	76	18.6	152	15	US-10-104-047-2372	Sequence 2372, Ap
38	75	18.3	101	9	US-09-764-853-432	Sequence 432, App
39	75	18.3	119	9	US-09-764-847-696	Sequence 696, App
40	75	18.3	119	14	US-10-092-154-696	Sequence 696, App
41	75	18.3	121	9	US-09-764-877-1641	Sequence 1641, Ap
42	75	18.3	121	15	US-10-242-515-1641	Sequence 1641, Ap
43	75	18.3	127	11	US-09-833-245-1427	Sequence 1427, Ap
44	74	18.1	310	9	US-09-864-921-12	Sequence 12, Appl
45	74	18.1	310	17	US-10-766-682-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1  
US-10-138-516-6  
; Sequence 6, Application US/10138516  
; Publication No. US20030003445A1  
; GENERAL INFORMATION:  
; APPLICANT: AVERBACK, PAUL  
; TITLE OF INVENTION: METHOD OF PREVENTING CELL DEATH USING ANTIBODIES TO  
; TITLE OF INVENTION: NEURAL THREAD PROTEINS  
; FILE REFERENCE: 59003.000004  
; CURRENT APPLICATION NUMBER: US/10/138.516  
; CURRENT FILING DATE: 2002-07-23  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 6  
; LENGTH: 75  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-138-516-6

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; Sequence 8, Application US/10146130
; Publication No. US20030004107A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; TITLE OF INVENTION: METHOD OF PREVENTING CELL DEATH USING SEGMENTS OF
; TITLE OF INVENTION: NEURAL THREAD PROTEINS
; FILE REFERENCE: 59003.000007
; CURRENT APPLICATION NUMBER: US/10/146,130
; CURRENT FILING DATE: 2002-08-06
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 75
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-146-130-8

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QY 61 ALLTINGHCTWLPAS 75
Db 61 ALLTINGHCTWLPAS 75

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US-10-092-934-7
; Sequence 7, Application US/10092934
; Publication No. US20030054990A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; TITLE OF INVENTION: METHODS OF USING NEURAL THREAD PROTEINS TO TREAT TUMORS
; TITLE OF INVENTION: AND CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 018792-0199
; CURRENT APPLICATION NUMBER: US/10/092,934
; CURRENT FILING DATE: 2002-06-05
; PRIOR APPLICATION NUMBER: 60/273,957
; PRIOR FILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 75
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Neural thread
US-10-092-934-7

Query Match      100.0%; Score 409; DB 14; Length 75;
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QY 61 ALLTINGHCTWLPAS 75
Db 61 ALLTINGHCTWLPAS 75

RESULT 4
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; Sequence 7, Application US/10153334
; Publication No. US20030096350A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 59003-000006
; CURRENT APPLICATION NUMBER: US/10/153,334
; CURRENT FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: 60/293,156
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 75
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-153-334-7

Query Match      100.0%; Score 409; DB 14; Length 75;
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QY 61 ALLTINGHCTWLPAS 75
Db 61 ALLTINGHCTWLPAS 75

RESULT 5
US-10-198-069-7
; Sequence 7, Application US/10198069
; Publication No. US20030096756A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 59003.000009
; CURRENT APPLICATION NUMBER: US/10/198,069
; CURRENT FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/306,161
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/306,150
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/331,477
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 48
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; LENGTH: 75
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; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Unknown NTP
US-10-198-069-7

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QY 61 ALLTINGHCTWLPAS 75
Db 61 ALLTINGHCTWLPAS 75

RESULT 6
US-10-153-334-7
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; Publication No. US20030096350A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 59003-000006
; CURRENT APPLICATION NUMBER: US/10/153,334
; CURRENT FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: 60/293,156
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 75
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; ORGANISM: Homo sapiens
US-10-153-334-7

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US-10-198-070-7
; Sequence 7, Application US/10198070
; Publication No. US20030109437A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; APPLICANT: GEMMEL, JACK
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 59003.00008
; CURRENT APPLICATION NUMBER: US/10/198.070
; CURRENT FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/306,161
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/306,150
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/331,477
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 7
; LENGTH: 75
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Unknown NTP
; OTHER INFORMATION: peptide
US-10-198-070-7

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RESULT 7
US-10-294-891-5
; Sequence 5, Application US/10294891
; Publication No. US2003016569A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; APPLICANT: GEMMEL, JACK
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF CELLS
; FILE REFERENCE: 59003.000010
; CURRENT APPLICATION NUMBER: US/10/294.891
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: 60/331,447
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 75
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-294-891-5

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Qy 61 ALLTINGHCTWLPAS 75
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RESULT 7
US-10-294-891-5
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; Publication No. US2003016569A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; APPLICANT: GEMMEL, JACK
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF CELLS
; FILE REFERENCE: 59003.000010
; CURRENT APPLICATION NUMBER: US/10/294.891
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: 60/331,447
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 75
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-294-891-5

Query Match      100.0%; Score 409; DB 14; Length 75;
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US-10-198-070-7
; Sequence 7, Application US/10198070
; Publication No. US20030109437A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; APPLICANT: GEMMEL, JACK
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 59003.00008
; CURRENT APPLICATION NUMBER: US/10/198.070
; CURRENT FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/306,161
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/306,150
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/331,477
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 7
; LENGTH: 75
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Unknown NTP
; OTHER INFORMATION: peptide
US-10-198-070-7

Query Match      100.0%; Score 409; DB 14; Length 75;
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Db 61 ALLTINGHCTWLPAS 75

RESULT 7
US-10-294-891-5
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; Publication No. US2003016569A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; APPLICANT: GEMMEL, JACK
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF CELLS
; FILE REFERENCE: 59003.000010
; CURRENT APPLICATION NUMBER: US/10/294.891
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: 60/331,447
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-294-891-5

Query Match      100.0%; Score 409; DB 14; Length 75;
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US-10-920-313-5
; Sequence 5, Application US/10920313
; Publication No. US20050032704A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; APPLICANT: GEMMEL, JACK
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF CELLS
; FILE REFERENCE: 59003.000010
; CURRENT APPLICATION NUMBER: US/10/920.313
; CURRENT FILING DATE: 2004-08-18
; PRIOR APPLICATION NUMBER: 60/331,447
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 75
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-920-313-5

Query Match      100.0%; Score 409; DB 17; Length 75;
Best Local Similarity 100.0%; Pred. No. 3.6e-43;
Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSSGLPKCDYRHELLSLALMINFRVMCTFKQHIELRQKISIVPRKLCMGPVCPVKI 60
Db 1 SSSGLPKCDYRHELLSLALMINFRVMCTFKQHIELRQKISIVPRKLCMGPVCPVKI 60

Qy 61 ALLTINGHCTWLPAS 75
Db 61 ALLTINGHCTWLPAS 75

RESULT 8
US-10-920-313-5
; Sequence 5, Application US/10920313
; Publication No. US20050032704A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; APPLICANT: GEMMEL, JACK
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF CELLS
; FILE REFERENCE: 59003.000010
; CURRENT APPLICATION NUMBER: US/10/920.313
; CURRENT FILING DATE: 2004-08-18
; PRIOR APPLICATION NUMBER: 60/331,447
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 75
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-920-313-5

Query Match      100.0%; Score 409; DB 17; Length 75;
Best Local Similarity 100.0%; Pred. No. 3.6e-43;
Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSSGLPKCDYRHELLSLALMINFRVMCTFKQHIELRQKISIVPRKLCMGPVCPVKI 60
Db 1 SSSGLPKCDYRHELLSLALMINFRVMCTFKQHIELRQKISIVPRKLCMGPVCPVKI 60

Qy 61 ALLTINGHCTWLPAS 75
Db 61 ALLTINGHCTWLPAS 75

RESULT 9
US-09-764-869-1057
; Sequence 1057, Application US/09764869
; Patent No. US20020061521A1
; GENERAL INFORMATION:
; APPLICANT: ROSEN ET AL.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC007
; CURRENT APPLICATION NUMBER: US/09/764.869
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2442
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1057
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (71)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (82)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-869-1057

Query Match      22.5%; Score 92; DB 9; Length 86;
Best Local Similarity 56.2%; Pred. No. 0.0015;
Matches 18; Conservative 3; Mismatches 7; Indels 4; Gaps 1;

Qy 1 SSSGLPKCDYRHELLSLALMINFRVMCTFKQHIELRQKISIVPRKLCMGPVCPVKI 32
Db 7 SSSGLPKCDYRHELLSLALMINFRVMCTFKQHIELRQKISIVPRKLCMGPVCPVKI 34
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RESULT 10
US-10-091-504-1057
; Sequence 1057, Application US/10091504
; Publication No. US2003005908A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC007C1
; CURRENT APPLICATION NUMBER: US/10/091,504
; NUMBER OF SEQ ID NOS: 2442
; Prior Application removed - See File Wrapper or Palm
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1057
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (71)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: misc_feature
; LOCATION: (82)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-091-504-1057

Query Match      22.5%; Score 92; DB 14; Length 86;
Best Local Similarity 56.2%; Pred. No. 0.0015;
Matches 18; Conservative 3; Mismatches 7; Indels 4; Gaps 1;

Qy 1 SSSLGPKCWDYRHELLSLALMIFRVMCTF 32
   ||| ||||| ||||| ||| : |||
Db 7 SSCLSLPKCWDYRHEPLYMAYIF----LRCTF 34

RESULT 11
US-10-227-577-1057
; Sequence 1057, Application US/10227577
; Publication No. US20040005575A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC007C2
; CURRENT APPLICATION NUMBER: US/10/227,577
; CURRENT FILING DATE: 2002-08-26
; PRIOR FILING DATE: 2002-03-07
; PRIOR FILING DATE: 2002-03-07
; PRIOR FILING DATE: 2001-01-17
; PRIOR FILING DATE: 2000-01-31
; PRIOR FILING DATE: 2000-02-04
; PRIOR FILING DATE: 2000-06-28
; PRIOR FILING DATE: 2000-07-11
; PRIOR FILING DATE: 2000-07-11
; PRIOR FILING DATE: 2000-08-14
; PRIOR FILING DATE: 2000-07-26
; PRIOR FILING DATE: 2000-07-26
; PRIOR FILING DATE: 2000-07-11
; PRIOR FILING DATE: 2000-07-11
; PRIOR FILING DATE: 2000-08-14
; PRIOR FILING DATE: 2000-08-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2442
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1057
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Homo sapiens

Query Match      22.5%; Score 92; DB 14; Length 86;
Best Local Similarity 56.2%; Pred. No. 0.0015;
Matches 18; Conservative 3; Mismatches 7; Indels 4; Gaps 1;

Qy 1 SSSLGPKCWDYRHELLSLALMIFRVMCTF 32
   ||| ||||| ||||| ||| : |||
Db 7 SSCLSLPKCWDYRHEPLYMAYIF----LRCTF 34

RESULT 12
US-10-294-891-39
; Sequence 39, Application US/10294891
; Publication No. US20030166569A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; APPLICANT: GEMMEL, JACK
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; FILE REFERENCE: 59003.000010
; CURRENT APPLICATION NUMBER: US/10/294,891
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: 60/331,447
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 39
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-294-891-39

Query Match      22.0%; Score 90; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.00042;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 46 PRKLCCMGVPCVKI 60
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Db 1 PRKLCCMGVPCVKI 15

RESULT 13
US-10-920-313-39
; Sequence 39, Application US/10920313
; Publication No. US20050032704A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; APPLICANT: GEMMEL, JACK
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; FILE REFERENCE: 59003.000010
; CURRENT APPLICATION NUMBER: US/10/920,313
; CURRENT FILING DATE: 2004-08-18
; PRIOR APPLICATION NUMBER: 60/331,447
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 39
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-920-313-39

Query Match      22.0%; Score 90; DB 17; Length 15;
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Best Local Similarity 100.0%; Pred. No. 0.00042; DB 14; Length 15;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 46 PRKLCMGPVCPVKI 60  
| | | | | | | | | | | | | | |  
Db 1 PRKLCMGPVCPVKI 15

## RESULT 14

US-10-294-891-36  
; Sequence 36, Application US/10294891  
; Publication No. US20030166569A1  
; GENERAL INFORMATION:  
; APPLICANT: AVERBACK, PAUL  
; APPLICANT: GEMMEL, JACK  
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER  
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF CELLS  
; FILE REFERENCE: 59003.000010  
; CURRENT APPLICATION NUMBER: US/10/294,891  
; CURRENT FILING DATE: 2002-11-15  
; PRIOR APPLICATION NUMBER: 60/331,447  
; PRIOR FILING DATE: 2001-11-16  
; NUMBER OF SEQ ID NOS: 49  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 36  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-294-891-36

Query Match 21.8%; Score 89; DB 14; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.00057; DB 15;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSSLGLPKCWDYRHE 15  
| | | | | | | | | | | | | | |  
Db 1 SSSLGLPKCWDYRHE 15

## RESULT 15

US-10-920-313-36  
; Sequence 36, Application US/10920313  
; Publication No. US20050032704A1  
; GENERAL INFORMATION:  
; APPLICANT: AVERBACK, PAUL  
; APPLICANT: GEMMEL, JACK  
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER  
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF CELLS  
; FILE REFERENCE: 59003.000010  
; CURRENT APPLICATION NUMBER: US/10/920,313  
; CURRENT FILING DATE: 2004-08-18  
; PRIOR APPLICATION NUMBER: 60/331,447  
; PRIOR FILING DATE: 2001-11-16  
; NUMBER OF SEQ ID NOS: 49  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 36  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-920-313-36

Query Match 21.8%; Score 89; DB 17; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.00057; DB 15;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSSLGLPKCWDYRHE 15  
| | | | | | | | | | | | | | |  
Db 1 SSSLGLPKCWDYRHE 15

Search completed: October 11, 2005, 07:39:46  
Job time : 126.735 secs

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Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	409	100.0	75	2	US-08-454-557C-48	Sequence 48, Appl
2	409	100.0	75	2	US-08-340-426D-48	Sequence 48, Appl
3	409	100.0	75	2	US-08-450-673C-48	Sequence 48, Appl
4	409	100.0	75	3	PCT-US95-17111A-48	Sequence 48, Appl
5	86	21.0	72	3	US-09-227-357-578	Sequence 578, App
6	81.5	19.9	55	4	US-09-513-999C-7795	Sequence 7795, Ap
7	75.5	18.5	82	4	US-09-513-999C-5298	Sequence 5298, Ap
8	73	17.8	135	4	US-09-685-166A-884	Sequence 884, App
9	73	17.8	135	4	US-09-679-426-884	Sequence 884, App
10	73	17.8	135	4	US-09-759-143-884	Sequence 884, App
11	72	17.6	24	4	US-09-461-325-436	Sequence 436, App
12	72	17.6	24	4	US-10-012-543-436	Sequence 436, App
13	72	17.6	24	4	US-10-115-123-436	Sequence 436, App
14	71.5	17.5	397	5	PCT-US95-17111A-121	Sequence 121, App
15	70	17.1	132	4	US-09-636-215-573	Sequence 573, App
16	70	17.1	132	4	US-09-685-166A-573	Sequence 573, App
17	70	17.1	132	4	US-09-679-426-573	Sequence 573, App
18	70	17.1	132	4	US-09-759-143-573	Sequence 573, App
19	70	17.1	132	4	US-09-651-236-573	Sequence 573, App
20	69	16.9	71	4	US-09-513-999C-6619	Sequence 6619, Ap
21	68	16.6	73	4	US-09-513-999C-4484	Sequence 4484, Ap
22	67.5	16.5	108	4	US-09-621-976-5858	Sequence 5858, Ap
23	67	16.4	99	4	US-09-621-976-6393	Sequence 6393, Ap
24	66	16.1	91	4	US-09-621-976-5929	Sequence 5929, Ap
25	64.5	15.8	375	2	US-08-454-557C-121	Sequence 121, App
26	64.5	15.8	375	2	US-08-340-426D-121	Sequence 121, App
27	64.5	15.8	375	2	US-08-450-673C-121	Sequence 121, App

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Db 61 ALLTINGHCTWLPAS 75

RESULT 2
US-08-340-426D-48
; Sequence 48, Application US/08340426D
; Patent No. 5948634
; GENERAL INFORMATION:
; APPLICANT: de la Monte, Suzanne
; TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
; TITLE OF INVENTION: of Alzheimer's Disease
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/340,426D
; FILING DATE: 14-NOV-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ludwig, Steven R.
; REGISTRATION NUMBER: 36,203
; REFERENCE/DOCKET NUMBER: 0609.3840002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 75 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-340-426D-48

Query Match 100.0%; Score 409; DB 2; Length 75;
Best Local Similarity 100.0%; Pred. No. 1.8e-46;
Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSSGLPKCWDYRHLLSLALMINFRVMCTFKQHIELRQKISIVPRKLCMGPVCPVKI 60
Db 1 SSSGLPKCWDYRHLLSLALMINFRVMCTFKQHIELRQKISIVPRKLCMGPVCPVKI 60
QY 61 ALLTINGHCTWLPAS 75
Db 61 ALLTINGHCTWLPAS 75

RESULT 4
PCT-US95-17111A-48
; Sequence 48, Application PC/TUS951711A
; GENERAL INFORMATION:
; APPLICANT: de la Monte, Suzanne
; APPLICANT: Wands, Jack R.
; TITLE OF INVENTION: Neural Thread Protein Gene Expression and
; TITLE OF INVENTION: Detection of Alzheimer's Disease
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/17111A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/340,426
; FILING DATE: 14-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ludwig, Steven R.
; REGISTRATION NUMBER: 36,203
; REFERENCE/DOCKET NUMBER: 0609.3840002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; US-08-450-673C-48

Query Match 100.0%; Score 409; DB 2; Length 75;
Best Local Similarity 100.0%; Pred. No. 1.8e-46;
Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSSGLPKCWDYRHLLSLALMINFRVMCTFKQHIELRQKISIVPRKLCMGPVCPVKI 60
Db 1 SSSGLPKCWDYRHLLSLALMINFRVMCTFKQHIELRQKISIVPRKLCMGPVCPVKI 60
QY 61 ALLTINGHCTWLPAS 75
Db 61 ALLTINGHCTWLPAS 75

RESULT 3
US-08-450-673C-48
; Sequence 48, Application US/08450673C
; Patent No. 5948888
; GENERAL INFORMATION:
; APPLICANT: de la Monte, Suzanne
; APPLICANT: Wands, Jack R.
; TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
; TITLE OF INVENTION: of Alzheimer's Disease
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,673C
; FILING DATE: 30-MAY-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Ludwig, Steven R.
; REGISTRATION NUMBER: 36,203
; REFERENCE/DOCKET NUMBER: 0609.3840004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 75 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-450-673C-48

Query Match 100.0%; Score 409; DB 2; Length 75;
Best Local Similarity 100.0%; Pred. No. 1.8e-46;
Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSSGLPKCWDYRHLLSLALMINFRVMCTFKQHIELRQKISIVPRKLCMGPVCPVKI 60
Db 1 SSSGLPKCWDYRHLLSLALMINFRVMCTFKQHIELRQKISIVPRKLCMGPVCPVKI 60
QY 61 ALLTINGHCTWLPAS 75
Db 61 ALLTINGHCTWLPAS 75
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Db      106 SACLGLPKCWGYRHKPPHPACHILLNYQV 134
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RESULT 9
US-09-679-426-884
; Sequence 884, Application US/09679426
; Patent No. 6759515
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C20
; CURRENT APPLICATION NUMBER: US/09/679,426
; CURRENT FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 895
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 884
; LENGTH: 135
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-679-426-884
Query Match          17.8%; Score 73; DB 4; Length 135;
Best Local Similarity 48.3%; Pred. No. 0.065;
Matches 14; Conservative 7; Mismatches 6; Indels 2;

Oy      1 SSSIGLPCWIDYRHLLSLA--LMINFRV 27
|:||||||| |:|::|::|
Db      106 SACLGLPKCWGYRHKPPHPACHILLNYQV 134
|:||||||| |:|::|::|
RESULT 10
US-09-759-143-884
; Sequence 884, Application US/09759143
; Patent No. 6800746
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C23
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; CURRENT APPLICATION NUMBER: US/09/759,143
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 884
; LENGTH: 135
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-759-143-884

Query Match      17.8%; Score 73; DB 4; Length 135;
Best Local Similarity 48.3%; Pred. No. 0.065;
Matches 14; Conservative 7; Mismatches 6; Indels 2; Gaps 1;

Qy 1 SSSGLPKCWDYRHEILSLA--LMINFRV 27
Db 106 SACLGLPKCWGYRKHPPHPACHILLNYQV 134

RESULT 11
US-09-461-325-436
; Sequence 436, Application US/09461325A
; Patent No. 6475753
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 94 Human Secreted Proteins
; FILE REFERENCE: P2029P1
; CURRENT APPLICATION NUMBER: US/09/461,325A
; CURRENT FILING DATE: 1999-12-14
; EARLIER APPLICATION NUMBER: PCT/US99/13418
; EARLIER FILING DATE: 1999-06-15
; EARLIER APPLICATION NUMBER: 60/089,507
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: 60/089,508
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: 60/089,509
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: 60/089,510
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: 60/090,112
; EARLIER FILING DATE: 1998-06-22
; EARLIER APPLICATION NUMBER: 60/090,113
; EARLIER FILING DATE: 1998-06-22
; NUMBER OF SEQ ID NOS: 532
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 436
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-461-325-436

Query Match      17.6%; Score 72; DB 4; Length 24;
Best Local Similarity 85.7%; Pred. No. 0.012;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 SSSGLPKCWDYRHE 15
Db 1 SCLGLPKCWDYRQE 14

RESULT 12
US-10-012-542-436
; Sequence 436, Application US/10012542
; Patent No. 6627741
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 94 Human Secreted Proteins
; FILE REFERENCE: P2029P1
; CURRENT APPLICATION NUMBER: US/10/012,542
; CURRENT FILING DATE: 2001-12-12
; EARLIER APPLICATION NUMBER: 09/461,325
; EARLIER FILING DATE: 1999-12-14
; EARLIER APPLICATION NUMBER: 60/089,507
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; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,508
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,509
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,510
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/090,112
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/090,113
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-22
; NUMBER OF SEQ ID NOS: 532
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 436
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-012-542-436

Query Match      17.6%; Score 72; DB 4; Length 24;
Best Local Similarity 85.7%; Pred. No. 0.012;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 SSSGLPKCWDYRHE 15
Db 1 SCLGLPKCWDYRQE 14

RESULT 13
US-10-115-123-436
; Sequence 436, Application US/10115123
; Patent No. 8774216
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 94 Human Secreted Proteins
; FILE REFERENCE: P2029G30AP1D2
; CURRENT APPLICATION NUMBER: US/10/115,123
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: PCT/US99/13418
; PRIOR FILING DATE: 1999-06-15
; PRIOR APPLICATION NUMBER: 60/089,507
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089,508
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089,509
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089,510
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/090,112
; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: 60/090,113
; PRIOR FILING DATE: 1998-06-22
; NUMBER OF SEQ ID NOS: 532
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 436
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-115-123-436

Query Match      17.6%; Score 72; DB 4; Length 24;
Best Local Similarity 85.7%; Pred. No. 0.012;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 SSSGLPKCWDYRHE 15
Db 1 SCLGLPKCWDYRQE 14

RESULT 14
PCT-US95-17111A-121
; Sequence 121, Application PC/TUS9517111A
; GENERAL INFORMATION:
```

; APPLICANT: de la Monte, Suzanne  
; APPLICANT: Wands, Jack R.  
; TITLE OF INVENTION: Neural Thread Protein Gene Expression and  
; TITLE OF INVENTION: Detection of Alzheimer's Disease  
; NUMBER OF SEQUENCES: 121  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.  
; STREET: 1100 New York Avenue, Suite 600  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/17111A  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/340,426  
; FILING DATE: 14-NOV-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ludwig, Steven R.  
; REGISTRATION NUMBER: 36,203  
; REFERENCE/DOCKET NUMBER: 0609.3840002  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 371-2600  
; TELEFAX: (202) 371-2540  
; INFORMATION FOR SEQ ID NO: 121:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 397 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
PCT-US95-17111A-121

Query Match 17.5%; Score 71.5; DB 5; Length 397;  
Best Local Similarity 28.2%; Pred. No. 0.36; Mismatches 29; Indels 23; Gaps 3;  
Matches 24; Conservative 9;  
QY 1 SSSLGLPKCWDYRHLLSLALMNFVMAC-----TFKHTELROKISIVPR 47  
Db 119 STCLSLPKCWDYRAAVPGILFFLHRLRPTLTQDEVQWCDHSSLOPSTLRSSI-LLPQ 177  
QY 48 KLCCMGFVCPVKIALTLTNGHCTWL 72  
Db 178 -----PPKVAGTKDMHHTWL 193

RESULT 15  
US-09-636-215-573  
; Sequence 573, Application US/09636215  
; Patent No. 6620922  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Harlocker, Susan L.  
; APPLICANT: Jiang, Yuqi  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Retter, Marc W.  
; APPLICANT: Stolk, John A.  
; APPLICANT: Day, Craig H.  
; APPLICANT: Vedvick, Thomas S.  
; APPLICANT: Carter, Darrick  
; APPLICANT: Li, Samuel  
; APPLICANT: Wang, Aijun  
; APPLICANT: Skeiky, Yasir A.W.

; APPLICANT: Hepler, William  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER  
; FILE REFERENCE: 210121.42717C17  
; CURRENT APPLICATION NUMBER: US/09/636,215  
; CURRENT FILING DATE: 2000-08-10  
; NUMBER OF SEQ ID NOS: 852  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 573  
; LENGTH: 132  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-636-215-573  
Query Match 17.1%; Score 70; DB 4; Length 132;  
Best Local Similarity 73.3%; Pred. No. 0.16; Mismatches 2; Indels 0; Gaps 0;  
Matches 11; Conservative 2;  
QY 1 SSSLGLPKCWDYRHE 15  
Db 106 SACLGLPKCMGYRHK 120

Search completed: October 11, 2005, 07:42:51  
Job time : 18.1457 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 11, 2005, 06:57:07 ; Search time 10.5455 Seconds  
(without alignments)  
620.432 Million cell updates/sec

Title: US-10-092-934-8  
Perfect score: 393  
Sequence: 1 MFVFCLLLNREKIKGNSSP.....FYCLVDKAAFECHWFYSFDT 68

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79:.\*  
1: pir1:.\*  
2: pir2:.\*  
3: pir3:.\*  
4: pir4:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	66.5	16.9	131	2 I56894	complement regulat
2	63.5	16.2	1162	2 T49191	hypothetical prote
3	62.5	15.9	358	2 E84611	hypothetical prote
4	62.5	15.9	531	2 T11074	NADH2 dehydrogenas
5	62	15.8	182	2 T17625	hypothetical prote
6	62	15.8	428	2 T48167	hypothetical prote
7	61.5	15.6	277	2 T21630	hypothetical prote
8	61.5	15.6	348	2 S64041	probable membrane
9	61.5	15.6	657	2 D71351	probable primosoma
10	61	15.5	160	2 S45981	probable membrane
11	61	15.5	320	2 AC2432	hypothetical prote
12	60.5	15.4	3020	2 A43932	mucin 2 precursor,
13	60	15.3	324	2 T24645	hypothetical prote
14	60	15.3	457	2 T11124	NADH2 dehydrogenas
15	59.5	15.1	274	2 T12791	hypothetical prote
16	59.5	15.1	308	2 F87912	protein B0205.2 [i
17	59.5	15.1	845	1 JBVLSK	DNA-directed DNA p
18	59.5	15.1	1472	2 A84470	hypothetical prote
19	59	15.0	527	2 S26037	NADH2 dehydrogenas
20	58.5	14.9	192	2 S22981	T-cell surface gly
21	58.5	14.9	1095	2 E96744	probable oligopept
22	58.5	14.9	2278	1 S56274	FAB1 protein - yea
23	58	14.8	128	1 RWHU59	surface glycoprote
24	58	14.8	340	2 T16729	hypothetical prote
25	58	14.8	707	2 F84943	primosomal protei
26	58	14.8	711	2 T05148	protein kinase hom
27	57.5	14.6	458	2 A29361	DG17 protein - sli
28	57.5	14.6	502	1 I30010	NADH2 dehydrogenas
29	57.5	14.6	591	2 T29974	hypothetical prote

30	57.5	14.6	1504	2 T49896	glycine/proline-ri
31	57.5	14.6	1513	2 A54895	mucin 2, intestina
32	57	14.5	414	2 G71680	penicillin-binding
33	57	14.5	439	2 F87490	NADH2 dehydrogenase
34	57	14.5	487	1 S52261	NADH2 dehydrogenas
35	57	14.5	536	2 F86251	hypothetical prote
36	56.5	14.4	279	2 T24606	hypothetical prote
37	56.5	14.4	431	1 A39588	NADH2 dehydrogenas
38	56.5	14.4	846	2 A12336	primosomal protein
39	56	14.2	202	2 JC4635	tumor-associated L
40	56	14.2	202	2 JC6205	cell surface anti
41	56	14.2	325	2 T32282	hypothetical prote
42	56	14.2	371	1 H22848	ubiquinol-cytochro
43	56	14.2	433	2 B81992	NADH2 dehydrogenas
44	56	14.2	433	2 D81222	NADH dehydrogenase
45	56	14.2	590	1 S34960	NADH2 dehydrogenas

ALIGNMENTS

RESULT 1

I56894  
complement regulatory protein - common squirrel monkey  
C:Species: Saimiri sciureus (common squirrel monkey)  
C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004  
C:Accession: I56894  
R:Roeder, R.P.; Rollins, S.A.; Fodor, W.L.; Albrecht, J.C.; Setter, E.; Fleckenstein, B.  
J. Virol. 68, 730-737, 1994  
A:Title: Inhibition of complement-mediated cytolysis by the terminal complement inhibitor  
A:Reference number: I56894; MUID:94118421; PMID:7507185  
A:Accession: I56894  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-131 <RES>  
A:Cross-references: UNIPROT:P47777; GB:L22859; NID:g404796; PIDN:AAA16747.1; PID:g404797  
C:Genetics:  
A:Gene: CDS9  
C:Superfamily: Ly-6 antigen, Ly-6 homology  
F:26-105/Domain: Ly-6 homology <LY6>

Query Match	16.9%	Score 66.5;	DB 2;	Length 131;
Best Local Similarity	27.9%	Pred. No. 1.6;		
Matches	19;	Conservative	9;	Mismatches 23; Indels 17; Gaps 3;
Qy	13	IKGNSSSF---FLLSFFSFQNCQCFQRTTEGYAVECF-----YCLVDKAA--	57	
Db	3	IQGGSVLFGLLLVLAVFCHSGNSLQCYSCPLPTWESMECTASTNCTSNLDSCLIAGSG	62	
Qy	58	--FECWWF 63		
Db	63	VYRCWKRF 70		

RESULT 2

T49191  
hypothetical protein MAA21.130 - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 02-Jun-2000 #sequence\_revision 02-Jun-2000 #text\_change 09-Jul-2004  
C:Accession: T49191  
R:Rieger, M.; Mueller-Auer, S.; Zipp, M.; Schaefer, M.; Mewes, H.W.; Rudd, S.; Lemcke, K.  
submitted to the Protein Sequence Database, April 2000  
A:Reference number: 225018  
A:Accession: T49191  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1162 <RIE>  
A:Cross-references: UNIPROT:Q9LY65; EMBL:AL163818; GSPDB:GN00061; ATSP:MAA21.130  
A:Experimental source: cultivar Columbia; BAC clone MAA21  
C:Genetics:  
A:Gene: ATSP:MAA21.130  
A:Map position: 3  
A:Introns: 975/1

Query Match	15.9%	Score 62.5;	DB 2;	Length 531;
Best Local Similarity	22.2%;	Pred. No. 14;		
Matches 14;	Conservative 11;	Mismatches 21;	Indels 17;	Gaps 2;

C;Species: Caenorhabditis elegans  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C;Accession: T21630  
R;White, S.  
submitted to the EMBL Data Library, November 1996  
A;Reference number: Z19452  
A;Accession: T21630  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-277 <WIL>  
A;Cross-references: UNIPROT:O62200; EMBL:Z81522; PIDN:CAB04230.1; GSPDB:GN00019; CESP:F3324  
C;Genetics:  
A;Gene: CESP:F32B4.5  
A;Map position: 1  
A;Introns: 131/3; 237/3  
C;Superfamily: Caenorhabditis elegans hypothetical protein F32B4.5

Query Match 15.6%; Score 61.5; DB 2; Length 277;  
Best Local Similarity 63.6%; Pred. No. 11;  
Matches 14; Conservative 2; Mismatches 5; Indels 1; Gaps 1;

QY 9 NREKIKGNS-S-PFLLSFFFSF 29  
DB 190 NPEPVKGTTS-PFLLSFFFPF 211

RESULT 8  
S64041  
probable membrane protein YGL039w - yeast (Saccharomyces cerevisiae)  
N;Alternate names: hypothetical protein G3620  
C;Species: Saccharomyces cerevisiae  
C;Date: 17-May-1996 #sequence\_revision 17-May-1996 #text\_change 09-Jul-2004  
C;Accession: S64041  
R;Hebling, U.; Hofmann, B.; Delius, H.  
submitted to the Protein Sequence Database, May 1996  
A;Reference number: S64003  
A;Accession: S64041  
A;Molecule type: DNA  
A;Residues: 1-348 <HEB>  
A;Cross-references: UNIPROT:P53183; EMBL:Z72561; NID:gl322521; PID:gl322522; GSPDB:GN00040  
A;Experimental source: strain S288C  
C;Genetics:  
A;Gene: MIPS:YGL039w  
A;Cross-references: SGD:S0003007  
A;Map position: 7L  
C;Superfamily: dihydrokaempferol 4-reductase  
C;Keywords: transmembrane protein  
F;6-22/Domain: transmembrane #status predicted <TMM>

Query Match 15.6%; Score 61.5; DB 2; Length 348;  
Best Local Similarity 31.9%; Pred. No. 13;  
Matches 23; Conservative 10; Mismatches 16; Indels 23; Gaps 6;

QY 3 VFCL-----IINRE--KIKG-----GNSSFFLLSFFFSFQCCQFCQRTTE--GVAV 46  
DB 274 MFCQEQALDIINEFPQLKGKIATGEPGSGTFLT-----KNCKCDNRKTNLLGFQF 327

QY 47 ECFY-CLVDKAA 57  
DB 328 NKFRDCIVDTAS 339

RESULT 9  
D71351  
probable primosomal protein N (p18a) - syphilis spirochete  
C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete)  
C;Date: 24-Jul-1998 #sequence\_revision 24-Jul-1998 #text\_change 09-Jul-2004  
C;Accession: D71351  
R;Fraser, C.M.; Norris, S.J.; Weinstein, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwinther, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McDo-  
they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.  
Science 281, 375-388, 1998

A;Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.  
A;Reference number: A71250; MUID:98332770; PMID:9665876  
C;Accession: D71351  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-657 <COL>  
A;Cross-references: UNIPROT:O83258; GB:AE001204; GB:AE000520; NID:g3322492; PIDN:AAC6521  
A;Experimental source: strain Nichols  
C;Genetics:  
A;Gene: TP0230

Query Match 15.6%; Score 61.5; DB 2; Length 657;  
Best Local Similarity 30.0%; Pred. No. 22;  
Matches 24; Conservative 8; Mismatches 23; Indels 25; Gaps 4;

QY 8 LNREKIKGNS-S-PFLLSFFFSFQCCQFCQRTTEG-----AVECF 49  
DB 341 IRKTEAGYQSMFLNRRGFSYS-----FQCRSC-GYTLCCTQCAVPLTWHKRVGAMQCH 394

QY 50 YCLVDKAAFE-CWVFYSFDT 68  
DB 395 YCGRQEAPPESCPCHSFDT 414

RESULT 10  
S45981  
probable membrane protein YBR113w - yeast (Saccharomyces cerevisiae)  
N;Alternate names: hypothetical protein YBR0908E  
C;Species: Saccharomyces cerevisiae  
C;Date: 26-Aug-1994 #sequence\_revision 09-Sep-1994 #text\_change 09-Jul-2004  
C;Accession: S45981  
R;Feldmann, H.; Mannhaupt, G.; Schwarzlouse, C.; Vetter, I.  
submitted to the Protein Sequence Database, August 1994  
A;Reference number: S45927  
A;Accession: S45981  
A;Molecule type: DNA  
A;Residues: 1-160 <FEL>  
A;Cross-references: UNIPROT:P38267; EMBL:Z35981; NID:G536449; PID:G536451; GSPDB:GN00002  
A;Experimental source: strain S288C  
C;Genetics:  
A;Gene: MIPS:YBR113w  
A;Cross-references: SGD:S0000317  
A;Map position: 2R  
C;Superfamily: Saccharomyces cerevisiae probable membrane protein YBR113w  
C;Keywords: transmembrane protein  
F;32-64/Domain: transmembrane #status predicted <TM1>  
F;67-89/Domain: transmembrane #status predicted <TM2>  
F;113-142/Domain: transmembrane #status predicted <TM3>

Query Match 15.5%; Score 61; DB 2; Length 160;  
Best Local Similarity 48.4%; Pred. No. 7.9;  
Matches 15; Conservative 4; Mismatches 10; Indels 2; Gaps 2;

QY 19 SFLLSFFFS-FQNCQFCQRTT-EGYAVE 47  
DB 68 SFLLIFFFQSCFVCCCCSCCSLSLKAYSSE 98

RESULT 11  
AC2432  
hypothetical protein all5011 [imported] - Nostoc sp. (strain PCC 7120)  
C;Species: Nostoc sp. PCC 7120  
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120  
C;Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Jul-2004  
C;Accession: AC2432  
R;Kaneke, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi  
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, S.  
DNA Res. 8, 205-213, 2001  
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana-  
baena sp. strain PCC 7120  
A;Reference number: AB1807; MUID:21595285; PMID:11759840  
A;Accession: AC2432  
A;Status: preliminary  
A;Molecule type: DNA

A:Residues: 1-320 <XUR>  
A:Cross-references: UNIPROT:QBYMC3; GB:BA000019; PIDN:BAB76710.1; PID:g17134149; GSPDB:B2  
A:Experimental source: strain PCC 7120  
C:Genetics:  
A:Gene: all5011

Query Match 15.5%; Score 61; DB 2; Length 320;  
Best Local Similarity 32.3%; Pred. No. 14;  
Matches 20; Conservative 6; Mismatches 30; Indels 6; Gaps 3;

QY 10 REKIKGNSSFFLLSFFFSFQNCOCFCQCRTEGYAVECFYCLVDKAAF---ECWFFYSF 66  
DB 229 RKANGG--GVLLAILPHYDQOOQMIQAYNEEGYCL-AGYCDVGKRYFLKNHCWYCPSF 285  
QY 67 DT 68  
DB 286 ST 287

RESULT 12  
A43932  
mucin 2 precursor, intestinal - human (fragments)  
N:Alternate names: mucin SMUC-41  
C:Species: Homo sapiens (man)  
C:Date: 10-Mar-1993 #sequence.revision 12-Apr-1996 #text\_change 09-Jul-2004  
C:Accession: A49963; A45106; B45106; A43932; B33532; A61257; PQ0328; PQ0329  
R:Gum Jr., J.R.; Hicks, J.W.; Toribara, N.W.; Siddiki, B.; Kim, Y.S.  
J. Biol. Chem. 269, 2440-2446, 1994  
A:Title: Molecular cloning of human intestinal mucin (MUC2) cDNA. Identification of the  
A:Reference number: A49963; MUID:94132002; PMID:8300571  
A:Accession: A49963  
A:Molecule type: mRNA  
A:Residues: 1-639 <GU1>  
A:Cross-references: UNIPROT:Q02817; UNIPROT:Q14884; GB:L21998  
R:Gum Jr., J.R.; Hicks, J.W.; Toribara, N.W.; Rothe, E.W.; Lagace, R.E.; Kim, Y.S.  
J. Biol. Chem. 267, 21375-21383, 1992  
A:Title: The human MUC2 intestinal mucin has cysteine-rich subdomains located both upstr  
A:Reference number: A45106; MUID:93016075; PMID:1400449  
A:Accession: A45106  
A:Status: not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 626-1895 <GU2>  
A:Cross-references: GB:M94131; NID:g186395; PIDN:AAA59163.1; PID:g186396  
A:Note: sequence extracted from NCBI backbone (NCBIP:116706)  
A:Accession: B45106  
A:Status: not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 2037-3020 <GU3>  
A:Cross-references: GB:M94132; NID:g186397; PIDN:AAA59164.1; PID:g186398  
A:Experimental source: colon  
A:Note: sequence extracted from NCBI backbone (NCBIP:116698)  
R:Toribara, N.W.; Gum Jr., J.R.; Culhane, P.J.; Lagace, R.E.; Hicks, J.W.; Petersen, G.M  
J. Clin. Invest. 88, 1005-1013, 1991  
A:Title: MUC-2 human small intestinal mucin gene structure. Repeated arrays and polymor  
A:Reference number: A43932; MUID:91358717; PMID:1885763  
A:Accession: A43932  
A:Molecule type: DNA  
A:Residues: 1343-1350, 'L', 1352-1411, 'S', 1413-1448, 'P', 1450-1503, 'T', 1505-1915 <TOR>  
A:Cross-references: GB:M74027; NID:g188863; PIDN:AAA59875.1; PID:g188864  
A:Note: sequence inconsistent with the nucleotide translation  
A:Note: sequence extracted from NCBI backbone (NCBIN:55749, NCBIP:55750)  
R:Gum, J.R.; Byrd, J.C.; Hicks, J.W.; Toribara, N.W.; Lampert, D.T.A.; Kim, Y.S.  
J. Biol. Chem. 264, 6480-6487, 1989  
A:Title: Molecular cloning of human intestinal mucin cDNAs. Sequence analysis and eviden  
A:Reference number: A43532; MUID:89197956; PMID:2703501  
A:Accession: B33532  
A:Molecule type: mRNA  
A:Residues: 1916-2193 <GU4>  
A:Cross-references: GB:M22405; NID:g188873; PIDN:AAA36334.1; PID:g188874  
A:Experimental source: intestine  
R:Jany, B.H.; Gallup, M.W.; Yan, P.S.; Gum, J.R.; Kim, Y.S.; Basbaum, C.B.  
J. Clin. Invest. 87, 77-82, 1991  
A:Title: Human bronchus and intestine express the same mucin gene.

C;Accession: Tl1124  
R;Scouras, A.; Smith, M.J.  
submitted to the EMBL Data Library, February 1998

A;Description: The complete mitochondrial genome of the crinoid *Florometra serratissima*.

A;Reference number: Z17249

A;Accession: Tl1124

A;Status: preliminary; translated from GB/EMBL/DDBBJ

A;Molecule type: DNA

A;Residues: 1-457 <SUN>

A;Cross-references: UNIPROT:O63595; EMBL:AF049132; NID:g2970420; PID:g2970431; PIDN:AADDO

C;Genetics:

A;Genome: mitochondrion

C;Superfamily: NADH dehydrogenase (ubiquinone) chain 4

C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;

Query Match 15.3%; Score 60; DB 2; Length 457;  
Best Local Similarity 30.4%; Pred.No. 24;  
Matches 14; Conservative 5; Mismatches 13; Indels 14; Gaps 1;

Qy 21 FLISFFPSFNCOCFCQCRTTEGVAVECFCLVDKAAFECEWFWYSF 66  
          ||||| : ||||| :  
Db 170 FLGLSPFPFNVCYIFB-----LYNSFSLSLWWFFTF 201  
               :|||

RESULT 15

Tl2791

hypothetical protein yomD - Bacillus subtilis phase SPBc2

C;Species: Bacillus subtilis phase SPBc2

C;Date: 13-Aug-1999 #sequence\_revision 13-Aug-1999 #text\_change 09-Jul-2004

C;Accession: Tl2791; D69910

R;Lazarevic, V.; Duesterhoeft, A.; Soldo, B.; Hilbert, H.; MaueI, C.; Karamata, D.

submitted to the EMBL Data Library, August 1997

A;Description: The complete nucleotide sequence of the *Bacillus subtilis* SPbetac2 prophage

A;Reference number: Z17583

A;Accession: Tl2791

A;Status: translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-274 <LAZ>

A;Cross-references: UNIPROT:O64041; EMBL:AF020713; NID:g3025478; PID:g3025505; PIDN:AACILC  
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berther  
C.; Bron, S.; Bouilliet, S.; Bruschii, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd  
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.  
Nature 390, 249-256, 1997

A;Authors: Foulgner, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallen  
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holtsappel, S.; Hosono, S.; Hulio, M.F.  
Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,  
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mauel  
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; PohI, T.M.; Portetelle  
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,  
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seron  
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpestra, P.; Tognoni, A.; Tosato, V.; Uchiyama, K.  
T.; Winters, P.; Wiopat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.  
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.

A;Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*.  
A;Reference number: A69580; MUID:98044033; PMID:9384377

A;Accession: D69910

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-274 <GUN>

A;Cross-references: GB:D39115; GB:AL009126; NID:g2634478; PIDN:CAB14058.1; PID:g2634560

A;Experimental source: strain 168

C;Genetics:

A;Gene: yomD

C;Superfamily: Bacillus subtilis phase SPBc2 hypothetical protein yomD

Query Match 15.1%; Score 59.5; DB 2; Length 274;  
Best Local Similarity 39.6%; Pred.No. 18;  
Matches 19; Conservative 5; Mismatches 15; Indels 9; Gaps 3;

Qy 22 LLSEFFFFNCOCFCQCRTTEGVAVECFCLVDKAAFECEWFWYS-FPT 68  
          ||||| : ||||| :  
Db 120 LPNFFFGE---ECFOCKAKKYTVGC-----QAFAESDRGFPLPFT 159  
               :|||

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 11, 2005, 06:57:07 ; Search time 40.8182 Seconds  
(without alignments)  
853.085 Million cell updates/sec

Title: US-10-092-934-8  
Perfect score: 393  
Sequence: 1 MFVFCILLNREKIKGNSSP.....FYCLVDKAAPECWFFYSFDT 68

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_03.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	74.5	19.0	462	2 Q5FL9	Q5FL9 leptospira
2	74.5	19.0	462	2 Q5EX1	Q5EX1 leptospira
3	70.5	17.9	2063	2 Q7R0L1	Q7R0L1 plasmodium
4	69	17.6	168	2 Q6YQ78	Q6YQ78 onion yello
5	67.5	17.2	1116	2 Q7FA2	Q7FA2 oryza sativ
6	67	17.0	133	2 Q5FL93	Q5FL93 candida gla
7	66.5	16.9	131	1 CD59_SAI5C	P47777 salmirel sci
8	66	16.8	122	2 Q6MSW2	Q6MSW2 mycoplasma
9	66	16.8	275	2 Q8S204	Q8S204 oryza sativ
10	65	16.5	304	2 Q894Q5	Q894Q5 clostridium
11	64.5	16.4	834	2 Q91C56	Q91C56 hepatitis b
12	64	16.3	1798	2 Q6ZM73	Q6ZM73 brachydanio
13	63.5	16.2	144	2 Q97454	Q97454 drosophila
14	63.5	16.2	975	2 Q84T13	Q84T13 arabidopsis
15	63.5	16.2	1162	2 Q9LY65	Q9LY65 arabidopsis
16	63	16.0	128	1 CD59_AOTTR	P51447 actus trivi
17	62.5	15.9	358	2 Q9SJZ9	Q9SJZ9 arabidopsis
18	62.5	15.9	531	2 Q47582	Q47582 onchocerca
19	62.5	15.9	531	2 Q70UR6	Q70UR6 dirofilaria
20	62.5	15.9	734	1 CD97_BOVIN	Q8SQA4 bos taurus
21	62.5	15.9	827	2 Q702T4	Q702T4 bos taurus
22	62	15.8	182	2 Q84455	Q84455 paramacium
23	62	15.8	428	2 Q9M029	Q9M029 arabidopsis
24	62	15.8	444	2 Q6DBH0	Q6DBH0 arabidopsis
25	62	15.8	844	2 Q8C804	Q8C804 mus musculu
26	62	15.8	1912	2 Q95226	Q95226 homo sapien
27	62	15.8	1966	1 CCAF_HUMAN	Q60840 homo sapien
28	62	15.8	1977	2 Q9UHB1	Q9UHB1 homo sapien
29	62	15.8	1981	2 Q92327	Q92327 rattus norv
30	62	15.8	1984	2 Q7TN13	Q7TN13 mus musculu
31	62	15.8	1985	1 CCAF_MOUSE	Q9JIS7 mus musculu

32	61.5	15.6	277	2 O62200	O62200 caenorhabdi
33	61.5	15.6	348	1 YGD9_YEAST	P53183 saccharomyc
34	61.5	15.6	657	1 PRIA_TREPA	O83258 treponema p
35	61.5	15.6	838	2 Q91C47	Q91C47 hepatitis b
36	61	15.5	128	1 CD59_CALSQ	P46657 callithrix
37	61	15.5	160	1 YBW3_YEAST	P38267 saccharomyc
38	61	15.5	231	2 Q813X1	Q813X1 plasmodium
39	61	15.5	234	2 Q8JJP7	O8JJP7 porcine lym
40	61	15.5	320	2 Q8YMC3	O8YMC3 anabaena sp
41	60.5	15.4	780	2 Q9WPF1	Q9WPF1 hepatitis b
42	60.5	15.4	5179	1 MUC2_HUMAN	Q02817 homo sapien
43	60	15.3	80	2 O21898	O21898 bacterioph
44	60	15.3	324	2 Q22283	Q22283 caenorhabdi
45	60	15.3	431	2 Q8XXQ6	Q8XXQ6 talstonia s

ALIGNMENTS

RESULT 1

ID	Q75FL9	PRELIMINARY;	PRT;	462 AA.
AC	Q75FL9;			
DT	05-JUL-2004 (TrEMBLrel. 27, Created)			
DT	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)			
DE	Hypothetical protein.			
GN	OrderedLocusNames=LIC20163;			
OS	Leptospira interrogans (serogroup Icterohaemorrhagiae / serovar Copenhageni).			
OC	Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.			
OX	NCBI_TaxID=44275;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Fiocruz L1-130;			
RX	PubMed=15028702; DOI=10.1128/JB.186.7.2164-2172.2004;			
RA	Nascimento A.L.T.O., Ko A.I., Martins E.A.L., Monteiro-Vitorello C.B., Ho P.L., Haake D.A., Verjovsky-Almeida S., Hartskeerl R.A., Marques M.V., Oliveira M.C., Menck C.F.M., Leite L.C.C., Carrer H., Coutinho L.L., Degraive W.M., Dellagostin O.A., El-Dorfi H., Ferro E.S., Ferro M.I.T., Furlan L.R., Gamberini M., Gigliotti E.A., Goes-Neto A., Goldman G.H., Goldman M.H.S., Harakava R., Jeronimo S.M.B., Junqueira-de-Azevedo J.L.M., Kimura E.T., Kuramae E.E., Lemos E.G.M., Lemos M.V.F., Marino C.L., Nunes L.R., de Oliveira R.C., Pereira G.G., Reis M.S., Schriefer A., Siqueira W.J., Sommer P., Tsai S.M., Simpson A.J.G., Ferro J.A., Camargo L.E.A., Kitajima J.P., Setubal J.C., Van Sluys M.A.; "Comparative genomics of two Leptospira interrogans serovars reveals novel insights into physiology and pathogenesis.";			
RT	J. Bacteriol. 186:2164-2172(2004).			
RL	EMBL; AE016824; AAS72191.1; -.			
KW	Complete proteome.			
SQ	SEQUENCE 462 AA; 54921 MW; 2FD430227AEC35F0 CRC64;			

Query Match 19.0%; Score 74.5; DB 2; Length 462;  
Best Local Similarity 26.5%; Pred. No. 1.9;  
Matches 22; Conservative 12; Mismatches 20; Indels 29; Gaps 4;

Qy	8 LNREKIKGG-----NSSFFLL---SFFSFONCCQCFQRTEGVAV 46
Db	286 LNFGEVGNGLRVLRHLSWEQRESLPYLNLTFWILFCTFFFNFKNIWKRFQIET-----I 340
Qy	47 ECFYCLVDKAAFEQW---FVSF 66
Db	341 LLLFWLPSILFYTWEGYFFEF 363

RESULT 2

ID	Q8EXK1	PRELIMINARY;	PRT;	462 AA.
AC	Q8EXK1;			
DT	01-MAR-2003 (TrEMBLrel. 23, Created)			
DT	01-MAR-2003 (TrEMBLrel. 23, Last sequence update)			

DT	01-MAR-2003 (TrEMBLrel. 23, Last annotation update)	DR	GO; GO:0003677; F:DNA binding; IEA.
DE	Hypothetical protein.	DR	GO; GO:0003774; F:motor activity; IEA.
GN	OrderedLocusNames=LB207;	DR	GO; GO:000160; P:two-component signal transduction system (p. . .; IEA.
OS	Leptospira interrogans.	DR	InterPro; IPR001451; Hexapep.transf.
OC	Bacteria; Spirochaetes; Spirochaetales; Leptospiaceae; Leptospira.	DR	InterPro; IPR001609; Myosin.head
OX	NCBI_TaxID=173;	DR	InterPro; IPR002078; Sig54.interact.
RN	[1]	DR	Pfam; PF00063; Myosin.head; 5.
RP	SEQUENCE FROM N.A.	DR	PRINTS; PR00193; MYOSINHEAVY.
RC	STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar lai;	DR	ProDom; PD000355; Myosin.head; 1.
RX	MEDLINE=22598143; PubMed=12712204; DOI=10.1038/nature01597;	DR	PROSITE; PS00101; HEXAPEP.TRANSFERASES; UNKNOWN_2.
RA	Ren S.-X., Fu G., Jiang X.-G., Zeng R., Miao Y.-G., Xu H.,	DR	PROSITE; PS00675; SIGWAS4.INTERACT.1; 1.
RA	Zhang Y.-X., Xiong H., Lu G., Lu L.-F., Jiang H.-Q., Jia J., Tu Y.-F.,	SQ	SEQUENCE 2063 AA; 240303 MW; 4DCB8E3B8E7D2ABA CRC64;
RA	Jiang J.-X., Gu W.-Y., Zhang Y.-Q., Cai Z., Sheng H.-H., Yin H.-F.,		
RA	Zhang Y., Zhu G.-F., Wan M., Huang H.-L., Qian Z., Wang S.-Y., Ma W.,		
RA	Yao Z.-J., Shen Y., Qiang B.-Q., Xia Q.-C., Guo X.-K., Danchin A.,		
RA	Saint Girons I., Somerville R.L., Wen Y.-M., Shi M.-H., Chen Z.,		
RA	Xu J.-G., Zhao G.-P.;		
RT	"Unique physiological and pathogenic features of Leptosira		
RT	interrogans revealed by whole-genome sequencing.";		
RL	Nature 422:888-893(2003).		
EMBL	AE011608; AAN51766.1; -.		
KW	Complete proteome.		
SQ	SEQUENCE 462 AA; 54887 MW; AFE8659C2B986B4C CRC64;		
	Query Match 19.0%; Score 74.5; DB 2; Length 462;		
	Best Local Similarity 26.5%; Pred. No. 1.9;		
	Matches 22; Conservative 12; Mismatches 20; Indels 29; Gaps 4;		
QY	8 LNREKIKGG-----NSSFFLL-----SFFSFQNCQCQCQTTEGYAV 46	QY	7 ILNREKIKGNSFFLLSFFSFQNCQCQCQTTEGYAVECFYCLVDKAAFCWPFYSF 66
DB	286 LNFEGVNGVRVLRHLSWEQRESFYNLNLTFWILFCTFFFNKNIWRFQIET-----I 340	DB	1095 IVNKNKIKINES----IKOFFNPFYNCCKPYAI-CTKGYENLCYTSFAKRLTMGSDIFQSI 1149
QY	47 ECFYCLVDKAAFCW---FYSF 66	QY	67 DT 68
DB	341 LLLFWLIPSLFYTWEGYFEF 363	DB	1150 ET 1151
RESULT 3		RESULT 4	
Q7RQL1	PRELIMINARY; PRT; 2063 AA.	Q6YQ78	PRELIMINARY; PRT; 168 AA.
AC	Q7RQL1	AC	Q6YQ78
DT	01-MAR-2004 (TrEMBLrel. 26, Created)	DT	05-JUL-2004 (TrEMBLrel. 27, Created)
DT	01-MAR-2004 (TrEMBLrel. 26, Last sequence update)	DT	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE	Myosin heavy chain.	DE	Hypothetical protein.
GN	Names=PY01085;	GN	OrderedLocusNames=PAM497;
OS	Plasmodium yoelii yoelii.	OS	Onion yellows phytoplasma.
OC	Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.	OC	Bacteria; Firmicutes; Mollicutes; Acholeplasmatales;
OX	NCBI_TaxID=73239;	OC	Acholeplasmataceae; Candidatus Phytoplasma.
RN	[1]	OX	NCBI_TaxID=100379;
RP	SEQUENCE FROM N.A.	RN	[1]
RC	STRAIN=17XNL;	RP	SEQUENCE FROM N.A.
RX	PubMed=12368865; DOI=10.1038/nature01099;	RC	STRAIN=OY-M;
RA	Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Perteza M.,	RA	PubMed=14661021; DOI=10.1038/ng1277;
RA	Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,	RA	Oshima K., Kakizawa S., Nishigawa H., Jung H.-Y., Wei W., Suzuki S.,
RA	Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,	RA	Arashida R., Nakata D., Miyata S.-I., Ugaki M., Namba S.;
RA	Shallom S.J., van Aken S.B., Riedmuller S.B., Feldblyum T.V.,	RT	"Reductive evolution suggested from the complete genome sequence of a
RA	Cho J.K., Quackenbush J., Sedegah M., Shoabi A., Cummings L.M.,	RT	plant-pathogenic phytoplasma.";
RA	Florens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A.,	RL	Nat. Genet. 36:27-29(2004).
RA	Cunningham D.A., Preiser P.R., Bergman L.W., Valcya A.B.,	DR	EMBL; AF006628; BAD04582.1; -.
RA	van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,	KW	Complete proteome.
RA	Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,	SQ	SEQUENCE 168 AA; 19313 MW; D7038A05C94A149E CRC64;
RA	Carucci D.J.;		
RT	"Genome sequence and comparative analysis of the model rodent malaria		
RT	parasite Plasmodium yoelii yoelii.";		
RL	Nature 419:512-519(2002).		
CC	-1- CAUTION: The sequence shown here is derived from an		
CC	EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is		
CC	preliminary data.		
DR	EMBL; AABL01000287; EAA20190.1; -.	QY	19 SFFLSFFSFQNCQCQCQCQTTEGYAVECFY-----CLVDKAAFCW----WFYS 65
DR	HSSP; Q02440; 10E9	DB	27 NFFSFFFSY-----CPSCCISFGSG--CSYFSFNSCATISKFNCFYVKLWFSS 75
DR	GO; GO:0016459; C:myosin; IEA.		
DR	GO; GO:0005524; F:ATP binding; IEA.		
		RESULT 5	
		Q7FAF2	PRELIMINARY; PRT; 1116 AA.
		ID	Q7FAF2
		AC	Q7FAF2
		DT	05-JUL-2004 (TrEMBLrel. 27, Created)
		DT	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
		DE	OSJNB0026E15.4 protein.
		GN	Names=OSJNB0026E15.4;
		OS	Oryza sativa (japonica cultivar-group).
		OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
		OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;



DR EMBL; CR380958; CAG61971.1; -. C2CA08223BE312A1 CRC64;  
SQ SEQUENCE 133 AA; 15668 MW; 2

Query Match 17.0%; Score 67; DB 2; Length 133;  
Best Local Similarity 28.2%; Pred. No. 4.7;  
Matches 20; Conservative 10; Mismatches 31; Indels 10; Gaps 2

QY 1 MFVFCILINREKIKGNSFFLLSP-----FFSFQNCOCFQRTTEGVAVCFYCLV 56  
DB 41 LLAICLLLHTRKPHLQSHAFNYFSISLFFDFENSCLVTVIQTYYVCACYYLLFYRG 100  
QY 57 AFECMWFYSFD 67  
DB 101 -----FHLFD 105

RESULT 7  
CD59\_SAISC STANDARD; PRT; 131 AA.  
ID\_CD59\_SAISC STANDARD; PRT; 131 AA.  
AC P47777;  
DT 01-FEB-1996 (Rel. 33, Created)  
DT 01-FEB-1996 (Rel. 33, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE CD59 glycoprotein precursor (Membrane attack complex inhibition factor) (MACIF) (MACIF) (MAC-inhibitory protein) (MAC-IP) (Protectin).  
DE Names=CD59;  
OS Saimiri sciureus (Common squirrel monkey).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Saimiri.  
OX NCBI\_TaxID=9521;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lung;  
RX MEDLINE=94118421; PubMed=75071185;  
RA Rother R.P., Rollins S.A., Fodor W.L., Albrecht J.-C., Setter E.,  
RA Fleckenstein B., Squinto S.P.,  
RT "Inhibition of complement-mediated cytolysis by the terminal  
complement inhibitor of herpesvirus saimiri.";  
RL J. Virol. 68:730-737(1994).  
CC -!- FUNCTION: Potent inhibitor of the complement membrane attack  
complex (MAC) action. Acts at or after the C5b-8 stage of MAC  
assembly.  
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (By  
similarity).  
CC -!- SIMILARITY: Contains 1 UPAR/Ly6 domain.  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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CC -----  
DR EMBL; L22859; AAA16747.1; -.  
DR PIR; I56894; I56894.  
DR HSP; P13987; 1CDS.  
DR InterPro; IPR001632; Ly-6 CD59.  
DR InterPro; IPR001526; Ly6\_UPAR.  
DR Pfam; PF00021; UPAR\_Ly6; 1.  
DR ProDom; PD003128; Ly-6\_CD59; 1.  
DR SMART; SM00134; LU; 1.  
DR PROSITE; PS00983; Ly6\_UPAR; FALSE NEG.  
KW Antigen; Glycoprotein; GPI-anchor; Lipoprotein; Signal.  
FT SIGNAL 1 25 By similarity.  
FT CHAIN 26 105 CD59 glycoprotein.  
FT PROPEP 106 131 Removed in mature form (By similarity).  
FT DOMAIN 26 111 UPAR/Ly6.  
FT DISULFID 28 54 By similarity.  
FT DISULFID 31 41 By similarity.  
FT DISULFID 47 67 By similarity.  
FT DISULFID 73 91 By similarity.  
FT DISULFID 92 97 By similarity.

OC Ehrhartoideae; Oryzeae; Oryza.  
OX NCBI\_TaxID=39947;  
RN [1]  
RP SEQUENCE FROM N.A.  
QY 4 FCILINREKIKGNSFFLLSP-FFSFQNCOCFQRT-----TEGVAVCFYCLV 53  
DB 387 YVAVQNRESIRPEN-YFVQWAFAGACIHAFQCSRMILCVDVAGADPKIIPVAFGV 444  
QY 54 DXAAFEQW-WF 63  
DB 445 ESENYESWLWF 455

RESULT 6  
Q6FL93 PRELIMINARY; PRT; 133 AA.  
ID\_Q6FL93 PRELIMINARY; PRT; 133 AA.  
AC Q6FL93;  
DT 05-JUL-2004 (TEMBLrel. 27, Created)  
DT 05-JUL-2004 (TEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TEMBLrel. 27, Last annotation update)  
DE Similarity.  
DE ORFNames=CAGL01052149;  
DE Candida glabrata CBS138.  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.  
OX NCBI\_TaxID=284593;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CBS138;  
RG Genolevures;  
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,  
RA Lafontaine J., de Montigny J., Marck C., Neuveglise C., Falla E.,  
RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,  
RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,  
RA Boismans A., Boyer J., Cattolico L., Confantolieri F., de Daruvar A.,  
RA Despons L., Fabre B., Fairhead C., Ferry-Dunast H., Groppi A.,  
RA Hantraye F., Hennequin C., Jaumiaux N., Joyet P., Kachouri R.,  
RA Kerrist A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,  
RA Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,  
RA Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,  
RA Sennene D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,  
RA Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,  
RA Bouchier C., Caudron B., Scarpell C., Gaillardin C., Weissenbach J.,  
RA Wincker P., Souciet J.L.;  
RT "Genome evolution in yeasts."  
RL Nature 430:35-44(2004).

DR EMBL; CR380958; CAG61971.1; -. C2CA08223BE312A1 CRC64;  
SQ SEQUENCE 133 AA; 15668 MW; 2

Query Match 17.0%; Score 67; DB 2; Length 133;  
Best Local Similarity 28.2%; Pred. No. 4.7;  
Matches 20; Conservative 10; Mismatches 31; Indels 10; Gaps 2

QY 1 MFVFCILINREKIKGNSFFLLSP-----FFSFQNCOCFCQRTTEGVAVCFYCLV 56  
DB 41 LLAICLLLHTRKPHLQSHAFNYFSISLFFDFENSILCVTIQTYVYVCACYLLFYRG 100  
QY 57 AFECMWFYSFD 67  
DB 101 -----FHLFD 105

RESULT 7  
CD59\_SAISC STANDARD; PRT; 131 AA.  
AC P47777;  
DT 01-FEB-1996 (Rel. 33, Created)  
DT 01-FEB-1996 (Rel. 33, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE CD59 glycoprotein precursor (Membrane attack complex inhibition factor) (MACIF) (MACIF) (MAC-inhibitory protein) (MAC-IP) (Protectin).  
DE Names=CD59;  
OS Saimiri sciureus (Common squirrel monkey).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Saimiri.  
OX NCBI\_TaxID=9521;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lung;  
RX MEDLINE=94118421; PubMed=75071185;  
RA Rother R.P., Rollins S.A., Fodor W.L., Albrecht J.-C., Setter E.,  
RA Fleckenstein B., Squinto S.P.,  
RT "Inhibition of complement-mediated cytolysis by the terminal  
complement inhibitor of herpesvirus saimiri";  
RL J. Virol. 68:730-737(1994).  
CC -!- FUNCTION: Potent inhibitor of the complement membrane attack  
complex (MAC) action. Acts at or after the C5b-8 stage of MAC  
assembly.  
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (By  
similarity).  
CC -!- SIMILARITY: Contains 1 UPAR/Ly6 domain.  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
between the Swiss Institute of Bioinformatics and the EMBL outstation  
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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; L22859; AAA16747.1; -.  
DR PIR; I56894; I56894.  
DR HSP; P13987; 1CDS.  
DR InterPro; IPR001632; Ly-6 CD59.  
DR InterPro; IPR001526; Ly6\_UPAR.  
DR Pfam; PF00021; UPAR\_Ly6; 1.  
DR ProDom; PD003128; Ly-6\_CD59; 1.  
DR SMART; SM00134; LU; 1.  
DR PROSITE; PS00983; Ly6\_UPAR; FALSE NEG.  
KW Antigen; Glycoprotein; GPI-anchor; Lipoprotein; Signal.  
FT SIGNAL 1 25 By similarity.  
FT CHAIN 26 105 CD59 glycoprotein.  
FT PROPEP 106 131 Removed in mature form (By similarity).  
FT DOMAIN 26 111 UPAR/Ly6.  
FT DISULFID 28 54 By similarity.  
FT DISULFID 31 41 By similarity.  
FT DISULFID 47 67 By similarity.  
FT DISULFID 73 91 By similarity.  
FT DISULFID 92 97 By similarity.

OC Ehrhartoideae; Oryzeae; Oryza.  
OX NCBI\_TaxID=39947;  
RN [1]  
RP SEQUENCE FROM N.A.  
QY 4 FCILINREKIKGNSFFLLSP-FFSFQNCOCFCQRT-----TEGVAVCFYCLV 53  
DB 387 YVAVQNRSIRPEN-YFVQWAFAGACIHAFQSRPMLCVDVAGADPKIIPVAFGV 444  
QY 54 DXAAFEQW-WF 63  
DB 445 ESENYESWLWF 455

RESULT 6  
Q6FL93 PRELIMINARY; PRT; 133 AA.  
ID Q6FL93  
AC Q6FL93;  
DT 05-JUL-2004 (TEMBLrel. 27, Created)  
DT 05-JUL-2004 (TEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TEMBLrel. 27, Last annotation update)  
DE Similarity.  
DE ORFNames=CAGL01052149;  
GN Candida glabrata CBS138.  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.  
OX NCBI\_TaxID=284593;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CBS138;  
RG Genolevures;  
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,  
RA Lafontaine J., de Montigny J., Marck C., Neuveglise C., Falla E.,  
RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,  
RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,  
RA Boismans A., Boyer J., Cattolico L., Confantolieri F., de Daruvar A.,  
RA Despons L., Fabre B., Fairhead C., Ferry-Dumazet H., Groppi A.,  
RA Hantraye F., Hennequin C., Jaumiaux N., Joyet P., Kachouri R.,  
RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,  
RA Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,  
RA Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,  
RA Sennenne D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,  
RA Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,  
RA Bouchier C., Caudron B., Scarpell C., Gaillardin C., Weissenbach J.,  
RA Wincker P., Souciet J.L.;  
RT "Genome evolution in yeasts."  
RL Nature 430:35-44(2004).

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FT CARBOHYD 46 46 N-linked (GlcNAc...) (Potential).
FT LIPID 105 105 GPI-anchor amidated asparagine (By
FT similarity).
SQ SEQUENCE 131 AA; 14355 MW; 47A739CBE9B4609E CRC64;

Query Match 16.9%; Score 66.5; DB 1; Length 131;
Best Local Similarity 27.9%; Pred. No. 5.3;
Matches 19; Conservative 9; Mismatches 23; Indels 17; Gaps 3;

QY 13 IKGNSSF---FLLSFFSFQNCQFCQRTTEGYAVECF-----YCLVDVAAA-- 57
Db 3 IQGGSVLFGLLLVLAFCVCHSGNSLQCYSCPLPTMESWECTASTNCTNSLDCLIAKAGSG 62
QY 58 --FECWVF 63
Db 63 VYRCWK 70

RESULT 8
Q6MSW2 PRELIMINARY; PRT; 122 AA.
AC Q6MSW2
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical transmembrane protein.
GN OrderedLocusNames=MSC_0655;
OS Mycoplasma mycoides (subsp. mycoides SC).
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=44101;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PG1;
RX PubMed=14762060; DOI=10.1101/gr.1673304;
RA Westberg J., Persson A., Holmberg A., Goemann A., Lundeberg J.,
RA Johansson K.-E., Pettersson B., Uhlen M.;
RT "The genome sequence of Mycoplasma mycoides subsp. mycoides SC type
RT strain PG1T, the causative agent of contagious bovine pleuropneumonia
RT (CBPP).";
RL Genome Res. 14:221-227(2004).
DR ENBL; BX842644; CAF77276.1; -.
DR InterPro; IPR006121; HeavyMe transp.
DR PROSITE; PS01047; HMA_1; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 122 AA; 14492 MW; 8A57797DCACB3107 CRC64;

Query Match 16.8%; Score 66; DB 2; Length 122;
Best Local Similarity 25.0%; Pred. No. 5.7;
Matches 14; Conservative 9; Mismatches 11; Indels 22; Gaps 2;

QY 22 LLSFFSFQNCQFCQRTTEGYAVECFYCLVDKAA-----FECWVFSEF 67
Db 1 MLNHFNLWLCSS-----NCSFLFNKLYWNSCNLINFSCWNFNSFN 44

RESULT 9
Q8S204 PRELIMINARY; PRT; 275 AA.
AC Q8S204
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE P0468B07.4 protein.
GN Name=P0468B07.4;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=12447438; DOI=10.1038/nature01184;
RA Sasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y.,

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RA Wu J., Nilmura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H.,
RA Hosokawa S., Masukawa M., Arikawa K., Chiden Y., Hayashi M.,
RA Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C.,
RA Hijishita S., Honda M., Ichikawa Y., Idonuma A., Iijima M., Ikeda M.,
RA Ikono M., Itoh S., Itoh T., Itoh Y., Itoh Y., Iwabuchi A., Kamiya K.,
RA Karsawa W., Katagiri S., Kikuta A., Kobayashi N., Kono I.,
RA Machita K., Maehara T., Mizuno H., Mizubayashi T., Nakai Y.,
RA Nagasaki H., Nakashima M., Nakama Y., Nakamichi Y., Nakamura M.,
RA Namiki N., Negishi M., Ohta I., Ono N., Saji S., Sakai, K, Shibata M.,
RA Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Tsuji K.,
RA Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K.,
RA Zhong H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.I., Eun M.Y.,
RA Yano M., Jiang J., Gojobori T.;
RT "The genome sequence and structure of rice chromosome 1.";
RL Nature 420:312-316(2002).
DR EMBL; AP003260; BAB89625.1; -.
DR Gramene; Q8S204; -.
DR InterPro; IPR006209; EGF_like.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
SQ SEQUENCE 275 AA; 30430 MW; 480644D61BF9B121 CRC64;

Query Match 16.8%; Score 66; DB 2; Length 275;
Best Local Similarity 33.3%; Pred. No. 12;
Matches 21; Conservative 7; Mismatches 23; Indels 12; Gaps 3;

QY 2 FVFCILNREKIKGNSSFLLS-----FFFSFQNCQFCQRTTEGYAVECFYCL-VDK 55
Db 186 FVYSLIITAVNHGPDRTGTGVPATVQAFSSANLNCNCFSPSL-----IFVCLATDR 239
QY 56 AAF 58
Db 240 ALF 242

RESULT 10
Q894Q5 PRELIMINARY; PRT; 304 AA.
AC Q894Q5
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Conserved protein, putative ferredoxin-type protein naph.
GN Name=naph; OrderedLocusNames=CtC01480;
OS Clostridium tetani.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1513;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Massachusetts / E88;
RX MEDLINE=22457253; PubMed=12552129; DOI=10.1073/pnas.0335853100;
RA Brueggemann H., Baumer S., Fricke W.F., Wierer A., Liesegang H.,
RA Decker I., Herzberg C., Martinez-Arias R., Merkl R., Henne A.,
RA Gottschalk G.;
RT "The genome sequence of Clostridium tetani, the causative agent of
RT tetanus disease.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:1316-1321(2003).
DR EMBL; AE015941; AAO36037.1; -.
DR HSSP; P24184; 1KQF.
DR GO; GO:0005489; F:electron transporter activity; IEA.
DR GO; GO:0005506; F:iron ion binding; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR001450; 4Fe4S_ferredoxin.
DR Pfam; PF00037; Fer4; 2.
DR PRINTS; PR00353; 4FE4SFRDOXIN.
DR PROSITE; PS00198; 4FE4S_FERREDOXIN; 1.
KW 4Fe-4S; Complete proteome; Iron; Iron-sulfur; Metal-binding.
SQ SEQUENCE 304 AA; 34263 MW; 03E4B0F10EDC52EA CRC64;

Query Match 16.5%; Score 65; DB 2; Length 304;
Best Local Similarity 27.9%; Pred. No. 17;
Matches 19; Conservative 6; Mismatches 25; Indels 18; Gaps 3;

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QY 15 GGNSSFF-----LLSFFSFQNCOCFOCR-----TTGAYVECFYCL--VDKA 56
Db 221 GAFYSFNKISLSYDFNKDCNVCKGRVCKRMDVDITKSTTHNECIRGCEIKVCPTK 280
QY 57 AFECWFY 64
Db 281 AISTFWGY 288

RESULT 11
Q91C56 PRELIMINARY; PRT; 834 AA.
AC Q91C56;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Polymerase.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21361467; PubMed=11468728; DOI=10.1002/jmv.1070;
RA Owiredu W.K., Kramvis A., Kew M.C.;
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR GO; GO:0005786; C:signal recognition particle (sensu Eukaryota); IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0003887; F:DNA-directed DNA polymerase activity; IEA.
DR GO; GO:0004523; F:ribonuclease H activity; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006050; P:protein targeting; IEA.
DR GO; GO:0006278; P:RNA-dependent DNA replication; IEA.
DR Pfam; PF00336; DNA_pol_viral_C; 1.
DR Pfam; PF00242; DNA_pol_viral_N; 1.
DR Pfam; PF00078; RVT_1; 2.
DR PrdDom; PD000814; DNAPol_viral_C; 1.
DR RNA-directed DNA polymerase; Transferase.
SQ SEQUENCE 834 AA; 93927 MW; CEEA31F2A2230515 CRC64;

Query Match 16.4%; Score 64.5; DB 2; Length 834;
Best Local Similarity 37.1%; Pred. No. 47;
Matches 13; Conservative 6; Mismatches 7; Indels 9; Gaps 2;

QY 36 FQCHTTGAYVECFYCLVDKAA-----FECHW 62
Db 283 FEKHSNGHAYE-FHCLAPSSAGSQRGSVFPCW 316

RESULT 12
Q62M73 PRELIMINARY; PRT; 1798 AA.
AC Q62M73;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE SI:zK70P6.5 (Novel protein similar to vertebrate voltage-dependent
DE calcium channel P/Q type alpha 1 subunit (CACNA1)) (Fragment).
GN Name=cacna1f; Synonyms=SI:zK70P6.5;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; danio.
OX NCBI_TaxID=7955;
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RN [1]
RP SEQUENCE FROM N.A.
RA Beasley H.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
CC -I- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -I- SIMILARITY: Belongs to the calcium channel alpha-1 subunits
CC family.
DR EMBL; AL331748; CAE50430.1; -.
DR ZFIN; ZDB-GENE-031104-1; cacna1f.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005891; C:voltage-gated calcium channel complex; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0005245; F:voltage-gated calcium channel activity; IEA.
DR GO; GO:0006816; P:calcium ion transport; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR InterPro; IPR001682; Ca_Na_pore.
DR InterPro; IPR002111; Cat_channel_TripL.
DR InterPro; IPR002077; Ca_channel_alpha.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR000463; Fatty_acid_BP.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR005446; LVDCALphal.
DR InterPro; IPR005820; M+channel_nlg.
DR Pfam; PF00520; Ion_trans_4.
DR PRINTS; PR00167; CCHANNEL.
DR PRINTS; PR01630; LVDCALPHAL.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
DR PROSITE; PS00214; FASP; UNKNOWN_1.
KW Calcium; Calcium channel; Calcium transport; Calcium-binding;
KW Ion transport; Ionic channel; Transmembrane; Transport;
KW Voltage-gated channel.
FT NON_TER 1
SQ SEQUENCE 1798 AA; 202714 MW; 7E9EF983772AF2DD CRC64;

Query Match 16.3%; Score 64; DB 2; Length 1798;
Best Local Similarity 36.0%; Pred. No. 1.le+02;
Matches 18; Conservative 7; Mismatches 19; Indels 6; Gaps 3;

QY 15 GGNSSFFLLSFFSFQNCOCFOCRTTGAYVECFYCLVDKAAFECHWY 64
Db 217 GGITNFD--NFFAM--LTVFCITMEGW-TDVLWNDAIGFELPWVY 260

RESULT 13
O97454 PRELIMINARY; PRT; 144 AA.
AC O97454;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE CG1639-PA (L(1)10Bb) (RE22390p).
GN Name=l(1)10Bb; Synonyms=lethal(1)10Bb; ORFNames=CG1639;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Ananidis P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandal M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Abell J.F., Agbayani A., An H.J., Andrews-Frankoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
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Job time : 43.812 secs

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OM protein - protein search, using sw model

Run on: October 11, 2005, 06:57:07 ; Search time 50.3636 Seconds  
(without alignments)  
522.196 Million cell updates/sec

Title: US-10-092-934-8  
Perfect score: 393  
Sequence: 1 MFVFCILILNREKIKGNSSF.....FYCLVDKAAECWFWFYSDT 68

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq16Dec04:.\*  
1: Geneseqp1980s:.\*  
2: Geneseqp1990s:.\*  
3: Geneseqp2000s:.\*  
4: Geneseqp2001s:.\*  
5: Geneseqp2002s:.\*  
6: Geneseqp2003as:.\*  
7: Geneseqp2003bs:.\*  
8: Geneseqp2004s:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	393	100.0	68	2 AAR63236	Aar63236 Neural th
2	393	100.0	68	2 AAR95915	Aar95915 AD 2-2 hu
3	393	100.0	68	5 AAE29149	Aae29149 Neural th
4	393	100.0	68	6 ABR63247	AbR63247 68 amino
5	393	100.0	68	6 ABU02979	Abu02979 Human neu
6	393	100.0	68	6 ABP59929	Abp59929 Human 68
7	393	100.0	68	6 AAE33196	Aae33196 Neural th
8	393	100.0	68	6 ABJ19452	Abj19452 68-mer ne
9	393	100.0	68	7 ADB37526	Adb37526 Neural th
10	393	100.0	68	7 ADL96027	Adl96027 Human neu
11	143	36.4	23	6 ABP59919	Abp59919 Human neu
12	143	36.4	23	7 ADL96065	Adl96065 Human neu
13	95	24.2	15	6 ABP59918	Abp59918 Human neu
14	95	24.2	15	7 ADL96064	Adl96064 Human neu
15	78	19.8	15	6 ABP59916	Abp59916 Human neu
16	78	19.8	15	7 ADL96062	Adl96062 Human neu
17	77	19.6	15	6 ABP59917	Abp59917 Human neu
18	77	19.6	15	7 ADL96063	Adl96063 Human neu
19	74.5	19.0	89	4 AAO02088	Aao02088 Human pol
20	67	17.0	322	4 AAU30371	Aau30371 Novel hum
21	66.5	16.9	109	7 ADC94958	Adc94958 E. faeciu
22	66.5	16.9	131	2 AAR66985	Aar66985 Squirrel
23	66.5	16.9	131	2 AAR86311	Aar86311 Ly-6 term
24	66	16.8	298	7 ADC87387	Adc87387 Human GPC
25	64.5	16.4	294	7 ADC87411	Adc87411 Human GPC

26	64.5	16.4	296	8 ADJ66555	Adj66555 Her4 prot
27	64	16.3	50	2 AAY41329	Aay41329 Human sec
28	63.5	16.2	144	4 ABB58329	Abb58329 Drosophil
29	63.5	16.2	887	8 ADN72853	Adn72853 Thale cre
30	63	16.0	30	8 ADS33534	Ads33534 CMET-HGF
31	63	16.0	128	2 AAR66986	Aar66986 Owl Monke
32	63	16.0	128	2 AAR86312	Aar86312 Ly-6 term
33	62	15.8	1824	3 AAY49431	Aay49431 Murine CA
34	62	15.8	1912	3 AAY49429	Aay49429 Human CAC
35	62	15.8	1977	3 AAY49430	Aay49430 Human CAC
36	61.5	15.6	58	2 AAB30720	Aab30720 Amino aci
37	61.5	15.6	163	3 AAB53407	Aab53407 Human col
38	61.5	15.6	301	4 AAB87732	Aab87732 Human T2R
39	61.5	15.6	301	8 ADR29064	Adr29064 Taste rec
40	61.5	15.6	302	8 ADJ84484	Adj84484 Human T2R
41	61.5	15.6	348	2 AAY05773	Aay05773 Saccharom
42	61.5	15.6	348	7 ADF39747	Adf39747 Yeast Ygl
43	61.5	15.6	449	7 ADC87301	Adc87301 Human GPC
44	61	15.5	96	4 AAM94740	Aam94740 Human rep
45	61	15.5	96	4 AAU22762	Aau22762 Human pro

ALIGNMENTS

RESULT 1

AAR63236	Neural thread protein AD2-2 T7.
ID AAR63236	standard; protein; 68 AA.
XX	
AC AAR63236;	
XX	
DT 25-MAR-2003	(revised)
DT 06-JUL-1995	(first entry)
XX	
DE	Neural thread protein AD2-2 T7.
XX	
KW	Neural thread protein AD2-2 T7; Alzheimer's; neuroectodermal tumours;
KW	malignant astrocytomas; glioblastomas.
XX	
OS	Rattus rattus.
XX	
PH	Key
FT	Location/Qualifiers
FT	Misc-difference 67..68
FT	/note= "corresponding codons GCA CAT CAC GAC ATT TTA TAA"
XX	
PN	W09423756-A1.
XX	
PD	27-OCT-1994.
XX	
XX	
PF	20-APR-1994; 94WO-US0004321.
XX	
PR	20-APR-1993; 93US-00050559.
XX	
PA	(GEHO ) GEN HOSPITAL CORP.
XX	
PI	De La Monte SM, Wands JR;
XX	
DR	WPI; 1994-341497/42.
XX	
DR	N-PSDB; AAQ77872.
XX	
PT	Detection of neural thread proteins - to detect sporadic and familial
PT	Alzheimer's disease, neuroectodermal tumours, malignant astrocytomas and
PT	glioblastomas (Eng).
XX	
PS	Example 4; Fig 16a; 158pp; English.
XX	
CC	AAQ77872 encodes AAR63236 the AD2-2 T7 neural thread protein (NTP). These
CC	sequences were used in the development of an antibody dependent method,
CC	for the detection of NTPs. This new method could be used to diagnose
CC	Alzheimer's disease (differentiating between sporadic and familial),
CC	neuroectodermal tumours, malignant astrocytomas and glioblastomas.
XX	(Updated on 25-MAR-2003 to correct PN field.)

```

SQ Sequence 68 AA;
Query Match 100.0%; Score 393; DB 2; Length 68;
Best Local Similarity 100.0%; Pred. No. 5.8e-37;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFVFCILNREKIKGNSPFLLSFFPFCQCFQCRTEGYAVECFCLVDKAAFE 60
DB 1 MFVFCILNREKIKGNSPFLLSFFPFCQCFQCRTEGYAVECFCLVDKAAFE 60

QY 61 WWFYSPDT 68
DB 61 WWFYSPDT 68

RESULT 2
AAR95915
ID AAR95915 standard; protein; 68 AA.
XX AC AAR95915;
XX DT 14-NOV-1996 (first entry)
XX DE AD 2-2 human neural thread protein clone (partial sequence).
XX KW Neural thread protein; NTP; diagnosis; detection; Alzheimer's disease;
KW neuroectodermal tumour; malignant astrocytoma; monoclonal antibody;
KW binding fragment.
XX OS Homo sapiens.
XX PN WO9615272-A1.
XX PD 23-MAY-1996.
XX PF 14-NOV-1995; 95WO-US017111.
XX PR 14-NOV-1994; 94US-00340426.
XX PA (GEHO ) GEN HOSPITAL CORP.
XX PI De La Monte S, Wands JR;
XX DR WPI; 1996-259865/26.
XX DR N-PSDB; AAT27754.
XX PT Detection of neural thread protein in diagnosis of Alzheimer's disease -
XX also NTP DNA and protein sequences used in gene and anti:sense therapy.
XX PS Example 4c; Fig 16A; 238pp; English.
XX CC A method for detecting the presence of neural thread protein (NTP) having
XX a molecular weight of 8, 14, 17, 21, 26 or 42 kD in a human subject
XX comprises (a) contacting a sample from a human subject that is suspected
XX of containing the NTP with at least one molecule capable of binding to
XX the protein; and (b) detecting any of the molecule bound to the protein.
XX The binding molecule is selected from an antibody free of natural
XX impurities, a monoclonal antibody or a binding fragment of either of
XX these. The method may be used for diagnosing the presence of Alzheimer's
XX disease, neuroectodermal tumours and a malignant astrocytoma in a human.
XX A number of clones of neural thread protein were isolated from healthy 17
XX -18 week old foetal human brain (HB) 2 year old temporal lobe neocortex
XX and end stage Alzheimer's disease (AD) cerebral cortex. See AAT27753-75
XX
SQ Sequence 68 AA;
Query Match 100.0%; Score 393; DB 2; Length 68;
Best Local Similarity 100.0%; Pred. No. 5.8e-37;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFVFCILNREKIKGNSPFLLSFFPFCQCFQCRTEGYAVECFCLVDKAAFE 60
DB 1 MFVFCILNREKIKGNSPFLLSFFPFCQCFQCRTEGYAVECFCLVDKAAFE 60

QY 61 WWFYSPDT 68
DB 61 WWFYSPDT 68

RESULT 3
AAE29149
ID AAE29149 standard; protein; 68 AA.
XX AC AAE29149;
XX DT 27-JAN-2003 (first entry)
XX DE Neural thread protein (NTP) #7.
XX KW Neural thread protein; NTP; hyperplasia; hypertrophy; arteriosclerosis;
KW haemorrhoid; gene therapy; tumour; vascular disease; atherosclerosis;
KW inflammatory disease; nutritional deficiency disease; genetic disease;
KW autoimmune disease; metabolic disease; traumatic disease; intoxication;
KW infectious disease; congenital malformation; enzyme deficiency disease;
KW amyloid disease; fibrosis disease; storage disease; radiation disease;
KW poisoning; environmental disease; endocrine disease; protein therapy;
KW degenerative disease; mechanical disease.
XX OS Unidentified.
XX PN WO200274323-A2.
XX PD 26-SEP-2002.
XX PF 08-MAR-2002; 2002WO-IB001959.
XX PR 08-MAR-2003; 2001US-0273957P.
XX PA (AVER/) AVERBACK P.
XX PI Averbach P;
XX DR WPI; 2002-759864/82.
XX PT Treating a condition in a patient requiring removal or destruction of
XX cells, such as a benign or malignant tumor of a tissue or an inflammatory
XX disease, comprises administering a neural thread protein (NTP) or a NTP
XX gene to a mammal.
XX PS Claim 23; Fig 8; 70pp; English.
XX CC The invention relates to a method for treating a condition in a patient
XX requiring removal or destruction of cells. The method involves
XX administering to a mammal a neural thread protein (NTP), or administering
XX to a tumour or other target cell a NTP gene, where the expression of the
XX NTP gene is induced resulting in expression of the NTP protein. The
XX method and NTP are useful for treating a condition in a patient requiring
XX removal or destruction of cells, such as a benign or malignant tumour of
XX a tissue, a hyperplasia, hypertrophy, or overgrowth of a tissue.
XX Preferably tonsillar hypertrophy or prostatic hyperplasia, a virally,
XX bacterially, or parasitically altered tissue, or a malformation of a
XX tissue. Other conditions include a cosmetic modification to a tissue,
XX such as removal of unwanted facial hair, warts or unwanted fatty tissue,
XX a vascular disease, particularly atherosclerosis or arteriosclerosis,
XX haemorrhoids, or varicose veins, an inflammatory disease, autoimmune
XX disease, metabolic disease, hereditary/genetic disease, traumatic disease
XX or physical injury, nutritional deficiency disease, infectious disease,
XX congenital malformation, amyloid disease, fibrosis disease, storage
XX disease, enzyme deficiency disease, poisoning, intoxication, degenerative
XX disease, radiation disease, environmental disease, endocrine disease or
XX mechanical disease. The invention is useful in protein therapy and gene
XX therapy. The present sequence is NTP protein
XX
SQ Sequence 68 AA;
Query Match 100.0%; Score 393; DB 5; Length 68;

```



Best Local Similarity 100.0%; Pred. No. 5.8e-37;  
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFVFLILNREKIKGNSFFLLSFFSFQNCOCFQCRTEGYAVECFYCLVDKAAFEK 60  
DB 1 MFVFLILNREKIKGNSFFLLSFFSFQNCOCFQCRTEGYAVECFYCLVDKAAFEK 60

QY 61 WWFYSDFT 68  
DB 61 WWFYSDFT 68

RESULT 4  
ABR63247  
ID ABR63247 standard; protein; 68 AA.  
XX AC ABR63247;  
XX DT 28-AUG-2003 (first entry)  
XX DE 68 amino acid neural thread protein.  
XX CYTOSTATIC; Antibacterial; Immunosuppressive; Antiinflammatory;  
KW neural thread protein; NTP; tumour.  
XX Unidentified.  
XX WO2003008443-A2.  
XX 30-JAN-2003.  
XX 19-JUL-2002; 2002WO-CA001105.  
XX 19-JUL-2001; 2001US-0306150P.  
XX 19-JUL-2001; 2001US-0306161P.  
XX 16-NOV-2001; 2001US-0331477P.  
XX (NYMO-) NYMOX CORP.  
XX AVERBACK PA;  
XX WPI; 2003-247999/24.  
XX Novel neural thread protein peptide, referred as cell death peptide,  
PT useful for treating prostatic hyperplasia, psoriasis, eczema, dermatosis,  
PT atherosclerosis, cosmetic modification to skin, throat, mouth, muscle.  
XX Disclosure; Fig 8; 77pp; English.

XX The present invention relates to a neural thread protein (NTP) peptide  
CC referred to as cell death peptide. Thought to be cytostatic,  
CC antibacterial, immunosuppressive and antiinflammatory. It is useful for  
CC treating a condition in a patient requiring removal or destruction of  
CC cells, for treating a condition such as benign or malignant tumor,  
CC inflammatory disease, autoimmune disease and infectious disease. The  
CC peptide useful for treatment is derived from the amino acid sequence for  
CC a pancreatic thread protein. The peptide is conjugated, linked or bound  
CC to a molecule chosen from antibody or its fragment, antibody-like binding  
CC molecule, where the molecule has a higher affinity for binding to a tumor  
CC or other target than binding to other cells. Treatment using NTP peptides  
CC can remove benign tumors with less risk and fewer of the undesirable side  
CC effects of surgery. The present sequence is an NTP amino acid sequence

SQ Sequence 68 AA;  
Query Match 100.0%; Score 393; DB 6; Length 68;  
Best Local Similarity 100.0%; Pred. No. 5.8e-37;  
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFVFLILNREKIKGNSFFLLSFFSFQNCOCFQCRTEGYAVECFYCLVDKAAFEK 60  
DB 1 MFVFLILNREKIKGNSFFLLSFFSFQNCOCFQCRTEGYAVECFYCLVDKAAFEK 60

QY 61 WWFYSDFT 68  
DB 61 WWFYSDFT 68

RESULT 5  
ABU02979  
ID ABU02979 standard; protein; 68 AA.  
XX AC ABU02979;  
XX DT 20-JAN-2003 (first entry)  
XX DE Human neural thread protein AD7C-NTP, protein fragment #7.  
XX KW Neural thread protein; NTP-peptide; AD7C-NTP; surgical excision;  
KW transplantation; grafting; chemotherapy; immunotherapy; vaccination;  
KW ablation; cryotherapy; laser therapy; phototherapy; gene therapy;  
KW radiation; tumour; hyperplasia; hypertrophy; overgrowth of tissue;  
KW malformation of tissue; tonsillary hypertrophy; prostatic hyperplasia;  
KW cosmetic modification; vascular disease; atherosclerosis;  
KW arteriosclerosis; haemorrhoid; varicose vein; inflammatory disease;  
KW autoimmune disease; metabolic disease; traumatic disease;  
KW physical injury; nutritional deficiency disease; infectious disease;  
KW amyloid disease; fibrosis disease; storage disease;  
KW congenital malformation; enzyme deficiency disease; poisoning;  
KW intoxication; environmental disease; radiation disease;  
KW endocrine disease; degenerative disease; mechanical disease.  
XX Homo sapiens.  
XX OS  
XX WO200297030-A2.  
XX 05-DEC-2002.  
XX 24-MAY-2002; 2002WO-CA000759.  
XX 25-MAY-2001; 2001US-0293156P.  
XX (NYMO-) NYMOX CORP.  
XX AVERBACK PA;  
XX WPI; 2003-041406/03.  
XX Novel peptides similar in amino acid sequence to neural thread proteins  
PT (NTP), useful for treating unwanted cellular proliferations such as  
PT malignant tumors and prostatic hyperplasia.  
XX Disclosure; Fig 8; 78pp; English.

XX The invention describes an NTP-peptide (I) comprising at least one amino  
CC acid sequence corresponding to part of the amino acid sequence of a  
CC neural thread protein, AD7C-NTP. The invention provides a method of  
CC treating a condition requiring removal or destruction of cells of a  
CC mammal comprising administering to a mammal, a therapeutic amount of (I).  
CC The treatment is administered to the mammal before, during or after  
CC surgical excision, transplantation, grafting, chemotherapy,  
CC immunotherapy, vaccination, thermal or electrical ablation, cryotherapy,  
CC laser therapy, phototherapy, gene therapy and/or radiation. The method is  
CC useful for treatment of benign or malignant tumour; hyperplasia,  
CC hypertrophy or overgrowth of tissue; virally, bacterially or  
CC parasitically altered tissue; malformation of tissue selected from lung,  
CC breast, stomach, pancreas, prostate, bladder, bone, ovary, skin, kidney,  
CC sinus, colon, intestine, rectum, esophagus, heart, spleen, salivary  
CC gland, blood, brain and its coverings, spinal cord, muscle, connective  
CC tissue, adrenal, parathyroid, thyroid, uterus, testis, pituitary, and  
CC reproductive organs, liver, hair, gall bladder, eye, ear, nose, throat,  
CC tonsils, mouth and lymph nodes and lymphoid system; tonsillary  
CC hypertrophy; prostatic hyperplasia; cosmetic modification to a tissue;  
CC vascular disease (atherosclerosis or arteriosclerosis); haemorrhoids;  
CC varicose veins; inflammatory disease; autoimmune disease; metabolic  
CC disease; hereditary/genetic disease; traumatic disease; physical injury;

CC nutritional deficiency disease, infectious disease, amyloid disease;  
CC fibrosis disease, storage disease, congenital malformation, enzyme  
CC deficiency disease, poisoning, intoxication, disease,  
CC radiation disease, endocrine disease, degenerative disease and chemical  
CC disease. This is the amino acid sequence of a human neural thread protein  
CC AD7C-NTP protein fragment  
XX  
SO Sequence 68 AA;

```
Query Match      100.0%; Score 393; DB 6; Length 68;
Best Local Similarity 100.0%; Pred. No. 5.8e-37;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

[illegible]

Qy 61 WFEYSFDT 68  
Db 61 WFEYSFDT 68

RESULT 6  
ABP59929  
ID ABP59929 standard; protein; 68 AA.

DT 08-SEP-2003 (first entry)

Human 68 amino acid neural thread protein; DE

Human; tumour; cancer; neural thread protein; NTP; cell removal;  
 cell destruction; antiporiatic; antimicrobial; immunosuppressive;  
 antiinflammatory; dermatological; antiarteriosclerotic; vasotropic;  
 gene therapy.

xx  
OS  
Homo sapiens.

WO200304053-A2

30-MAY-2003.

18-NOV-2002: 2002WO-CA001757.

PR 16-NOV-2001: 2001US-0331477P.

PA (NYMO-) NYMOX CORP.

PI Averbach P, Gemmell J;

DR WPI; 2003-457592/43.

New neural thread protein (NTP), useful for preparing a composition for treating or preventing a condition in a mammal requiring removal or destruction of cells, e.g. psoriasis, eczema, atherosclerosis or inflammatory disease.

PS Disclosure: Fig 6: 98pp: English.

The present invention relates to peptides derived from the human neural thread protein (NTP). The peptides are useful for preparing a composition for treating or preventing a condition in a mammal requiring removal or destruction of cells, comprising tonsillary hypertrophy, prostatic hyperplasia, psoriasis, eczema, dermatosis, cosmetic modification to a breast, connective, skin, eye, ear, nose, throat, mouth or muscle tissue, varicose veins, atherosclerosis, inflammatory, metabolic, infectious, fibrosis, endocrine or autoimmune disease, or stenosis, restenosis, occlusion or blockage of an artery or of a stent placed or implanted in an artery. The present sequence is an NTP protein used to produce peptides of the invention

Sequence 68 AA;

```

Query Match      100.0%; Score 393; DB 6; Length 68;
Best Local Similarity 100.0%; Pred. No. 5.8e-37;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFVFCLILNREKIKGNSSFFLLSFFPSFQNCFCQRTTEGYAVCEFCYCLVDKAAAFEC 60
    |||||
Db 1 MFVFCLILNREKIKGNSSFFLLSFFPSFQNCFCQRTTEGYAVCEFCYCLVDKAAAFEC 60
    |||||

Qy 61 WWFYSPDT 68
    |||||
Db 61 WWFYSPDT 68
    |||||

```

## RESULT 7

AAE33196

ID AAE33196 standard; protein; 68 AA.

AAE33196:

16-APR-2003 (first entry)

DE Neural thread protein (NTP) #7

Cell death; tissue necrosis; neural thread protein; NTP; amyloidosis;  
KW stroke; brain tumour; Pick's disease; Parkinson's disease; glaucoma;  
KW Alzheimer's disease; gene therapy.

OS Unidentified.

PN WO200289841-A2.

14-NOV-2002

XX  
PF  
06-MAY-2002. 2002WO-CA000681XX  
PP 04-MAY-2001: 2001US-0388463PXX  
PA (NYMO-) NYMOY COPRXX  
DT      November 1944

XX  
DB WBT: 2003-120506/11

Preventing, controlling, modulating, ameliorating and/or treating cell death or tissue necrosis using antibodies to neural thread proteins, PT useful in disorders such as stroke, brain tumor, glaucoma and Alzheimer's disease

XX  
PS  
Disc]asure: Fig 11: 60nn: English

The invention relates to a method of preventing, and/or inhibiting cell death and/or tissue necrosis in live tissue containing neural thread proteins (NTP). The method involves contacting the live tissue with at least one antibody, fragment or derivative that recognises NTP, where the antibody, fragment or derivative is present to prevent, control, ameliorate and/or inhibit cell death and/or tissue necrosis caused by the presence of NTP. Methods and compositions of the invention are useful for preventing, modulating, controlling and/or treating disorders associated with cell death and/or tissue necrosis such as stroke, brain tumour, Pick's disease, Parkinson's disease, amyloidosis, glaucoma and Alzheimer's disease. The invention is useful in gene therapy. The present sequence is NTP protein.

Sequence 68 AA;

Query Match	100.0%	Score 393;	DB 6;	Length 68;
Best Local Similarity	100.0%;	Pred. No. 5.8e-37;		
Matches 68;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy 1 MFVFCLILNREKIKGNSFFLLSFFSFQNCQCFCQRTTGYAVEGFCYCLVDKAAFC 60

Dp 1 MFVFCLILNREKIKGNSFFLLSFFSFQNCQCFCQRTTGYAVEGFCYCLVDKAAFC 60

Qy 61 WWFYSPDT 68  
 Db 61 WWFYSPDT 68

RESULT 8  
 ABJ19452  
 ID ABU19452 standard; protein; 68 AA.  
 XX AC ABJ19452;  
 XX DT 27-MAR-2003 (first entry)  
 XX DE 68-mer neural thread protein.  
 XX KW Nootropic; neuroprotective; cell death; tissue necrosis; NTP;  
 XX KW neural thread protein; neurodegenerative disorder; Alzheimer's disease.  
 XX OS Unidentified.  
 XX PN WO200292115-A2.  
 XX XX 21-NOV-2002.  
 XX PF 16-MAY-2002; 2002WO-CA000712.  
 XX PR 16-MAY-2001; 2001US-0290971P.  
 XX PA (NYMO-) NYMOX CORP.  
 XX PI Averbach PA;  
 XX DR WPI; 2003-129234/12.  
 XX PT Preventing and/or inhibiting cell death and/or tissue necrosis in a  
 PT tissue for treating a neurodegenerative disorder, e.g. Alzheimer's  
 PT disease, by contacting the live tissue with at least one segment of  
 PT neural thread proteins (NTP).  
 XX PS Disclosure; Fig 8; 60pp; English.  
 XX CC The invention relates to a novel method for preventing and/or inhibiting  
 CC cell death and/or tissue necrosis in a tissue comprising contacting the  
 CC live tissue with at least one segment of neural thread proteins (NTP).  
 CC The methods are composition are useful for treating a neurodegenerative  
 CC disorder, such as Alzheimer's disease. This sequence represents an NTP  
 CC protein of the invention  
 XX SQ Sequence 68 AA;  
 Query Match 100.0%; Score 393; DB 6; Length 68;  
 Best Local Similarity 100.0%; Pred. No. 5.8e-37;  
 Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 MFVFCILINREKIKGNSFFLLSFFSFQNCOCFQCRTEGVAVECFCLVDKAAAFEC 60  
 Db 1 MFVFCILINREKIKGNSFFLLSFFSFQNCOCFQCRTEGVAVECFCLVDKAAAFEC 60

Qy 61 WWFYSPDT 68  
 Db 61 WWFYSPDT 68

RESULT 9  
 ADB37526  
 ID ADB37526 standard; protein; 68 AA.  
 XX AC ADB37526;  
 XX DT 04-DEC-2003 (first entry)  
 XX DE Neural thread protein #5.

XX KW Cytostatic; Antitumour; Antiprosclerotic; Dermatological;  
 KW Antiatherosclerotic; Antiarteriosclerotic; Vasotropic; Antiinflammatory;  
 KW Immunosuppressive; Tranquillizer; Antiemetic; Virucide; AD7c-NTP;  
 KW neural thread protein; neuritic sprouting.  
 XX OS Unidentified.  
 XX PN WO2003008444-A2.  
 XX XX 30-JAN-2003.  
 XX PF 19-JUL-2002; 2002WO-CA001106.  
 XX PR 19-JUL-2001; 2001US-0306150P.  
 XX PR 19-JUL-2001; 2001US-0306161P.  
 XX PR 16-NOV-2001; 2001US-0331477P.  
 XX PA (NYMO-) NYMOX CORP.  
 XX PI Averbach PA, Gemmell J;  
 XX XX WPI; 2003-248000/24.  
 XX PT Novel Related peptide or AD7c-neural thread peptide, useful for treating  
 PT unwanted cellular proliferations, glandular hyperplasia, unwanted facial  
 PT hair, warts and unwanted fatty tissue.  
 XX PS Disclosure; Fig 8; 109pp; English.  
 XX CC The present invention relates to AD7c-neural thread protein (NTP) and  
 CC related proteins and peptides (I; ADB37528-ADB37641). The sequences are  
 CC useful for treating a condition in a patient requiring removal or  
 CC destruction of cells. The condition can be selected from benign or  
 CC malignant tumour of a tissue, hyperplasia, hypertrophy or overgrowth of a  
 CC tissue, virally, bacterially or parasitically altered tissue, or  
 CC malformation of a tissue, where the tissue is selected from lung, breast,  
 CC stomach, pancreas, prostate, bladder, bone, ovary, skin, kidney, sinus,  
 CC colon, intestine, stomach, rectum, oesophagus, heart, spleen, salivary  
 CC gland, blood, brain and its coverings, spinal cord and its coverings,  
 CC muscle, connective tissue, adrenal, parathyroid, thyroid, uterus, testis,  
 CC pituitary, reproductive organs, liver, gall bladder, eye, ear, nose,  
 CC throat, tonsils, mouth, lymph nodes and lymphoid tissue. The condition is  
 CC preferably tonsillary hypertrophy, prostatic hyperplasia, psoriasis,  
 CC eczema, dermatosis, cosmetic modification to a tissue (skin, eye, ear,  
 CC nose, throat, mouth, muscle, connective, hair or breast tissue), vascular  
 CC disease (atherosclerosis or arteriosclerosis), haemorrhoids, varicose  
 CC veins, inflammatory disease, autoimmune disease, metabolic disease,  
 CC hereditary/genetic disease, traumatic disease or physical injury,  
 CC nutritional deficiency disease, infectious disease, amyloid disease,  
 CC fibrosis disease, storage disease, congenital malformation, enzyme  
 CC deficiency disease, poisoning, intoxication, environmental disease,  
 CC radiation disease, endocrine disease, degenerative disease and mechanical  
 CC disease. The peptides are useful for treating unwanted cellular  
 CC proliferations, glandular (e.g. prostate) hyperplasia, unwanted facial  
 CC hair, warts and unwanted fatty tissue, or for preparing antibodies that  
 CC recognize and/or bind to Related proteins, Related peptides or NTP  
 CC peptides. The present sequence was used to illustrate the invention.  
 XX SQ Sequence 68 AA;  
 Query Match 100.0%; Score 393; DB 7; Length 68;  
 Best Local Similarity 100.0%; Pred. No. 5.8e-37;  
 Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 MFVFCILINREKIKGNSFFLLSFFSFQNCOCFQCRTEGVAVECFCLVDKAAAFEC 60  
 Db 1 MFVFCILINREKIKGNSFFLLSFFSFQNCOCFQCRTEGVAVECFCLVDKAAAFEC 60

Qy 61 WWFYSPDT 68  
 Db 61 WWFYSPDT 68

RESULT 10  
ADL96027  
ID ADL96027 standard; protein; 68 AA.  
XX  
AC ADL96027;  
XX  
DT 20-MAY-2004 (first entry)  
XX  
DE Human neural thread protein, NTP68.  
XX  
KW Human; neural thread protein; NTP123; NTP112; NTP106; NTP98; NTP75;  
KW NTP68; NTP61; stenosis; stent; tumour; prostatic hyperplasia; psoriasis;  
KW eczema; haemorrhoid; atherosclerosis; inflammatory disease;  
KW autoimmune disease; metabolic disease; hereditary disease;  
KW genetic disease; traumatic disease; physical injury;  
KW nutritional deficiency disease; infectious disease; amyloid disease;  
KW Alzheimer's disease; storage disease; congenital malformation;  
KW enzyme deficiency disease; poisoning; intoxication;  
KW environmental disease; radiation disease; endocrine disease;  
KW degenerative disease; mechanical disease.  
XX  
OS Homo sapiens.  
XX  
PN US2003166569-A1.  
XX  
PD 04-SEP-2003.  
XX  
XX 15-NOV-2002; 2002US-00294891.  
XX  
PR 16-NOV-2001; 2001US-0331477P.  
XX  
PA (AVER/) AVERBACK P.  
PA (GEMM/) GEMMELL J.  
XX  
PI Averbach P, Gemmell J;  
XX  
DR WPI; 2003-898099/82.  
XX  
XX New neural thread protein or its variants, useful for treating tumors and  
PT other conditions requiring the removal or destruction of cells (e.g.  
PT prostatic hyperplasia, psoriasis, eczema, hemorrhoids or  
PT atherosclerosis).  
XX  
PS Disclosure; SEQ ID NO 6; 32pp; English.  
XX  
CC The invention relates to a peptide, or its homologue, derivative,  
CC fragment, variant or mimetic, comprising at least one neural thread  
CC protein (NTP) peptide appearing as ADL96029-ADL96069, derived from  
CC NTP122, 112, 106, 98, 75, 68 or 61. Also included are a nucleic acid  
CC encoding an amino acid sequence corresponding to the above peptide,<sup>a</sup>  
CC composition comprising one or more peptides or nucleic acids cited above  
CC and a carrier, a method of treating a condition in a mammal requiring  
CC removal or destruction of cells (comprising administering to the mammal  
CC an amount of the peptide cited above) and a method of preventing or  
CC inhibiting the stenosis, occlusion or blockage of a stent, comprising  
CC coating the stent with an amount of the above peptide. The peptide  
CC further comprises an amino acid in a reverse-D order based on the above  
CC amino acid sequences. The composition and methods are useful in treating  
CC tumours and other conditions requiring the removal or destruction of  
CC cells (e.g. prostatic hyperplasia, psoriasis, eczema, haemorrhoids or  
CC atherosclerosis). These may also be used in treating inflammatory  
CC diseases, autoimmune diseases, metabolic diseases, hereditary/genetic  
CC diseases, traumatic diseases or physical injuries, nutritional deficiency  
CC diseases, infectious diseases, amyloid diseases e.g. Alzheimer's disease,  
CC storage diseases, congenital malformation, enzyme deficiency diseases,  
CC poisoning, intoxication, environmental diseases, radiation diseases,  
CC endocrine diseases, degenerative diseases or mechanical diseases. The  
CC present sequence is a human NTP protein from which the peptides of the  
CC invention are derived.  
XX  
XX Sequence 68 AA;

Query Match 100.0%; Score 393; DB 7; Length 68;  
Best Local Similarity 100.0%; Pred. No. 5.8e-37;  
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MFVFCILNREKIKGNSSFFLLSFFFSFQNCQCFQCRTEGYAVECFYCLVDKAAPEC 60  
DB 1 MFVFCILNREKIKGNSSFFLLSFFFSFQNCQCFQCRTEGYAVECFYCLVDKAAPEC 60  
QY 61 WMFYSDFT 68  
DB 61 WMFYSDFT 68  
RESULT 11  
ABP59919  
ID ABP59919 standard; peptide; 23 AA.  
XX  
AC ABP59919;  
XX  
DT 28-AUG-2003 (first entry)  
XX  
DE Human neural thread protein NTP(68) peptide #4.  
XX  
KW Human; tumour; cancer; neural thread protein; NTP; cell removal;  
KW cell destruction; antipsoriatic; antimicrobial; immunosuppressive;  
KW antiinflammatory; dermatological; antiarteriosclerotic; vasotropic;  
KW gene therapy.  
XX  
OS Homo sapiens.  
XX  
PN WO2003044053-A2.  
XX  
PD 30-MAY-2003.  
XX  
PF 18-NOV-2002; 2002WO-CA001757.  
XX  
PR 16-NOV-2001; 2001US-0331477P.  
XX  
PA (NYMO-) NYMOX CORP.  
XX  
PI Averbach P, Gemmell J;  
XX  
DR WPI; 2003-457592/43.  
XX  
XX New neural thread protein (NTP), useful for preparing a composition for  
PT treating or preventing a condition in a mammal requiring removal or  
PT destruction of cells, e.g. psoriasis, eczema, atherosclerosis or  
PT inflammatory disease.  
XX  
PS Claim 1; Page 39; 98pp; English.  
XX  
CC The present invention relates to peptides derived from the human neural  
CC thread protein (NTP). The peptides are useful for preparing a composition  
CC for treating or preventing a condition in a mammal requiring removal or  
CC destruction of cells, comprising consilary hypertrophy, prostatic  
CC hyperplasia, psoriasis, eczema, dermatosis, cosmetic modification to a  
CC breast, connective, skin, eye, ear, nose, throat, mouth or muscle tissue,  
CC varicose veins, atherosclerosis, inflammatory, metabolic, infectious,  
CC fibrosis, endocrine or autoimmune disease, or stenosis, restenosis,  
CC occlusion or blockage of an artery or of a stent placed or implanted in  
CC an artery. The present sequence is a peptide of the invention  
XX  
XX Sequence 23 AA;

Query Match 36.4%; Score 143; DB 6; Length 23;  
Best Local Similarity 100.0%; Pred. No. 4.2e-09;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 46 VECFYCLVDKAAAFECWFWYSFDT 68  
DB 1 VECFYCLVDKAAAFECWFWYSFDT 23

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RESULT 12
ADL96065
ID ADL96065 standard; peptide; 23 AA.
XX AC
XX ADL96065;
XX DT
XX 20-MAY-2004 (first entry)
XX DE
XX Human neural thread protein, NTP68, peptide #4.
XX KW
XX Human; neural thread protein; NTP122; NTP112; NTP106; NTP98; NTP75;
XX KW NTP68; NTP61; stenosis; stent; tumour; prostatic hyperplasia; psoriasis;
XX KW eczema; haemorrhoid; atherosclerosis; inflammatory disease;
XX KW autoimmune disease; metabolic disease; hereditary disease;
XX KW genetic disease; traumatic disease; physical injury;
XX KW nutritional deficiency disease; infectious disease; amyloid disease;
XX KW Alzheimer's disease; storage disease; congenital malformation;
XX KW enzyme deficiency disease; poisoning; intoxication;
XX KW environmental disease; radiation disease; endocrine disease;
XX KW degenerative disease; mechanical disease.
XX OS
XX Homo sapiens.
XX XX
XX US2003166569-A1.
XX PN
XX 04-SEP-2003.
XX PD
XX 15-NOV-2002; 2002US-00294891.
XX PF
XX 16-NOV-2001; 2001US-0331477P.
XX PR
XX (AVER/) AVERBACK P.
XX PA (GEMM/) GEMMELL J.
XX XX
XX Averbach P, Gemmell J;
XX PI WPI; 2003-898099/82.
XX XX
XX New neural thread protein or its variants, useful for treating tumors and
XX PT other conditions requiring the removal or destruction of cells (e.g.
XX PT prostatic hyperplasia, psoriasis, eczema, hemorrhoids or
XX PT atherosclerosis).
XX XX
XX Claim 1; SEQ ID NO 44; 32pp; English.
XX CC
XX The invention relates to a peptide, or its homologue, derivative,
XX CC fragment, variant or mimetic, comprising at least one neural thread
XX CC protein (NTP) peptide appearing as ADL96029-ADL96069, derived from
XX CC NTP122, 112, 106, 98, 75, 88 or 61. Also included are a nucleic acid
XX CC encoding an amino acid sequence corresponding to the above peptide, a
XX CC composition comprising one or more peptides or nucleic acids cited above
XX CC and a carrier, a method of treating a condition in a mammal requiring
XX CC removal or destruction of cells (comprising administering to the mammal
XX CC an amount of the peptide cited above) and a method of preventing or
XX CC inhibiting the stenosis, occlusion or blockage of a stent, comprising
XX CC coating the stent with an amount of the above peptide. The peptide
XX CC further comprises an amino acid in a reverse-D order based on the above
XX CC amino acid sequences. The composition and methods are useful in treating
XX CC tumours and other conditions requiring the removal or destruction of
XX CC cells (e.g. prostatic hyperplasia, psoriasis, eczema, haemorrhoids or
XX CC atherosclerosis). These may also be used in treating inflammatory
XX CC diseases, autoimmune diseases, metabolic diseases, hereditary/genetic
XX CC diseases, traumatic diseases or physical injuries, nutritional deficiency
XX CC diseases, infectious diseases, amyloid diseases e.g. Alzheimer's disease,
XX CC storage diseases, congenital malformation, enzyme deficiency diseases,
XX CC poisoning, intoxication, environmental diseases, radiation diseases,
XX CC endocrine diseases, degenerative diseases or mechanical diseases. The
XX CC present sequence is a NTP peptide of the invention.
XX SQ
XX Sequence 23 AA;
XX Query Match 36.4%; Score 143; DB 7; Length 23;
XX Best Local Similarity 100.0%; Pred. No. 4.2e-09;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 46 VECFYCLVDKAAAECEWFWFSFDT 68
AC
Db 1 VECFYCLVDKAAAECEWFWFSFDT 23

RESULT 13
ABP59918
ID ABP59918 standard; peptide; 15 AA.
XX AC
XX ABP59918;
XX DT
XX 28-AUG-2003 (first entry)
XX DE
XX Human neural thread protein NTP(68) peptide #3.
XX KW
XX Human; tumour; cancer; neural thread protein; NTP; cell removal;
XX KW cell destruction; antipsoriatic; antimicrobial; immunosuppressive;
XX KW antiinflammatory; dermatological; antiarteriosclerotic; vasotropic;
XX KW gene therapy.
XX OS
XX Homo sapiens.
XX XX
XX WO2003044053-A2.
XX PN
XX 30-MAY-2003.
XX PD
XX 18-NOV-2002; 2002WO-CA001757.
XX PF
XX 16-NOV-2001; 2001US-0331477P.
XX PR
XX (NYMO-) NYMOX CORP.
XX PA
XX Averbach P, Gemmell J;
XX PI WPI; 2003-457592/43.
XX XX
XX New neural thread protein (NTP), useful for preparing a composition for
XX PT treating or preventing a condition in a mammal requiring removal or
XX PT destruction of cells, e.g. psoriasis, eczema, atherosclerosis or
XX PT inflammatory disease.
XX XX
XX Claim 1; Page 39; 98pp; English.
XX CC
XX The present invention relates to peptides derived from the human neural
XX CC thread protein (NTP). The peptides are useful for preparing a composition
XX CC for treating or preventing a condition in a mammal requiring removal or
XX CC destruction of cells, comprising tonsillary hypertrophy, prostatic
XX CC hyperplasia, psoriasis, eczema, dermatosis, cosmetic modification to a
XX CC breast, connective, skin, eye, ear, nose, throat, mouth or muscle tissue,
XX CC varicose veins, atherosclerosis, inflammatory, metabolic, infectious,
XX CC fibrosis, endocrine or autoimmune disease, or stenosis, restenosis,
XX CC occlusion or blockage of an artery or of a stent placed or implanted in
XX CC an artery. The present sequence is a peptide of the invention
XX SQ
XX Sequence 15 AA;
XX Query Match 24.2%; Score 95; DB 6; Length 15;
XX Best Local Similarity 100.0%; Pred. No. 0.00075;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 31 NCCQCFQCRTEGYA 45
Db 1 NCCQCFQCRTEGYA 15

RESULT 14
ADL96064
ID ADL96064 standard; peptide; 15 AA.
XX AC
XX ADL96064;
XX XX
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DT 20-MAY-2004 (first entry)  
DE Human neural thread protein, NTP68, peptide #3.  
KW Human; neural thread protein; NTP122; NTP106; NTP98; NTP75;  
KW NTP68; NTP61; stenosis; stent; tumour; prostatic hyperplasia; psoriasis;  
KW eczema; haemorrhoid; atherosclerosis; inflammatory disease;  
KW autoimmune disease; metabolic disease; hereditary disease;  
KW genetic disease; traumatic disease; physical injury;  
KW nutritional deficiency disease; infectious disease; amyloid disease;  
KW Alzheimer's disease; storage disease; congenital malformation;  
KW enzyme deficiency disease; poisoning; intoxication;  
KW environmental disease; radiation disease; endocrine disease;  
KW degenerative disease; mechanical disease.  
XX  
OS Homo sapiens.  
XX  
XX US2003166569-A1.  
XX  
XX 04-SEP-2003.  
XX  
XX 15-NOV-2002; 2002US-00294891.  
XX  
XX 16-NOV-2001; 2001US-0331477P.  
XX (AVER/) AVERBACK P.  
XX (GEMM/) GEMMELL J.  
XX Averbach P, Gemmell J;  
XX WPI; 2003-898099/82.  
XX  
XX New neural thread protein or its variants, useful for treating tumors and  
XX other conditions requiring the removal or destruction of cells (e.g.  
XX prostatic hyperplasia, psoriasis, eczema, hemorrhoids or  
XX atherosclerosis).  
XX  
XX Claim 1; SEQ ID NO 43; 32pp; English.  
XX  
XX The invention relates to a peptide, or its homologue, derivative,  
XX fragment, variant or mimetic, comprising at least one neural thread  
XX protein (NTP) peptide appearing as ADL96029-ADL96069, derived from  
XX NTP122, 112, 106, 98, 75, 68 or 61. Also included are a nucleic acid  
XX encoding an amino acid sequence corresponding to the above peptide, a  
XX composition comprising one or more peptides or nucleic acids cited above  
XX and a carrier, a method of treating a condition in a mammal requiring  
XX removal or destruction of cells (comprising administering to the mammal  
XX an amount of the peptide cited above) and a method of preventing or  
XX inhibiting the stenosis, occlusion or blockage of a stent, comprising  
XX coating the stent with an amount of the above peptide. The peptide  
XX further comprises an amino acid in a reverse-D order based on the above  
XX amino acid sequences. The composition and methods are useful in treating  
XX tumours and other conditions requiring the removal or destruction of  
XX cells (e.g. prostatic hyperplasia, psoriasis, eczema, haemorrhoids or  
XX atherosclerosis). These may also be used in treating inflammatory  
XX diseases, autoimmune diseases, metabolic diseases, hereditary/genetic  
XX diseases, traumatic diseases or physical injuries, nutritional deficiency  
XX diseases, infectious diseases, amyloid diseases e.g. Alzheimer's disease,  
XX storage diseases, congenital malformation, enzyme deficiency diseases,  
XX poisoning, intoxication, environmental diseases, radiation diseases,  
XX endocrine diseases, degenerative diseases or mechanical diseases. The  
XX present sequence is a NTP peptide of the invention.  
XX  
XX Sequence 15 AA;

Query Match 24.2%; Score 95; DB 7; Length 15;  
Best Local Similarity 100.0%; Pred. NO. 0.00075;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 31 NCCQCFQCRTEGYA 45  
DB 1 NCCQCFQCRTEGYA 15  
|||||

RESULT 15  
ABP59916  
ID ABP59916 standard; peptide; 15 AA.  
XX  
XX AC ABP59916;  
XX  
XX DT 28-AUG-2003 (first entry)  
XX  
XX DE Human neural thread protein NTP(68) peptide #1.  
XX  
XX KW Human; tumour; cancer; neural thread protein; NTP; cell removal;  
KW cell destruction; antipsoriatic; antimicrobial; immunosuppressive;  
KW antiinflammatory; dermatological; antiarteriosclerotic; vasotropic;  
KW gene therapy.  
XX  
XX OS Homo sapiens.  
XX  
XX PN WO2003044053-A2.  
XX  
XX PD 30-MAY-2003.  
XX  
XX PF 18-NOV-2002; 2002WO-CA001757.  
XX  
XX PR 16-NOV-2001; 2001US-0331477P.  
XX  
XX PA (NYMO-) NYMOX CORP.  
XX  
XX PI Averbach P, Gemmell J;  
XX  
XX DR WPI; 2003-457592/43.  
XX  
XX PT New neural thread protein (NTP), useful for preparing a composition for  
PT treating or preventing a condition in a mammal requiring removal or  
PT destruction of cells, e.g. psoriasis, eczema, atherosclerosis or  
PT inflammatory disease.  
XX  
XX Claim 1; Page 38; 98pp; English.  
XX  
XX The present invention relates to peptides derived from the human neural  
XX thread protein (NTP). The peptides are useful for preparing a composition  
XX for treating or preventing a condition in a mammal requiring removal or  
XX destruction of cells, comprising tonsillary hypertrophy, prostatic  
XX hyperplasia, psoriasis, eczema, dermatosis, cosmetic modification to a  
XX breast, connective, skin, eye, ear, nose, throat, mouth or muscle tissue,  
XX varicose veins, atherosclerosis, inflammatory, metabolic, infectious,  
XX fibrosis, endocrine or autoimmune disease, or stenosis, restenosis,  
XX occlusion or blockage of an artery or of a stent placed or implanted in  
XX an artery. The present sequence is a peptide of the invention  
XX  
XX Sequence 15 AA;  
  
Query Match 19.8%; Score 78; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. NO. 0.063;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MFVFCILNREKIKG 15  
DB 1 MFVFCILNREKIKG 15  
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Search completed: October 11, 2005, 07:11:14  
Job time : 53.3636 secs

GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: October 11, 2005, 06:57:16 ; Search time 114 Seconds

(without alignments)

248.149 Million cell updates/sec

Title: US-10-092-934-8

Perfect score: 393

Sequence: 1 MFVFCILNREKIKGNSSFFLLSFFSFONCCOCFOCRRTTEGYAVECFYCLVDKAAPECWYFSFDT 68

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1854112 seqs, 416015017 residues

Total number of hits satisfying chosen parameters: 1854112

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

## Database :

Published Applications AA:\*  
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2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*  
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22: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	393	100.0	68	14	US-10-138-516-7
2	393	100.0	68	14	US-10-146-130-9
3	393	100.0	68	14	US-10-092-934-8
4	393	100.0	68	14	US-10-153-334-8
5	393	100.0	68	14	US-10-198-069-8
6	393	100.0	68	14	US-10-198-070-8
7	393	100.0	68	14	US-10-294-891-6
8	393	100.0	68	17	US-10-920-313-6
9	143	36.4	23	14	US-10-294-891-44
10	143	36.4	23	17	US-10-920-313-44
11	95	24.2	15	14	US-10-294-891-43

12	95	24.2	15	17	US-10-920-313-43	Sequence 43, Appl
13	78	19.8	15	14	US-10-294-891-41	Sequence 41, Appl
14	78	19.8	15	17	US-10-920-313-41	Sequence 41, Appl
15	77	19.6	15	14	US-10-294-891-42	Sequence 42, Appl
16	77	19.6	15	17	US-10-920-313-42	Sequence 42, Appl
17	68	17.3	172	15	US-10-424-599-158515	Sequence 158515,
18	67.5	17.2	1116	16	US-10-437-963-162468	Sequence 162468,
19	66	16.8	298	14	US-10-017-161-2194	Sequence 2194, Ap
20	66	16.8	298	15	US-10-292-798-1840	Sequence 1840, Ap
21	65	16.5	97	15	US-10-424-599-210426	Sequence 210426,
22	64.5	16.4	294	14	US-10-017-161-2218	Sequence 2218, Ap
23	64.5	16.4	294	15	US-10-292-798-1864	Sequence 1864, Ap
24	64	16.3	49	15	US-10-653-595-132	Sequence 132, App
25	64	16.3	50	10	US-09-397-945-132	Sequence 132, App
26	64	16.3	103	15	US-10-424-599-220535	Sequence 220535,
27	63.5	16.2	144	20	US-11-097-143-1779	Sequence 1779, App
28	63	16.0	30	18	US-10-792-582-187	Sequence 187, App
29	63	16.0	144	16	US-10-425-115-297883	Sequence 297883,
30	62	15.8	53	15	US-10-424-599-177729	Sequence 177729,
31	62	15.8	102	16	US-10-425-115-232872	Sequence 232872,
32	62	15.8	1966	18	US-10-828-868-5	Sequence 5, Appli
33	62	15.8	1966	18	US-10-828-868-6	Sequence 6, Appli
34	62	15.8	1977	18	US-10-828-868-7	Sequence 7, Appli
35	61.5	15.6	57	15	US-10-632-983-67	Sequence 121, App
36	61.5	15.6	84	15	US-10-632-983-121	Sequence 107755,
37	61.5	15.6	154	16	US-10-437-963-107755	Sequence 18, Appl
38	61.5	15.6	162	9	US-09-798-789-18	Sequence 428, App
39	61.5	15.6	162	14	US-10-218-103-428	Sequence 947, App
40	61.5	15.6	163	9	US-09-925-299-947	Sequence 947, App
41	61.5	15.6	163	10	US-09-925-299-947	Sequence 947, App
42	61.5	15.6	301	16	US-10-770-127-3	Sequence 3, Appli
43	61.5	15.6	302	9	US-09-393-634-37	Sequence 37, Appli
44	61.5	15.6	302	10	US-09-510-332-3	Sequence 37, Appli
45	61.5	15.6	302	14	US-10-383-982-37	Sequence 37, Appli

## ALIGNMENTS

## RESULT 1

US-10-138-516-7  
; Sequence 7, Application US/10138516  
; Publication No. US20030003445A1  
; GENERAL INFORMATION:  
; APPLICANT: AVERBACK, PAUL  
; TITLE OF INVENTION: METHOD OF PREVENTING CELL DEATH USING ANTIBODIES TO  
; TITLE OF INVENTION: NEURAL THREAD PROTEINS  
; FILE REFERENCE: 59003.000004  
; CURRENT APPLICATION NUMBER: US/10/138,516  
; CURRENT FILING DATE: 2002-07-23  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 7  
; LENGTH: 68  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-138-516-7

Query Match 100.0%; Score 393; DB 14; Length 68;  
Best Local Similarity 100.0%; Pred. No. 2.3e-38;  
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MFVFCILNREKIKGNSSFFLLSFFSFONCCOCFOCRRTTEGYAVECFYCLVDKAAPEC	60
Db	1	MFVFCILNREKIKGNSSFFLLSFFSFONCCOCFOCRRTTEGYAVECFYCLVDKAAPEC	60
Qy	61	WWFYSFDT	68
Db	61	WWFYSFDT	68

## RESULT 2

US-10-146-130-9





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US-10-198-070-8
; Sequence 8, Application US/10198070
; Publication No. US20030109437A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; APPLICANT: GEMMEL, JACK
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 59003.000008
; CURRENT APPLICATION NUMBER: US/10/198,070
; CURRENT FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/306,161
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/306,150
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/331,477
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Unknown NTP
; OTHER INFORMATION: peptide
US-10-198-070-8

Query Match      100.0%; Score 393; DB 14; Length 68;
Best Local Similarity 100.0%; Pred. No. 2.3e-38;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFVFCILINREKIKGNSFFLLSFFFSFQCCFCQRTTEGYAVECFYCLVDKAAPEC 60
Db 1 MFVFCILINREKIKGNSFFLLSFFFSFQCCFCQRTTEGYAVECFYCLVDKAAPEC 60

Qy 61 WWFYSFDT 68
Db 61 WWFYSFDT 68

RESULT 7
US-10-294-891-6
; Sequence 6, Application US/10294891
; Publication No. US20030166569A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; APPLICANT: GEMMEL, JACK
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF CELLS
; FILE REFERENCE: 59003.000010
; CURRENT APPLICATION NUMBER: US/10/294,891
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: 60/331,447
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-294-891-6

Query Match      100.0%; Score 393; DB 14; Length 68;
Best Local Similarity 100.0%; Pred. No. 2.3e-38;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFVFCILINREKIKGNSFFLLSFFFSFQCCFCQRTTEGYAVECFYCLVDKAAPEC 60
Db 1 MFVFCILINREKIKGNSFFLLSFFFSFQCCFCQRTTEGYAVECFYCLVDKAAPEC 60

Qy 61 WWFYSFDT 68
Db 61 WWFYSFDT 68

US-10-198-070-8
; Sequence 8, Application US/10198070
; Publication No. US20030109437A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; APPLICANT: GEMMEL, JACK
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 59003.000008
; CURRENT APPLICATION NUMBER: US/10/198,070
; CURRENT FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/306,161
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/306,150
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/331,477
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Unknown NTP
; OTHER INFORMATION: peptide
US-10-198-070-8

Query Match      100.0%; Score 393; DB 14; Length 68;
Best Local Similarity 100.0%; Pred. No. 2.3e-38;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFVFCILINREKIKGNSFFLLSFFFSFQCCFCQRTTEGYAVECFYCLVDKAAPEC 60
Db 1 MFVFCILINREKIKGNSFFLLSFFFSFQCCFCQRTTEGYAVECFYCLVDKAAPEC 60

Qy 61 WWFYSFDT 68
Db 61 WWFYSFDT 68

RESULT 7
US-10-294-891-6
; Sequence 6, Application US/10294891
; Publication No. US20030166569A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; APPLICANT: GEMMEL, JACK
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF CELLS
; FILE REFERENCE: 59003.000010
; CURRENT APPLICATION NUMBER: US/10/294,891
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: 60/331,447
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-294-891-6

Query Match      100.0%; Score 393; DB 14; Length 68;
Best Local Similarity 100.0%; Pred. No. 2.3e-38;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFVFCILINREKIKGNSFFLLSFFFSFQCCFCQRTTEGYAVECFYCLVDKAAPEC 60
Db 1 MFVFCILINREKIKGNSFFLLSFFFSFQCCFCQRTTEGYAVECFYCLVDKAAPEC 60

Qy 61 WWFYSFDT 68
Db 61 WWFYSFDT 68
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Db 61 WWFYSFDT 68

RESULT 8
US-10-920-313-6
; Sequence 6, Application US/10920313
; Publication No. US20050032704A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; APPLICANT: GEMMEL, JACK
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF CELLS
; FILE REFERENCE: 59003.000010
; CURRENT APPLICATION NUMBER: US/10/920,313
; CURRENT FILING DATE: 2004-08-18
; PRIOR APPLICATION NUMBER: 60/331,447
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-920-313-6

Query Match      100.0%; Score 393; DB 17; Length 68;
Best Local Similarity 100.0%; Pred. No. 2.3e-38;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFVFCILINREKIKGNSFFLLSFFFSFQCCFCQRTTEGYAVECFYCLVDKAAPEC 60
Db 1 MFVFCILINREKIKGNSFFLLSFFFSFQCCFCQRTTEGYAVECFYCLVDKAAPEC 60

Qy 61 WWFYSFDT 68
Db 61 WWFYSFDT 68

RESULT 9
US-10-294-891-44
; Sequence 44, Application US/10294891
; Publication No. US20030166569A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; APPLICANT: GEMMEL, JACK
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF CELLS
; FILE REFERENCE: 59003.000010
; CURRENT APPLICATION NUMBER: US/10/294,891
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: 60/331,447
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 44
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-294-891-44

Query Match      36.4%; Score 143; DB 14; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.4e-09;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 46 VECFYCLVDKAAPECWWFYSFDT 68
Db 1 VECFYCLVDKAAPECWWFYSFDT 23

RESULT 10
US-10-920-313-44
; Sequence 44, Application US/10920313
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```

; Publication No. US20050032704A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; APPLICANT: GEMMEL, JACK
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF CELLS
; FILE REFERENCE: 59003.000010
; CURRENT APPLICATION NUMBER: US/10/920,313
; PRIOR FILING DATE: 2004-08-18
; PRIOR APPLICATION NUMBER: 60/331,447
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 44
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-920-313-44

Query Match          36.4%; Score 143; DB 17; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.4e-09;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 46 VECFYCLVDKAAFECCWFFSFDT 69
      |||||
Db 1 VECFYCLVDKAAFECCWFFSFDT 23

RESULT 11
US-10-294-891-43
; Sequence 43, Application US/10294891
; Publication No. US20030166569A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; APPLICANT: GEMMEL, JACK
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF CELLS
; FILE REFERENCE: 59003.000010
; CURRENT APPLICATION NUMBER: US/10/294,891
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: 60/331,447
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 43
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-294-891-43

Query Match          24.2%; Score 95; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.00039;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 NCCQCFQCRTEGYA 45
      |||||
Db 1 NCCQCFQCRTEGYA 15

RESULT 12
US-10-920-313-43
; Sequence 43, Application US/10920313
; Publication No. US20050032704A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; APPLICANT: GEMMEL, JACK
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF CELLS
; FILE REFERENCE: 59003.000010
; CURRENT APPLICATION NUMBER: US/10/920,313
; PRIOR FILING DATE: 2004-08-18
; PRIOR APPLICATION NUMBER: 60/331,447
; PRIOR FILING DATE: 2001-11-16

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 11, 2005, 06:57:19 ; Search time 15.5455 Seconds  
(without alignments)  
326.535 Million cell updates/sec

Title: US-10-092-934-8

Perfect score: 393

Sequence: 1 MFVFCILNREKIKGNSSP.....FYCLVDKAAPECFWYFSDT 68

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents AA:\*  
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2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	393	100.0	68	2	US-08-454-557C-36
2	393	100.0	68	2	US-08-340-426D-36
3	393	100.0	68	2	US-08-450-673C-36
4	393	100.0	68	5	PCT-US95-17111A-36
5	234	59.5	75	4	US-09-621-976-5918
6	207	52.7	75	4	US-09-621-976-5886
7	66.5	16.9	109	4	US-09-107-532A-4585
8	64	16.3	119	4	US-09-270-767-37122
9	64	16.3	118	4	US-09-270-767-52339
10	64	16.3	188	4	US-09-270-767-40814
11	64	16.3	188	4	US-09-270-767-56030
12	62	15.8	1912	4	US-09-495-714C-2
13	62	15.8	1977	4	US-09-495-714C-4
14	62	15.8	1985	4	US-09-495-714C-6
15	61.5	15.6	58	4	US-09-716-129-67
16	61.5	15.6	84	4	US-09-716-129-121
17	61.5	15.6	302	4	US-09-393-634-37
18	61.5	15.6	348	4	US-09-415-277C-14
19	60.5	15.4	5179	4	US-09-538-092-1258
20	59.5	15.1	845	4	US-08-591-502B-57
21	59	15.0	404	2	US-08-070-301-15
22	58.5	14.9	105	3	US-08-858-207A-551
23	58	14.8	115	4	US-09-513-999C-7845
24	58	14.8	115	4	US-09-513-999C-7846
25	58	14.8	115	4	US-09-513-999C-7847
26	58	14.8	128	6	5179198-1
27	58	14.8	128	6	5521296-1

28	58	14.8	128	6	5179198-1	Patent No. 5179198
29	58	14.8	128	6	5521296-1	Sequence 9460, Ap
30	58	14.8	135	4	US-09-949-016-9460	Sequence 5367, Ap
31	58	14.8	270	4	US-09-134-000C-5367	Sequence 7455, Ap
32	58	14.8	437	4	US-09-543-681A-7455	Sequence 5115, Ap
33	56	14.2	123	3	US-09-134-001C-5115	Sequence 36649, A
34	56	14.2	141	4	US-09-270-767-36649	Sequence 51866, A
35	56	14.2	141	4	US-09-270-767-51866	Sequence 40352, A
36	56	14.2	282	4	US-09-270-767-40352	Sequence 55568, A
37	56	14.2	282	4	US-09-270-767-55568	Sequence 41523, A
38	56	14.2	301	4	US-09-270-767-41523	Sequence 2, Appli
39	56	14.2	2161	1	US-07-745-206A-2	Sequence 49, Appl
40	56	14.2	2161	1	US-08-455-543A-49	Sequence 49, Appl
41	56	14.2	2161	2	US-08-223-305C-49	Sequence 2, Appli
42	56	14.2	2161	2	US-08-311-363-2	Sequence 19825, A
43	55.5	14.1	258	4	US-09-252-991A-19825	Sequence 37179, A
44	55.5	14.1	424	4	US-09-270-767-37179	Sequence 52396, A
45	55.5	14.1	424	4	US-09-270-767-52396	

ALIGNMENTS

RESULT 1

US-08-454-557C-36  
; Sequence 36, Application US/08454557C  
; Patent No. 5830670  
; GENERAL INFORMATION:  
; APPLICANT: de la Monte, Suzanne  
; APPLICANT: Wands, Jack R.  
; TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection  
; NUMBER OF SEQUENCES: 121  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.  
; STREET: 1100 New York Avenue, Suite 600  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/454,557C  
; FILING DATE: 30-MAY-1995  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ludwig, Steven R.  
; REGISTRATION NUMBER: 36,203  
; REFERENCE/DOCKET NUMBER: 0609.3840003  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 371-2600  
; TELEFAX: (202) 371-2540  
; INFORMATION FOR SEQ ID NO: 36:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 68 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
US-08-454-557C-36

Query Match 100.0%; Score 393; DB 2; Length 68;  
Best Local Similarity 100.0%; Pred. No. 2.6e-41;  
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MFVFCILNREKIKGNSSFFLLSFFSFQNCOCFOCRITTEGYAVECFCLVDKAAPEC 60
Db	1	MFVFCILNREKIKGNSSFFLLSFFSFQNCOCFOCRITTEGYAVECFCLVDKAAPEC 60
Qy	61	WWFYSFDT 68



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; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -37...-1
; NAME/KEY: UNSURE
; LOCATION: 35
; OTHER INFORMATION: Xaa = * ,Tyr
; NAME/KEY: UNSURE
; LOCATION: 31
; OTHER INFORMATION: Xaa = Ala,Pro,Ser,Thr
; NAME/KEY: UNSURE
; LOCATION: 27
; OTHER INFORMATION: Xaa = Asn,Tyr
; NAME/KEY: UNSURE
; LOCATION: 25
; OTHER INFORMATION: Xaa = Gly,Trp
; NAME/KEY: UNSURE
; LOCATION: 10
; OTHER INFORMATION: Xaa = Lys,Arg
;
US-09-621-976-5886

Query Match          52.7%; Score 207; DB 4; Length 75;
Best Local Similarity 61.2%; Pred. No. 2.3e-18;
Matches 41; Conservative 1; Mismatches 25; Indels 0; Gaps 0;

QY 1 MFVFCILNREIKGNSSFFLLSFFFSFQNCQCFQCKTTGGYAVECFYCLVDKAAPEC 60
   |||||
Db 1 MFVFCILNREIKGNSSFFSFFSFFFTSKLLPVFSMDNRGICCKVFYCLVYKAAPEC 60
   |||||

QY 61 WHFYSPD 67
   |||||
Db 61 WXFSGFE 67
   |||||

RESULT 7
US-09-107-532A-4585
; Sequence 4585, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 4585:
; SEQUENCE CHARACTERISTICS:

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; LENGTH: 109 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...109
; SEQUENCE DESCRIPTION: SEQ ID NO: 4585:
US-09-107-532A-4585

Query Match      16.3%; Score 66.5; DB 4; Length 109;
Best Local Similarity 33.3%; Pred. No. 0.7;
Matches 17; Conservative 7; Mismatches 20; Indels 7; Gaps 3;

QY 19 SFLLSFFSFQ-NC--COCFOCRTEGVAVECFYCLVDKAAFECEWYFSP 66
Db 26 SCFLCYFHSYSYPCRCFLCYFHSYSYPCFRC---SCFLCYFHSY 72

RESULT 8
US-09-270-767-37122
; Sequence 37122, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 37122
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-37122

Query Match      16.3%; Score 64; DB 4; Length 119;
Best Local Similarity 29.2%; Pred. No. 1.6;
Matches 21; Conservative 10; Mismatches 19; Indels 22; Gaps 5;

QY 2 FVFCLILNREIKGNSSFFLLSFFSFQNCOCFOCRTEGVA--VECFYCL---VDKA 56
Db 17 FFFCLV-----FGWTFWFGF---CFCFFSRLFFSLAGVACFFSAGRRRSRS 61

QY 57 AFEC--WWFYSP 66
Db 62 SLFCFIWFFFSF 73

RESULT 9
US-09-270-767-52339
; Sequence 52339, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 52339
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-52339

Query Match      16.3%; Score 64; DB 4; Length 119;
Best Local Similarity 29.2%; Pred. No. 1.6;
Matches 21; Conservative 10; Mismatches 19; Indels 22; Gaps 5;

QY 2 FVFCLILNREIKGNSSFFLLSFFSFQNCOCFOCRTEGVA--VECFYCL---VDKA 56
Db 17 FFFCLV-----FGWTFWFGF---CFCFFSRLFFSLAGVACFFSAGRRRSRS 61

QY 57 AFEC--WWFYSP 66
Db 62 SLFCFIWFFFSF 73

RESULT 10
US-09-270-767-40814
; Sequence 40814, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 40814
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-40814

Query Match      16.3%; Score 64; DB 4; Length 188;
Best Local Similarity 29.6%; Pred. No. 2.5;
Matches 16; Conservative 11; Mismatches 15; Indels 12; Gaps 2;

QY 23 LSFFSFQNCOCFOCRTE-----GY-----AVECFYCLVDKAAFECEWYF 64
Db 97 LVFFYNFKTISKDFQSMGLEERIFGXIIGFWQISDSIKCFWVLITKAVFKLIIFY 150

RESULT 11
US-09-270-767-56030
; Sequence 56030, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 56030
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-56030

Query Match      16.3%; Score 64; DB 4; Length 188;
Best Local Similarity 29.6%; Pred. No. 2.5;
Matches 16; Conservative 11; Mismatches 15; Indels 12; Gaps 2;

QY 23 LSFFSFQNCOCFOCRTE-----GY-----AVECFYCLVDKAAFECEWYF 64
Db 97 LVFFYNFKTISKDFQSMGLEERIFGXIIGFWQISDSIKCFWVLITKAVFKLIIFY 150

RESULT 12
US-09-495-714C-2
; Sequence 2, Application US/09495714C
; Patent No. 6670465

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; GENERAL INFORMATION:
; APPLICANT: University Technologies International Inc.
; TITLE OF INVENTION: RETINAL CALCIUM CHANNEL (ALPHA) 1F-SUBUNIT GENE
; FILE REFERENCE: 45499.4 (formerly 45074.6)
; CURRENT APPLICATION NUMBER: US/09/495,714C
; CURRENT FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 1912
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-495-714C-2

Query Match          15.8%; Score 62; DB 4; Length 1912;
Best Local Similarity 34.0%; Pred. No. 52;
Matches 17; Conservative 8; Mismatches 19; Indels 6; Gaps 3;

QY 15 GGNSFFLLSFFSFQNCQCFCQRTTEGYAVECFYCLVDKAAFECEWFWY 64
Db 243 GGIITFD--NFFFM---LTVFQCVTMEGW-TDVLVWQDAMGYELPWWY 285

RESULT 13
US-09-495-714C-4
; Sequence 4, Application US/09495714C
; Patent No. 6670465
; GENERAL INFORMATION:
; APPLICANT: University Technologies International Inc.
; TITLE OF INVENTION: RETINAL CALCIUM CHANNEL (ALPHA) 1F-SUBUNIT GENE
; FILE REFERENCE: 45499.4 (formerly 45074.6)
; CURRENT APPLICATION NUMBER: US/09/495,714C
; CURRENT FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 1977
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-495-714C-4

Query Match          15.8%; Score 62; DB 4; Length 1977;
Best Local Similarity 34.0%; Pred. No. 54;
Matches 17; Conservative 8; Mismatches 19; Indels 6; Gaps 3;

QY 15 GGNSFFLLSFFSFQNCQCFCQRTTEGYAVECFYCLVDKAAFECEWFWY 64
Db 308 GGIITFD--NFFFM---LTVFQCVTMEGW-TDVLVWQDAMGYELPWWY 351

RESULT 14
US-09-495-714C-6
; Sequence 6, Application US/09495714C
; Patent No. 6670465
; GENERAL INFORMATION:
; APPLICANT: University Technologies International Inc.
; TITLE OF INVENTION: RETINAL CALCIUM CHANNEL (ALPHA) 1F-SUBUNIT GENE
; FILE REFERENCE: 45499.4 (formerly 45074.6)
; CURRENT APPLICATION NUMBER: US/09/495,714C
; CURRENT FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 1985
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-495-714C-6

Query Match          15.8%; Score 62; DB 4; Length 1985;
Best Local Similarity 34.0%; Pred. No. 54;
Matches 17; Conservative 8; Mismatches 19; Indels 6; Gaps 3;

QY 15 GGNSFFLLSFFSFQNCQCFCQRTTEGYAVECFYCLVDKAAFECEWFWY 64
```

```

Db 308 GGIITFD--NFFFM---LTVFQCVTMEGW-TDVLVWQDAMGYELPWWY 351

RESULT 15
US-09-716-129-67
; Sequence 67, Application US/09716129
; Patent No. 6632920
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 36 Human Secreted Proteins
; FILE REFERENCE: P2025P1
; CURRENT APPLICATION NUMBER: US/09/716,129
; CURRENT FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/076,053
; PRIOR FILING DATE: 1998-02-26
; PRIOR APPLICATION NUMBER: 60/076,057
; PRIOR FILING DATE: 1998-02-26
; PRIOR APPLICATION NUMBER: 60/076,052
; PRIOR FILING DATE: 1998-02-26
; PRIOR APPLICATION NUMBER: 60/076,054
; PRIOR FILING DATE: 1998-02-26
; PRIOR APPLICATION NUMBER: 60/076,051
; PRIOR FILING DATE: 1998-02-26
; NUMBER OF SEQ ID NOS: 186
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 67
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (58)
; OTHER INFORMATION: Xaa equals stop translation
US-09-716-129-67

Query Match          15.6%; Score 61.5; DB 4; Length 58;
Best Local Similarity 35.9%; Pred. No. 1.5;
Matches 14; Conservative 5; Mismatches 17; Indels 3; Gaps 1;

QY 19 SFFLLSFFSFQNCQCFCQRTTEGYAVECFYCLVDKAA 57
Db 19 SLFLQWLFFLGLQCCSSFLCKNES---QCFTRLKERSA 54

Search completed: October 11, 2005, 07:42:52
Job time : 16.5455 secs
```

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OM protein - protein search, using sw model

Run on: October 11, 2005, 06:57:07 ; Search time 9.45989 Seconds  
(without alignments)  
620.432 Million cell updates/sec

Title: US-10-092-934-9  
Perfect score: 326  
Sequence: 1 MEHTVAQGVPOHDLGSLQ.....NMNTALKRNRYTPETGRKS 61

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79:\*  
1: Pirl:\*  
2: Pirl2:\*  
3: Pirl3:\*  
4: Pirl4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	121.5	37.3	613	4 C40201	artifact-warning s
2	118	36.2	46	2 I54375	gene NF2 protein -
3	117.5	36.0	627	4 A40201	artifact-warning s
4	117	35.9	39	2 I54374	gene NF2 protein -
5	112	34.4	53	2 A42442	integrin beta-1 ch
6	97.5	29.9	673	4 F40201	artifact-warning s
7	76.5	23.5	597	4 E40201	artifact-accelerating
8	72	22.1	440	2 A26359	decay-accelerating
9	67	20.6	331	2 A54295	interferon alpha/b
10	67	20.6	331	2 S59501	interferon recepto
11	63	19.3	522	2 T08711	gamma-adaptin homo
12	60.5	18.6	660	2 H87325	hypothetical prote
13	60.5	18.6	814	2 A35206	glycosyl transfera
14	59.5	18.3	516	2 T32489	hypothetical prote
15	59	18.1	1239	2 A45648	DNA topoisomerase
16	57	17.5	446	2 E71057	probable thiamin b
17	57	17.5	747	2 T40728	hypothetical prote
18	56.5	17.3	245	2 S48363	hypothetical prote
19	56.5	17.3	718	2 H75485	hypothetical prote
20	56.5	17.3	1615	2 J06510	ras-responsive ele
21	56	17.2	691	2 S48390	hypothetical prote
22	55.5	17.0	427	2 T29872	hypothetical prote
23	55.5	17.0	747	2 T39879	hypothetical prote
24	55.5	17.0	947	2 G86420	probable receptor-
25	55.5	17.0	1196	2 S65245	translation elonga
26	55	16.9	189	2 F89753	protein FltC7.5 li
27	55	16.9	246	2 A70310	conserved hypothet
28	55	16.9	380	2 H69427	probable 2,3-bisph
29	55	16.9	394	2 H75372	conserved hypothet

30 55 16.9 454 2 T16429  
31 55 16.9 508 2 T00753  
32 55 16.9 1113 2 S73327  
33 54.5 16.7 197 2 T40144  
34 54.5 16.7 711 2 C83922  
35 54 16.6 314 2 G64940  
36 54 16.6 314 2 H85790  
37 54 16.6 314 2 D90942  
38 54 16.6 682 2 T15092  
39 54 16.6 929 2 JH0262  
40 53.5 16.4 210 2 G84499  
41 53.5 16.4 261 2 C72128  
42 53.5 16.4 261 2 F86494  
43 53.5 16.4 329 2 T17033  
44 53.5 16.4 354 2 S75877  
45 53.5 16.4 361 2 G83981

## ALIGNMENTS

RESULT 1  
C40201  
artifact-warning sequence (translated ALU class C) - human  
C:Species: Homo sapiens (man)  
C:Date: 31-Mar-1992 #sequence\_revision 11-Aug-1995 #text\_change 19-May-2000  
C:Accession: C40201  
R:Claverie, J.M.  
personal communication, 1992  
A:Reference number: A40201  
A:Accession: C40201  
A:Molecule type: DNA  
A:Residues: 1-613 <CUA>  
R:Claverie, J.M.  
Genomics 12, 838-841, 1992  
A:Title: Identifying coding exons by similarity search: Alu-derived and other potential  
A:Reference number: A40200; MUID:92241891; PMID:1572661  
A:Contents: annotation  
C:Comment: This "warning" entry is a conceptual translation in all 6 reading frames of  
in-frame stop codons are shown as 'X'.  
C:Comment: Any significant similarity of a predicted protein sequence to a portion of the

Query Match 37.3%; Score 121.5; DB 4; Length 613;  
Best Local Similarity 47.5%; Pred. No. 1.9e-07;  
Matches 28; Conservative 5; Mismatches 21; Indels 5; Gaps 1;  
Qy 2 EPHTVAQGVPOHDLGSLQSLPRKPFSCILIPKIDYRNMTA----LTKRNRYTP 55  
Db 318 EHSVTOAGVQVMDLGSQAPPMPFSCLSLRTWDYRPHHAQLIFCFSRNGVLP 376

RESULT 2  
I54375  
gene NF2 protein - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 01-Nov-1996 #sequence\_revision 01-Nov-1996 #text\_change 16-Aug-2004  
C:Accession: I54375  
R:Arakawa, H.; Hayashi, N.; Nagase, H.; Ogawa, M.; Nakamura, Y.  
Hum. Mol. Genet. 3, 565-568, 1994  
A:Title: Alternative splicing of the NF2 gene and its mutation analysis of breast and c  
A:Reference number: I54375; MUID:94348501; PMID:8069299  
A:Accession: I54375  
A>Status: preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: mRNA  
A:Residues: 1-46 <RES>  
A:Cross-references: UNIPROT:Q16230; GB:S73853; NID:g688372; PIDN:AAB31736.1; PID:g688373  
C:Genetics:  
A:Gene: GDB:NF2  
A:Cross-references: GDB:I20232; OMIM:101000  
A:Map position: 22q12.2-22q12.2  
C:Superfamily: laminin-type EGF-like homology



```

Query Match      20.6%; Score 67; DB 2; Length 331;
Best Local Similarity 50.0%; Pred. No. 0.9;
Matches 12; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

Cy      18  SLOSLLPRKRFSCSLILPKIWDYR 41
          :|||: |||: |||: |||:
Db      300  ALQSETPELQSSCLSPSSWDYK 323

RESULT 11
T08711
gamma-adaptin homolog DKFP564D066.1 - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 11-Jun-1999 #sequence revision 11-Jun-1999 #text change 13-Aug-1999

```



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OM protein - protein search, using sw model

Run on: October 11, 2005, 06:57:07 ; Search time 36.6163 Seconds  
(without alignments)  
853.085 Million cell updates/sec

Title: US-10-092-934-9

Perfect score: 326

Sequence: 1 MEHPTVAQAGVQPHDLGSLQ.....NMNTALIKRNYPTPTGRKS 61

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	155	47.5	128	2 Q8N862	Q8N862 homo sapien
2	141.5	43.4	165	2 Q6ZS53	Q6ZS53 homo sapien
3	141.5	43.4	165	2 Q6ZT71	Q6ZT71 homo sapien
4	140	42.9	434	2 Q8N213	Q8N213 homo sapien
5	140	42.9	440	2 Q8N273	Q8N273 homo sapien
6	136	41.7	142	2 Q6ZWD5	Q6ZWD5 homo sapien
7	135	41.4	83	2 Q96ID7	Q96ID7 homo sapien
8	135	41.4	151	2 Q6NS37	Q6NS37 homo sapien
9	134.5	41.3	591	1 ALU8_HUMAN	P39195 homo sapien
10	134	41.1	122	2 Q6ZNY9	Q6ZNY9 homo sapien
11	133.5	41.0	72	2 Q8TB48	Q8TB48 homo sapien
12	132.5	40.6	132	2 Q6ZNG3	Q6ZNG3 homo sapien
13	132	40.5	66	2 Q96HL9	Q96HL9 homo sapien
14	131	40.2	123	2 Q6ZV58	Q6ZV58 homo sapien
15	131	40.2	151	2 Q8ZV58	Q8ZV58 homo sapien
16	130.5	40.0	375	2 Q6O448	Q6O448 homo sapien
17	130	39.9	73	2 Q96AN9	Q96AN9 homo sapien
18	130	39.9	151	2 Q8N287	Q8N287 homo sapien
19	129.5	39.7	593	1 ALU7_HUMAN	P39194 homo sapien
20	129	39.6	131	2 Q8ZTD3	Q8ZTD3 homo sapien
21	128	39.3	123	2 Q6ZMQ3	Q6ZMQ3 homo sapien
22	128	39.3	193	2 Q6ZVX8	Q6ZVX8 homo sapien
23	128	39.3	630	2 Q8N7U6	Q8N7U6 homo sapien
24	127	39.0	118	2 Q9P195	Q9P195 homo sapien
25	127	39.0	659	2 Q70AC3	Q70AC3 homo sapien
26	127	39.0	726	2 Q708E2	Q708E2 homo sapien
27	125	38.3	788	2 Q6ZMV3	Q6ZMV3 homo sapien
28	124.5	38.2	170	2 Q6ZV14	Q6ZV14 homo sapien
29	124	38.0	102	2 Q9P147	Q9P147 homo sapien
30	124	38.0	132	2 Q6ZVC2	Q6ZVC2 homo sapien
31	123.5	37.9	587	1 ALU2_HUMAN	P39189 homo sapien

Query Match 47.5%; Score 155; DB 2; Length 128;  
Best Local Similarity 71.4%; Pred. No. 1.1e-11;  
Matches 30; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

32	123.5	37.9	587	1 ALU3_HUMAN	P39190 homo sapien
33	123.5	37.9	593	1 ALU6_HUMAN	P39193 homo sapien
34	123	37.7	506	2 Q9H6L7	Q9H6L7 homo sapien
35	122.5	37.6	157	2 Q8N845	Q8N845 homo sapien
36	122.5	37.6	208	2 Q9NWI4	Q9NWI4 homo sapien
37	122	37.4	122	2 Q6ZVH4	Q6ZVH4 homo sapien
38	122	37.4	158	2 Q8NAL9	Q8NAL9 homo sapien
39	122	37.4	602	2 Q6ZNH6	Q6ZNH6 homo sapien
40	121.5	37.3	585	1 ALU5_HUMAN	P39192 homo sapien
41	121	37.1	122	2 Q9BGW3	Q9BGW3 macaca fasc
42	121	37.1	164	2 Q9UQD6	Q9UQD6 homo sapien
43	120	36.8	138	2 Q8N874	Q8N874 homo sapien
44	120	36.8	198	2 Q6ZS18	Q6ZS18 homo sapien
45	120	36.8	840	2 Q6NY19	Q6NY19 homo sapien

#### ALIGNMENTS

RESULT 1

Q8N862	Q8N862	PRELIMINARY;	PRT;	128 AA.
AC	Q8N862:			
DT	01-OCT-2002 (TrEMBLrel. 22, Created)			
DT	01-OCT-2002 (TrEMBLrel. 22, Last sequence update)			
DE	Hypothetical protein FLJ3947.			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Spleen			
RX	PubMed=14702039; DOI=10.1038/ngi1285;			
RA	Ota Y., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,			
RA	Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,			
RA	Sekine M., Oabayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,			
RA	Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,			
RA	Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,			
RA	Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,			
RA	Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,			
RA	Abe K., Kamiyama K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,			
RA	Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y., Ishida S.,			
RA	Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,			
RA	Kanehori K., Takahashi-Fujii A., Hara H., Tanase T., Nomura Y.,			
RA	Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,			
RA	Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,			
RA	Yoshihawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,			
RA	Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,			
RA	Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,			
RA	Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,			
RA	Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,			
RA	Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,			
RA	Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,			
RA	Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,			
RA	Okitani R., Kawakami T., Noguchi S., Itoh T., Shigetani K., Senba T.,			
RA	Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,			
RA	Togashi T., Oyano M., Hata H., Watanabe M., Komatsu T.,			
RA	Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,			
RA	Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,			
RA	Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.,			
RT	"Complete sequencing and characterization of 21,243 full-length human			
RL	CDNAs."			
RL	Nat. Genet. 36:40-45(2004) .			
DR	EMBL: AK057266; BAC04988.1; -.			
SQ	SEQUENCE 128 AA; 13090 MW; CEF28D6A02AE709F CRC64;			





```
Matches 30; Conservative 7; Mismatches 20; Indels 0; Gaps 0;

QY 2 EPHTVAQGVQPHDLGSLQLPRFKRFSCLILPKIWDYRNMVTLKRNRYPTG 58
   : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
Db 357 DSRSAQAGVQWRNLGSLQLPLPGFKQFSLIPSSWDYRSVPLANFYFLVETG 413

RESULT 6
ID Q6ZWD5 PRELIMINARY; PRT; 142 AA.
AC Q6ZWD5;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DE Hypothetical protein FUJ41262.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=AmvGdala;
RA Ota T., Nakagawa S., Senoh A., Mizuguchi H., Inagaki H., Sugiyama T.,
RA Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J.,
RA Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K.,
RA Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,
RA Wagatsuma M., Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A.,
RA Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahari K.,
RA Masuno Y., Nagai K., Isogai T.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK123256; BAC85568.1;
SQ SEQUENCE 142 AA; 15764 MW; 7484BB8314099D1D CRC64;

Query Match 41.7%; Score 136; DB 2; Length 142;
Best Local Similarity 71.1%; Pred. No. 3.3e-09;
Matches 27; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 6 VAQAGVQPHDLGSLQLPRFKRFSCLILPKIWDYRNM 43
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 11 VAQAGVQPHDLGSLQLPRFKRFSCLILPKIWDYRNM 48

RESULT 7
ID Q96ID7 PRELIMINARY; PRT; 83 AA.
AC Q96ID7;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DE E2F2 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Touchman J.W., Green E.D., Dickinson M.C.,
RA Blakesley R.W., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Rodriguez A.C., Skaleka U., Smailus D.E., Schnerch A., Schein J.E.,
   (1)
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RA Strausberg R.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC007609; AAH07609.1;
DR InterPro; IPR001060; Cdc15_Fes_CIP4.
DR Pfam; PF00611; FCH; 2.
KW HYPOHETICAL protein.
SQ SEQUENCE 151 AA; 17439 MW; 07A07D986C6E6AA3 CRC64;

Query Match 41.4%; Score 135; DB 2; Length 151;
Best Local Similarity 63.4%; Pred. No. 4.8e-09;
Matches 26; Conservative 3; Mismatches 12; Indels 0; Gaps 0;
```

```
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
   and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RA Strausberg R.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC007609; AAH07609.1;
SQ SEQUENCE 83 AA; 9347 MW; 0CD8EFDA7F708C0D CRC64;

Query Match 41.4%; Score 135; DB 2; Length 83;
Best Local Similarity 66.7%; Pred. No. 2.5e-09;
Matches 28; Conservative 2; Mismatches 12; Indels 0; Gaps 0;

QY 1 MEPHTVAQGVQPHDLGSLQLPRFKRFSCLILPKIWDYRNM 42
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 MESRSVAQGVQPHDLGSLQLPRFKRFSCLILPKIWDYRNM 42

RESULT 8
ID Q6NS37 PRELIMINARY; PRT; 151 AA.
AC Q6NS37;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Touchman J.W., Green E.D., Dickinson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
   (1)
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RA Strausberg R.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC007490; AAH07490.1;
DR InterPro; IPR001060; Cdc15_Fes_CIP4.
DR Pfam; PF00611; FCH; 2.
KW HYPOHETICAL protein.
SQ SEQUENCE 151 AA; 17439 MW; 07A07D986C6E6AA3 CRC64;

Query Match 41.4%; Score 135; DB 2; Length 151;
Best Local Similarity 63.4%; Pred. No. 4.8e-09;
Matches 26; Conservative 3; Mismatches 12; Indels 0; Gaps 0;
```

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QY 1 MEPHTVAQGVPOHDLGSLQSLPRPKRFSCLILPKIWDYR 41
  ||:||||| |||||:| ||||| ||||| |||||
Db 93 MESHSVTQAGQWHDLSLQALPFGFMPFSCLSLPSFSSWYR 133

RESULT 9
ALU8 HUMAN
ID _ALU8_HUMAN STANDARD; PRT; 591 AA.
AC P39195;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Alu subfamily SX sequence contamination warning entry.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95021759; PubMed=7935834; DOI=10.1038/371752a0;
RA Claverie J.-M., Makalowski W.;
RT "Alu alert.";
RL Nature 371:752-752(1994).
RN [2]
RP CONCEPT.
RX MEDLINE=92241891; PubMed=1572661;
RA Claverie J.-M.;
RT "Identifying coding exons by similarity search: alu-derived and other
  potentially misleading protein sequences.";
RL Genomics 12:838-841(1992).
RN [3]
RP ALU FAMILIES CLASSIFICATION.
RX MEDLINE=88333009; PubMed=3138422;
RA Quentin Y.;
RT "The Alu family developed through successive waves of fixation closely
  connected with primate lineage history.";
RL J. Mol. Evol. 27:194-202(1988).
RN [4]
RP ALU FAMILIES CLASSIFICATION.
RX MEDLINE=91178815; PubMed=1706781;
RA Jurka J., Milosavljevic A.;
RT "Reconstruction and analysis of human Alu genes.";
RL J. Mol. Evol. 32:105-121(1991).
CC -1- MISCELLANEOUS: Various analyses indicate that Alu repeats fall
  into 8 subfamilies (Ref.3 and Ref.4). Therefore, 8 Alu warning
  consensus sequences have been constituted that contain all six
  frames conceptual translations of each of these classes of Alu
  repeats.
CC -1- MISCELLANEOUS: Isolated 'X' indicates the presence of a stop
  codon, 'XXX' is used to separate the various translation phases.
CC -1- CAUTION: This Alu entry is provided in order to avoid the further
  pollution of protein sequence databases with Alu-derived amino
  acid sequences.
CC -1- CAUTION: Alu repetitive sequences are interspersed in human and
  primate genomes with an average spacing of 4 kb. Some of them are
  actively transcribed by pol III. Normal transcripts may contain
  Alu-derived sequences in 5' or 3' untranslated regions. However,
  cDNA libraries also contain partial and/or rearranged cDNAs
  ligated with Alu-derived sequence in any orientation. Although Alu
  elements (especially situated on the complementary strand) have a
  great potential to create additional/alternative exons,
  consideration should be given to the possibility that the presence
  of an Alu in an open reading frame may have resulted from a
  cloning artifact or may be due to misinterpretation of sequencing
  data. This point has been overlooked on several occasions, with
  the consequence of erroneous Alu-derived amino acid sequences
  being reported.
CC -1- CAUTION: Any significant similarity of a putative protein sequence
  with an Alu-translated entry must be taken as a warning that a
  part of Alu repeat may have been artifactually included in the
  coding nucleotide sequence.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration

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CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
-----
CC EMBL; U14574; -; NOT_ANNOTATED_CDS.
DR KW Hypothetical protein.
FT DOMAIN 1 96 Frame-1.
FT DOMAIN 100 195 Frame-2.
FT DOMAIN 199 294 Frame-3.
FT DOMAIN 298 393 Frame-4.
FT DOMAIN 397 492 Frame-5.
FT DOMAIN 496 591 Frame-6.
SQ SEQUENCE 591 AA; 64395 MW; AC8154AD8ABGBB280 CRC64;

Query Match 41.3%; Score 134.5; DB 1; Length 591;
Best Local Similarity 50.8%; Pred. No. 2.5e-08;
Matches 30; Conservative 4; Mismatches 20; Indels 5; Gaps 1;

QY 2 EPHTVAAQGVPOHDLGSLQSLPRPKRFSCLILPKIWDYRN-----MNTALIKRNRYTP 55
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 500 ESRVAQAGVQWRDLGSLQPPPGFKRFSCLSPSSWDYRRAPPRPANFCFSRQGVSP 558

RESULT 10
Q6ZNY9 PRELIMINARY; PRT; 122 AA.
AC Q6ZNY9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein FLJ26869.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Prostate;
RA Ninomiya K., Wagatsuma M., Kanda K., Kondo H., Yokoi T., Kodaira H.,
RA Katsuya T., Takahashi M., Kikkawa E., Omura Y., Abe K., Kamihara K.,
RA Futaya N., Sato K., Tanikawa M., Yamazaki M., Suzuki Y., Hata H.,
RA Nakaigawa K., Mizuno S., Morinaga M., Kawamura M., Sugiyama T.,
RA Irie R., Osuki T., Sato H., Nishikawa T., Sugiyama A., Kawakami B.,
RA Nagai K., Isogai T., Sugano S.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK130379; BAC85336.1; -.
SQ SEQUENCE 122 AA; 13691 MW; F23AEA08FEF5CB9 CRC64;

Query Match 41.1%; Score 134; DB 2; Length 122;
Best Local Similarity 59.5%; Pred. No. 5.1e-09;
Matches 25; Conservative 6; Mismatches 11; Indels 0; Gaps 0;

QY 1 MEPHTVAQGVPOHDLGSLQSLPRPKRFSCLILPKIWDYRN 42
  ||:||||| |||||:| ||||| ||||| |||||
Db 67 LKSHSVAQAGVQWHDLSLSPQPPPPRPFKQFSCLSIPSSWDYRH 108

RESULT 11
Q8TB48 PRELIMINARY; PRT; 72 AA.
AC Q8TB48;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]

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RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Faney J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC024651; AAH24651.1; -
DR InterPro; IPR008957; FN_III-like.
KW Hypothetical protein.
SQ SEQUENCE 72 AA; 8162 MW; C14F28BD982C1F0 CRC64;

Query Match 41.0%; Score 133.5; DB 2; Length 72;
Best Local Similarity 48.3%; Pred. No. 3.3e-09;
Matches 29; Conservative 4; Mismatches 22; Indels 5; Gaps 1;

Qy 1 MEPTVAQGVQHDLSLQSLPRFKRFSCLILPKIWDYRN-----MNTALIKRNYTP 55
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MESHCIAQGVQVHGLGLQPPPPGKQFSCLSLPSWSDYRRAPSHLANFCIFSRDGVSP 60

RESULT 12
Q6ZNG3 PRELIMINARY; PRT; 132 AA.
AC Q6ZNG3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein FLJ16132.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Cerebellum;
RA Kawakami B., Sugiyama A., Takemoto M., Sugiyama T., Irie R.,
RA Otsubi T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M.,
RA Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A., Suzuki Y.,
RA Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK131229; BAD18412.1; -
DR InterPro; IPR004244; Transposase_22.
DR Pfam; PF02994; Transposase_22; 1.
SQ SEQUENCE 132 AA; 15232 MW; E97B0E76F9EB0B3 CRC64;

Query Match 40.6%; Score 132.5; DB 2; Length 132;
Best Local Similarity 52.8%; Pred. No. 8.6e-09;
Matches 28; Conservative 4; Mismatches 16; Indels 5; Gaps 1;

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Qy 8 QAGVPOHDLGSLQSLPRFKRFSCLILPKIWDYRN-----MNTALIKRNYTP 55
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 67 QAGVQVHDLGSLQSLPPPPGKQFSCLSLPSWSDYRRAPSHLANFCIFSRDGVSP 119

RESULT 13
Q96HL9 PRELIMINARY; PRT; 66 AA.
AC Q96HL9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE CHP protein.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Bladder;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Faney J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Bladder;
RA Strausberg R.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC008373; AAH08373.1; -
SQ SEQUENCE 66 AA; 7409 MW; 77F6F5AFAF7221B3 CRC64;

Query Match 40.5%; Score 132; DB 2; Length 66;
Best Local Similarity 62.8%; Pred. No. 4.7e-09;
Matches 27; Conservative 3; Mismatches 13; Indels 0; Gaps 0;

Qy 1 MEPTVAQGVQHDLSLQSLPRFKRFSCLILPKIWDYRN 43
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MESHSVTQAGVQWRDLGSLQPLPPGKQFSCLSLPSWSDYRRV 43

RESULT 14
Q6ZV58 PRELIMINARY; PRT; 123 AA.
ID Q6ZV58
AC Q6ZV58;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein FLJ42963.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Subthalamic nucleus;

```



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 11, 2005, 06:57:07 ; Search time 45.1791 Seconds  
(without alignments)  
522.196 Million cell updates/sec

Title: US-10-092-934-9  
Perfect score: 326  
Sequence: 1 MEHPTVAQGVQPHDLGSLQ.....NMWTLIKRNYPTETGRKS 61

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A Geneseq\_16Desc04:.\*  
1: Geneseqp1980s:.\*  
2: Geneseqp1990s:.\*  
3: Geneseqp2000s:.\*  
4: Geneseqp2001s:.\*  
5: Geneseqp2002s:.\*  
6: Geneseqp2003as:.\*  
7: Geneseqp2003bs:.\*  
8: Geneseqp2004s:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	326	100.0	61	5 AAE29150	Neural th
2	326	100.0	61	6 ABR63248	61 amino
3	326	100.0	61	6 ABU02980	Human neu
4	326	100.0	61	6 ABP59930	Human 61
5	326	100.0	61	6 AAE33197	Neural th
6	326	100.0	61	6 ABJ19453	61-mer ne
7	326	100.0	61	6 ADB37527	Neural th
8	326	100.0	61	7 ADL96028	Human neu
9	160.5	49.2	124	6 ABP75466	Human sec
10	160.5	49.2	124	6 ABP75933	Human sec
11	160.5	49.2	124	7 ADI40596	Human pur
12	156.5	48.0	73	4 AAB64652	Human sec
13	155	47.5	128	7 ADM05537	Human pro
14	154	47.2	109	7 ADM06040	Human pro
15	154	47.2	134	4 AAU31681	Novel hum
16	152	46.6	83	5 ABB98788	Ribosomal
17	150.5	46.2	129	4 AAO00806	Human pol
18	149.5	45.9	73	4 AAE04269	Human gen
19	148.5	45.6	114	7 ADB64269	Human pro
20	148	45.4	115	5 ABP57959	Human gua
21	147.5	45.2	146	6 ABP75894	Human sec
22	147.5	45.2	441	6 ABP75500	Human sec
23	147	45.1	104	7 ADB65611	Human pro
24	147	45.1	151	7 ADC86567	Human GPC
25	146.5	44.9	149	5 AAG80703	Human 2-h

26	146	44.8	112	4 AAU31904	Novel hum
27	144.5	44.3	76	4 AAB75337	Human sec
28	144	44.2	96	5 ABG72220	Pogo tran
29	143	43.9	92	5 ABB99219	Human try
30	142	43.6	218	4 AAE11963	Human c-m
31	141.5	43.4	165	8 ADR08721	Human pro
32	141.5	43.4	165	8 ADR09482	Human pro
33	141	43.3	109	4 AAO07076	Human pol
34	141	43.3	128	4 AAM51382	Human imm
35	140	42.9	54	3 AAG03438	Human sec
36	140	42.9	434	4 AAM93638	Human pol
37	140	42.9	434	8 ADL31456	Human pro
38	140	42.9	440	4 AAU29216	Human PRO
39	140	42.9	440	4 AAB87592	Human PRO
40	140	42.9	440	5 ABG95917	Human sec
41	140	42.9	440	6 ABU58592	Human PRO
42	140	42.9	440	6 ABU88140	Novel hum
43	140	42.9	440	6 ABU84455	Human sec
44	140	42.9	440	6 ABR66329	Human sec
45	140	42.9	440	6 ABR65719	Human sec

ALIGNMENTS

RESULT 1  
AAE29150  
ID AAE29150 standard; protein; 61 AA.

XX AAE29150;  
XX  
DT 27-JAN-2003 (first entry)  
XX  
DE Neural thread protein (NTP) #8.  
XX  
KW Neural thread protein; NTP; hyperplasia; hypertrophy; arteriosclerosis;  
KW haemorrhoid; gene therapy; tumour; vascular disease; atherosclerosis;  
KW inflammatory disease; nutritional deficiency disease; genetic disease;  
KW autoimmune disease; metabolic disease; traumatic disease; intoxication;  
KW infectious disease; congenital malformation; enzyme deficiency disease;  
KW amyloid disease; fibrosis disease; storage disease; radiation disease;  
KW poisoning; environmental disease; endocrine disease; protein therapy;  
KW degenerative disease; mechanical disease.  
XX  
OS Unidentified.

XX WO200274323-A2.

XX 26-SEP-2002.

XX 08-MAR-2002; 2002WO-IB001959.

XX 08-MAR-2001; 2001US-0273957P.

XX (AVER/) AVERBACK P.

XX Averbach P;

XX WPI; 2002-759864/82.

PT Treating a condition in a patient requiring removal or destruction of  
PT cells, such as a benign or malignant tumor of a tissue or an inflammatory  
PT disease, comprises administering a neural thread protein (NTP) or a NTP  
PT gene to a mammal.

XX Claim 23; Fig 9; 70pp; English.

XX The invention relates to a method for treating a condition in a patient  
CC requiring removal or destruction of cells. The method involves  
CC administering to a mammal a neural thread protein (NTP), or administering  
CC to a tumour or other target cell a NTP gene, where the expression of the  
CC NTP gene is induced resulting in expression of the NTP protein. The  
CC method and NTP are useful for treating a condition in a patient requiring

CC removal or destruction of cells, such as a benign or malignant tumour of  
CC a tissue, a hyperplasia, hypertrophy, or overgrowth of a tissue,  
CC preferably consillar hypertrophy or prostatic hyperplasia, a virally,  
CC bacterially, or parasitically altered tissue, or a malformation of a  
CC tissue. Other conditions include a cosmetic modification to a tissue,  
CC such as removal of unwanted facial hair, warts or unwanted fatty tissue,  
CC a vascular disease, particularly atherosclerosis or arteriosclerosis,  
CC hemorrhoids, or varicose veins, an inflammatory disease, autoimmune  
CC disease, metabolic disease, hereditary/genetic disease, traumatic disease  
CC or physical injury, nutritional deficiency disease, infectious disease,  
CC congenital malformation, amyloid disease, fibrosis disease, storage  
CC disease, enzyme deficiency disease, poisoning, intoxication, degenerative  
CC disease, radiation disease, environmental disease, endocrine disease or  
CC mechanical disease. The invention is useful in protein therapy and gene  
CC therapy. The present sequence is NTP protein  
XX  
SQ Sequence 61 AA;

Query Match 100.0%; Score 326; DB 5; Length 61;  
Best Local Similarity 100.0%; Pred. No. 9.4e-37;  
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPTVAQAGVPOHDLGSLQSLPRFKRFSCLILPKIWDYNNMTALIKENRYTPETGRK 60  
DB 1 MEPTVAQAGVPOHDLGSLQSLPRFKRFSCLILPKIWDYNNMTALIKENRYTPETGRK 60  
QY 61 S 61  
DB 61 S 61

RESULT 2  
ABRG3248  
ID ABRG3248 standard; protein; 61 AA.  
XX  
AC ABRG3248;  
XX  
DT 28-AUG-2003 (first entry)  
XX  
DE 61 amino acid neural thread protein.  
XX  
KW Cytostatic; Antibacterial; Immunosuppressive; Antiinflammatory;  
KW neural thread protein; NTP; tumour.  
XX  
OS Unidentified.  
XX  
PN W02003008443-A2.  
XX  
PD 30-JAN-2003.

PF 19-JUL-2002; 2002WO-CA001105.  
XX  
PR 19-JUL-2001; 2001US-0306150P.  
PR 19-JUL-2001; 2001US-0306161P.  
PR 16-NOV-2001; 2001US-0331477P.  
XX  
PA (NYMO-) NYMOX CORP.  
XX  
PI Averbach PA;  
XX  
DR WPI; 2003-247999/24.  
XX  
PT Novel neural thread protein peptide, referred as cell death peptide,  
PT useful for treating prostatic hyperplasia, psoriasis, eczema, dermatosis,  
PT atherosclerosis, cosmetic modification to skin, throat, mouth, muscle.  
XX  
PS Disclosure; Fig 9; 77pp; English.

XX The present invention relates to a neural thread protein (NTP) peptide  
CC referred to as cell death peptide. Thought to be cytostatic,  
CC antibacterial, immunosuppressive and antiinflammatory. It is useful for  
CC treating a condition in a patient requiring removal or destruction of  
CC cells, for treating a condition such as benign or malignant tumor,

CC inflammatory disease, autoimmune disease and infectious disease. The  
CC peptide useful for treatment is derived from the amino acid sequence for  
CC a pancreatic thread protein. The peptide is conjugated, linked or bound  
CC to a molecule chosen from antibody or its fragment, antibody-like binding  
CC molecule, where the molecule has a higher affinity for binding to a tumor  
CC or other target than binding to other cells. Treatment using NTP peptides  
CC can remove benign tumors with less risk and fewer of the undesirable side  
CC effects of surgery. The present sequence is an NTP amino acid sequence  
XX  
SQ Sequence 61 AA;

Query Match 100.0%; Score 326; DB 6; Length 61;  
Best Local Similarity 100.0%; Pred. No. 9.4e-37;  
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPTVAQAGVPOHDLGSLQSLPRFKRFSCLILPKIWDYNNMTALIKENRYTPETGRK 60  
DB 1 MEPTVAQAGVPOHDLGSLQSLPRFKRFSCLILPKIWDYNNMTALIKENRYTPETGRK 60  
QY 61 S 61  
DB 61 S 61

RESULT 3  
ABU02980  
ID ABU02980 standard; protein; 61 AA.  
XX  
AC ABU02980;  
XX  
DT 20-JAN-2003 (first entry)  
XX  
DE Human neural thread protein AD7C-NTP, protein fragment #8.  
XX  
KW Neural thread protein; NTP-peptide; AD7C-NTP; surgical excision;  
KW transplantation; grafting; chemotherapy; immunotherapy; vaccination;  
KW ablation; cryotherapy; laser therapy; phototherapy; gene therapy;  
KW radiation; tumour; hyperplasia; hypertrophy; overgrowth of tissue;  
KW malformation of tissue; tonsillary hypertrophy; prostatic hyperplasia;  
KW cosmetic modification; vascular disease; atherosclerosis;  
KW arteriosclerosis; haemorrhoid; varicose vein; inflammatory disease;  
KW autoimmune disease; metabolic disease; traumatic disease;  
KW physical injury; nutritional deficiency disease; infectious disease;  
KW amyloid disease; fibrosis disease; storage disease;  
KW congenital malformation; enzyme deficiency disease; poisoning;  
KW intoxication; environmental disease; radiation disease;  
KW endocrine disease; degenerative disease; mechanical disease.

XX Homo sapiens.  
OS  
XX WO200297030-A2.  
XX  
PD 05-DEC-2002.  
XX  
PF 24-MAY-2002; 2002WO-CA000759.  
XX  
PR 25-MAY-2001; 2001US-0293156P.  
XX  
PA (NYMO-) NYMOX CORP.  
XX  
PI Averbach PA;  
XX  
DR WPI; 2003-041406/03.  
XX  
PT Novel peptides similar in amino acid sequence to neural thread proteins  
PT (NTP), useful for treating unwanted cellular proliferations such as  
PT malignant tumors and prostatic hyperplasia.  
XX  
PS Disclosure; Fig 9; 78pp; English.  
XX  
CC The invention describes an NTP-peptide (1) comprising at least one amino  
CC acid sequence corresponding to part of the amino acid sequence of a  
CC neural thread protein, AD7C-NTP. The invention provides a method of

CC treating a condition requiring removal or destruction of cells of a  
CC mammal comprising administering to a mammal, a therapeutic amount of (I).  
CC The treatment is administered to the mammal before, during or after  
CC surgical excision, transplantation, grafting, chemotherapy,  
CC immunotherapy, vaccination, thermal or electrical ablation, cryotherapy,  
CC laser therapy, phototherapy, gene therapy and/or radiation. The method is  
CC useful for treatment of benign or malignant tumour; hyperplasia,  
CC hypertrophy or overgrowth of tissue; virally, bacterially or  
CC parasitically altered tissue; malformation of tissue selected from lung,  
CC breast, stomach, pancreas, prostate, bladder, bone, ovary, skin, kidney,  
CC sinus, colon, intestine, rectum, esophagus, heart, spleen, salivary  
CC gland, blood, brain and its coverings, spinal cord, muscle, connective  
CC tissue, adrenal, parathyroid, thyroid, uterus, testis, pituitary,  
CC reproductive organs, liver, hair, gall bladder, eye, ear, nose, throat,  
CC tonsils, mouth and lymph nodes and lymphoid system; tonsillary  
CC hypertrophy; prostatic hyperplasia; cosmetic modification to a tissue;  
CC vascular disease (atherosclerosis or arteriosclerosis); haemorrhoids;  
CC varicose veins; inflammatory disease; autoimmune disease; metabolic  
CC disease; hereditary/genetic disease; traumatic disease; physical injury;  
CC nutritional deficiency disease; infectious disease; amyloid disease;  
CC fibrosis disease; storage disease; congenital malformation; enzyme  
CC deficiency disease; poisoning; intoxication; environmental disease;  
CC radiation disease; endocrine disease; degenerative disease and mechanical  
CC disease. This is the amino acid sequence of a human neural thread protein  
CC AD7C-NTP protein fragment  
XX  
SQ Sequence 61 AA;

Query Match 100.0%; Score 326; DB 6; Length 61;  
Best Local Similarity 100.0%; Pred. No. 9.4e-37;  
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEPTVAQAGVPOHDLGSLQSLPRFRKFSCLILPKIWDYRNMTALIKRNYTPETGRK 60  
Db 1 MEPTVAQAGVPOHDLGSLQSLPRFRKFSCLILPKIWDYRNMTALIKRNYTPETGRK 60

Qy 61 S 61  
Db 61 S 61

## RESULT 4

ABP59930 ID ABP59930 standard; protein; 61 AA.

XX AC ABP59930;

XX DT 08-SEP-2003 (first entry)

XX DE Human 61 amino acid neural thread protein-like protein.

XX KW Human; tumour; cancer; neural thread protein; NTP; cell removal;  
XX KW cell destruction; antipsoriatic; antimicrobial; immunosuppressive;  
XX KW antiinflammatory; dermatological; antiarteriosclerotic; vasotropic;  
XX KW gene therapy.

XX OS Homo sapiens.

XX PN WO2003044053-A2.

XX PD 30-MAY-2003.

XX PF 18-NOV-2002; 2002WO-CA001757.

XX PR 16-NOV-2001; 2001US-0331477P.

XX FA (NYMO-) NYMOX CORP.

XX PI Averbach P, Gemmell J;

XX DR WPI; 2003-457592/43.

XX FT New neural thread protein (NTP), useful for preparing a composition for

PT treating or preventing a condition in a mammal requiring removal or  
PT destruction of cells, e.g. psoriasis, eczema, atherosclerosis or  
XX inflammatory disease.

XX PS Disclosure; Fig 7; 98pp; English.

XX CC The present invention relates to peptides derived from the human neural  
XX thread protein (NTP). The peptides are useful for preparing a composition  
XX for treating or preventing a condition in a mammal requiring removal or  
XX destruction of cells, comprising tonsillary hypertrophy, prostatic  
XX hyperplasia, psoriasis, eczema, dermatosis, cosmetic modification to a  
XX breast, connective, skin, eye, ear, nose, throat, mouth or muscle tissue,  
XX varicose veins, atherosclerosis, inflammatory, metabolic, infectious,  
XX fibrosis, endocrine or autoimmune disease, or stenosis, restenosis,  
XX occlusion or blockage of an artery or of a stent placed or implanted in  
XX an artery. The present sequence is an NTP protein used to produce  
XX peptides of the invention

SQ Sequence 61 AA;

Query Match 100.0%; Score 326; DB 6; Length 61;  
Best Local Similarity 100.0%; Pred. No. 9.4e-37;  
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEPTVAQAGVPOHDLGSLQSLPRFRKFSCLILPKIWDYRNMTALIKRNYTPETGRK 60  
Db 1 MEPTVAQAGVPOHDLGSLQSLPRFRKFSCLILPKIWDYRNMTALIKRNYTPETGRK 60

Qy 61 S 61  
Db 61 S 61

## RESULT 5

AAE33197 ID AAE33197 standard; protein; 61 AA.

XX AC AAE33197;

XX DT 16-APR-2003 (first entry)

XX DE Neural thread protein (NTP) #8.

XX KW Cell death; tissue necrosis; neural thread protein; NTP; amyloidosis;  
XX KW stroke; brain tumour; Pick's disease; Parkinson's disease; glaucoma;  
XX KW Alzheimer's disease; gene therapy.

XX OS Unidentified.

XX PN WO200289841-A2.

XX PD 14-NOV-2002.

XX PF 06-MAY-2002; 2002WO-CA000681.

XX PR 04-MAY-2001; 2001US-0288463P.

XX FA (NYMO-) NYMOX CORP.

XX PI Averbach PA;

XX DR WPI; 2003-120506/11.

XX FT Preventing, controlling, modulating, ameliorating and/or treating cell  
XX death or tissue necrosis using antibodies to neural thread proteins,  
XX useful in disorders such as stroke, brain tumor, glaucoma and Alzheimer's  
XX disease.

XX PS Disclosure; Fig 12; 60pp; English.

XX CC The invention relates to a method of preventing, and/or inhibiting cell  
XX death and/or tissue necrosis in live tissue containing neural thread  
XX proteins (NTP). The method involves contacting the live tissue with at



CC least one antibody, fragment or derivative that recognises NTP, where the  
 CC antibody, fragment or derivative is present to prevent, control,  
 CC ameliorate and/or inhibit cell death and/or tissue necrosis caused by the  
 CC presence of NTP. Methods and compositions of the invention are useful for  
 CC preventing, modulating, controlling and/or treating disorders associated  
 CC with cell death and/or tissue necrosis such as stroke, brain tumour,  
 CC Pick's disease, Parkinson's disease, amyloidosis, Glaucoma and  
 CC Alzheimer's disease. The invention is useful in gene therapy. The present  
 CC sequence is NTP protein

XX  
 SQ Sequence 61 AA;

Query Match 100.0%; Score 326; DB 6; Length 61;  
 Best Local Similarity 100.0%; Pred. NO. 9.4e-37;  
 Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPHTVAQAGVQPHDLGSLQSLPRFKRFSCLLPKIKWDYRNMMNTALIKENRYTPETGRK 60  
 |||||  
 Db 1 MEPHTVAQAGVQPHDLGSLQSLPRFKRFSCLLPKIKWDYRNMMNTALIKENRYTPETGRK 60  
 QY 61 S 61  
 |  
 Db 61 S 61

RESULT 6  
 ABJ19453  
 ID ABJ19453 standard; protein; 61 AA.

XX  
 AC ABJ19453;

XX 27-MAR-2003 (first entry)

XX 61-mer neural thread protein.

XX Nootropic; neuroprotective; cell death; tissue necrosis; NTP;  
 KW neural thread protein; neurodegenerative disorder; Alzheimer's disease.

XX Unidentified.

XX WO200292115-A2.

XX 21-NOV-2002.

XX 16-MAY-2002; 2002WO-CA000712.

XX 16-MAY-2001; 2001US-0290971P.

XX (NYMO-) NYMOX CORP.

XX Averbach PA;

XX WPI; 2003-129234/12.

XX Preventing and/or inhibiting cell death and/or tissue necrosis in a  
 PT tissue for treating a neurodegenerative disorder, e.g. Alzheimer's  
 PT disease, by contacting the live tissue with at least one segment of  
 PT neural thread proteins (NTP).

PS Disclosure; Fig 9; 60pp; English.

XX The invention relates to a novel method for preventing and/or inhibiting  
 CC cell death and/or tissue necrosis in a tissue comprising contacting the  
 CC live tissue with at least one segment of neural thread proteins (NTP).  
 CC The methods are composition are useful for treating a neurodegenerative  
 CC disorder, such as Alzheimer's disease. This sequence represents an NTP  
 CC protein of the invention

XX Sequence 61 AA;

Query Match 100.0%; Score 326; DB 6; Length 61;  
 Best Local Similarity 100.0%; Pred. NO. 9.4e-37;  
 Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPHTVAQAGVQPHDLGSLQSLPRFKRFSCLLPKIKWDYRNMMNTALIKENRYTPETGRK 60  
 |||||  
 Db 1 MEPHTVAQAGVQPHDLGSLQSLPRFKRFSCLLPKIKWDYRNMMNTALIKENRYTPETGRK 60  
 QY 61 S 61  
 |  
 Db 61 S 61

RESULT 7  
 ADB37527

ID ADB37527 standard; protein; 61 AA.

XX  
 AC ADB37527;

XX 04-DEC-2003 (first entry)

XX Neural thread protein-like protein #3.

XX Cytostatic; Antitumour; Antipsoriatic; Dermatological;  
 KW Antiatherosclerotic; Antiarteriosclerotic; Vasotropic; Antiinflammatory;  
 KW Immunosuppressive; Tranquillizer; Antiemetic; Virucide; AD7c-NTP;  
 KW neural thread protein; neuritic sprouting.

XX Unidentified.

XX WO2003008444-A2.

XX 30-JAN-2003.

XX 19-JUL-2002; 2002WO-CA001106.

XX 19-JUL-2001; 2001US-0306150P.

XX 19-JUL-2001; 2001US-0306161P.

XX 16-NOV-2001; 2001US-0331477P.

XX (NYMO-) NYMOX CORP.

XX Averbach PA, Gemmell J;

XX WPI; 2003-248000/24.

XX Novel Related peptide or AD7c-neural thread peptide, useful for treating  
 PT unwanted cellular proliferations, glandular hyperplasia, unwanted facial  
 PT hair, warts and unwanted fatty tissue.

PS Disclosure; Fig 9; 109pp; English.

XX The present invention relates to AD7c-neural thread protein (NTP) and  
 CC related proteins and peptides (I; ADB37528-ADB37641). The sequences are  
 CC useful for treating a condition in a patient requiring removal or  
 CC destruction of cells. The condition can be selected from benign or  
 CC malignant tumour of a tissue, hyperplasia, hypertrophy or overgrowth of a  
 CC tissue, virally, bacterially or parasitically altered tissue, or  
 CC malformation of a tissue, where the tissue is selected from lung, breast,  
 CC stomach, pancreas, prostate, bladder, bone, ovary, skin, kidney, sinus,  
 CC colon, intestine, stomach, rectum, oesophagus, heart, spleen, salivary  
 CC gland, blood, brain and its coverings, spinal cord and its coverings,  
 CC muscle, connective tissue, adrenal, parathyroid, thyroid, uterus, testis,  
 CC pituitary, reproductive organs, liver, gall bladder, eye, ear, nose,  
 CC throat, tonsils, mouth, lymph nodes and lymphoid tissue. The condition is  
 CC preferably tonsillary hypertrophy, prostatic hyperplasia, psoriasis,  
 CC eczema, dermatosis, cosmetic modification to a tissue (skin, eye, ear,  
 CC nose, throat, mouth, muscle, connective, hair or breast tissue), varicose  
 CC disease (atherosclerosis or arteriosclerosis), haemorrhoids, varicose  
 CC veins, inflammatory disease, autoimmune disease, metabolic disease,  
 CC hereditary/genetic disease, traumatic disease or physical injury.  
 CC nutritional deficiency disease, infectious disease, amyloid disease,  
 CC fibrosis disease, storage disease, congenital malformation, enzyme  
 CC deficiency disease, poisoning, intoxication, environmental disease,  
 CC radiation disease, endocrine disease, degenerative disease and mechanical  
 CC disease. The peptides are useful for treating unwanted cellular



CC proliferations, glandular (e.g. prostate) hyperplasia, unwanted facial  
 CC hair, warts and unwanted fatty tissue, or for preparing antibodies that  
 CC recognize and/or bind to related proteins, Related peptides or NTP  
 CC peptides. The present sequence was used to illustrate the invention.  
 XX  
 SQ Sequence 61 AA;  
 Query Match 100.0%; Score 326; DB 7; Length 61;  
 Best Local Similarity 100.0%; Pred. NO. 9.4e-37; Mismatches 0; Indels 0; Gaps 0;  
 Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 MEPTVAQAGVPOHDLGSLQSLPRFRFSCILIPKIWDYRNMTALIKENRYTPETGRK 60  
 Db 1 MEPTVAQAGVPOHDLGSLQSLPRFRFSCILIPKIWDYRNMTALIKENRYTPETGRK 60  
 Qy 61 S 61  
 Db 61 S 61  
 RESULT 8  
 ADL96028 standard; protein; 61 AA.  
 XX ADL96028;  
 XX 20-MAY-2004 (first entry)  
 XX Human neural thread protein, NTP61.  
 XX Human; neural thread protein; NTP122; NTP112; NTP106; NTP98; NTP75;  
 KW NTP68; NTP61; stenosis; stent; tumour; prostatic hyperplasia; psoriasis;  
 KW eczema; haemorrhoid; atherosclerosis; inflammatory disease;  
 KW autoimmune disease; metabolic disease; hereditary disease;  
 KW genetic disease; traumatic disease; physical injury;  
 KW nutritional deficiency disease; infectious disease; amyloid disease;  
 KW Alzheimer's disease; storage disease; congenital malformation;  
 KW enzyme deficiency disease; poisoning; intoxication;  
 KW environmental disease; radiation disease; endocrine disease;  
 KW degenerative disease; mechanical disease.  
 XX  
 OS Homo sapiens.  
 XX US2003166569-A1.  
 XX 04-SEP-2003.  
 XX 15-NOV-2002; 2002US-00294891.  
 XX 16-NOV-2001; 2001US-0331477P.  
 XX (AVER/) AVERBACK P.  
 XX (GEMM/) GEMMELL J.  
 XX Averbach P, Gemmell J;  
 XX WPI; 2003-898099/82.  
 XX New neural thread protein or its variants, useful for treating tumors and  
 XX other conditions requiring the removal or destruction of cells (e.g.  
 XX prostatic hyperplasia, psoriasis, eczema, hemorrhoids or  
 XX atherosclerosis).  
 XX Disclosure; SEQ ID NO 7; 32pp; English.  
 CC The invention relates to a peptide, or its homologue, derivative,  
 CC fragment, variant or mimetic, comprising at least one neural thread  
 CC protein (NTP) peptide appearing as ADL96029-ADL96069, derived from  
 CC NTP122, 112, 106, 98, 75, 68 or 61. Also included are a nucleic acid  
 CC encoding an amino acid sequence corresponding to the above peptide, a  
 CC composition comprising one or more peptides or nucleic acids cited above  
 CC and a carrier, a method of treating a condition in a mammal requiring  
 CC removal or destruction of cells (comprising administering to the mammal

CC an amount of the peptide cited above) and a method of preventing or  
 CC inhibiting the stenosis, occlusion or blockage of a stent, comprising  
 CC coating the stent with an amount of the above peptide. The peptide  
 CC further comprises an amino acid in a reverse-D order based on the above  
 CC amino acid sequences. The composition and methods are useful in treating  
 CC tumours and other conditions requiring the removal or destruction of  
 CC cells (e.g. prostatic hyperplasia, psoriasis, eczema, haemorrhoids or  
 CC atherosclerosis). These may also be used in treating inflammatory  
 CC diseases, autoimmune diseases, metabolic diseases, hereditary/genetic  
 CC diseases, traumatic diseases or physical injuries, nutritional deficiency  
 CC diseases, infectious diseases, amyloid diseases e.g. Alzheimer's disease,  
 CC storage diseases, congenital malformation, enzyme deficiency diseases,  
 CC poisoning, intoxication, environmental diseases, radiation diseases,  
 CC endocrine diseases, degenerative diseases or mechanical diseases. The  
 CC present sequence is a human NTP protein from which the peptides of the  
 XX invention are derived.  
 XX  
 SQ Sequence 61 AA;  
 Query Match 100.0%; Score 326; DB 7; Length 61;  
 Best Local Similarity 100.0%; Pred. NO. 9.4e-37; Mismatches 0; Indels 0; Gaps 0;  
 Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 MEPTVAQAGVPOHDLGSLQSLPRFRFSCILIPKIWDYRNMTALIKENRYTPETGRK 60  
 Db 1 MEPTVAQAGVPOHDLGSLQSLPRFRFSCILIPKIWDYRNMTALIKENRYTPETGRK 60  
 Qy 61 S 61  
 Db 61 S 61  
 RESULT 9  
 ABP75466  
 ID ABP75466 standard; protein; 124 AA.  
 XX AC ABP75466;  
 XX 10-FEB-2003 (first entry)  
 XX Human secretory polypeptide SPTM SEQ ID NO 650.  
 XX Human; SPTM; autoimmune disorder; inflammatory disorder; AIDS; anaemia;  
 KW asthma; Crohn's disease; neurological disorder; epilepsy; cancer;  
 KW Huntington's disease; Alzheimer's disease; Creutzfeldt-Jakob disease;  
 KW multiple sclerosis; Parkinson's disease; cell proliferative disorder;  
 KW anti-inflammatory; immunosuppressive; neuroprotective; neurotropic;  
 KW neuroleptic; anticonvulsant; cytostatic; antiparkinsonian; anxiolytic;  
 KW antipsoriatic; antianemic; anti-HIV; human immunodeficiency virus;  
 KW secretory polynucleotide; secretory protein.  
 XX  
 OS Homo sapiens.  
 XX WO200283876-A2.  
 XX 24-OCT-2002.  
 XX 27-MAR-2002; 2002WO-US009921.  
 XX 29-MAR-2001; 2001US-0280067P.  
 XX 29-MAR-2001; 2001US-0280068P.  
 XX 16-MAY-2001; 2001US-0291280P.  
 XX 17-MAY-2001; 2001US-0291829P.  
 XX 17-MAY-2001; 2001US-0291849P.  
 XX 19-JUN-2001; 2001US-0299428P.  
 XX 20-JUN-2001; 2001US-0299776P.  
 XX 20-JUN-2001; 2001US-0300001P.  
 XX (INCY-) INCYTE GENOMICS INC.  
 XX Daffo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;  
 PI Dufour GE, Hillman JL, Yu JY, Tuason O, Yap PE, Amshery SR;  
 PI Daughtery SC, Dam TC, Liu IF, Nguyen DA, Kleeferd Y, Gerstin EH;

PI Peralta CH, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B;  
 PI Flores V, Marwaha R, Lo A, Lan RY, Urashka ME;  
 XX WPI; 2003-075543/07.  
 DR N-PSDB; ABZ35914.  
 DR XX  
 XX New human secretory proteins and polynucleotides, useful for diagnosing,  
 PT treating or preventing autoimmune/inflammatory disorders (e.g. AIDS),  
 PT neurological disorders (e.g. Alzheimer's), or cell proliferations or  
 PT cancers.  
 XX  
 XX Claim 27; SEQ ID NO 650; 458pp + Sequence Listing; English.  
 PS  
 XX The invention relates to a secretory polynucleotide (designated sptm)  
 CC comprising any of 567 polynucleotide sequences (ABZ35837-ABZ36403), a  
 CC naturally occurring polynucleotide sequence at least 90 % identical to  
 CC the polynucleotide sequence, a polynucleotide complementary to them or an  
 CC RNA equivalent of them. The polypeptide or polynucleotide are useful for  
 CC treating, preventing or diagnosing a disease or condition associated with  
 CC the expression of functional SPTM. These are particularly useful for  
 CC diagnosing, treating or preventing autoimmune/inflammatory disorders  
 CC (e.g. acquired immunodeficiency syndrome, anaemia, asthma or Crohn's  
 CC disease), neurological disorders (e.g. epilepsy, Huntington's disease,  
 CC dementia, stroke, Alzheimer's disease, Creutzfeldt-Jakob disease,  
 CC multiple sclerosis, cerebral palsy, Parkinson's disease, anxiety,  
 CC schizophrenia or amnesia), or cell proliferative disorders (e.g.  
 CC psoriasis, polycythemia vera, or cancers including adenocarcinoma,  
 CC leukemia, lymphoma, melanoma, myeloma, sarcoma or cancers of the brain,  
 CC breast, cervix or prostate). The present sequence is one of the SPTM  
 CC proteins of the invention (ABP75384-ABP75962). Note: The sequence data  
 CC for this patent did not form part of the printed specification, but was  
 CC obtained in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 XX Sequence 124 AA;  
 SQ  
 Query Match 49.2%; Score 160.5; DB 6; Length 124;  
 Best Local Similarity 57.9%; Pred. No. 1.1e-13;  
 Matches 33; Conservative 6; Mismatches 13; Indels 5; Gaps 1;  
 QY 1 MEPHTVAQAGVQPHDGLGSLQSLPRFRKFSCLILPKIWDYR-----NMNTALIKRNR 52  
 Db 28 MKSHSVAQAGVQWCDLGLSLQPLLPFRKFSCLITPSSWDYRCTPCPVNFICFSRDR 84  
 RESULT 10  
 ABP75933  
 ID ABP75933 standard; protein; 124 AA.  
 XX  
 AC ABP75933;  
 XX  
 XX 10-FPB-2003 (first entry)  
 DT  
 XX Human secretory polypeptide SPTM SEQ ID NO 1117.  
 DE  
 XX Human; SPTM; autoimmune disorder; inflammatory disorder; AIDS; anaemia;  
 KW asthma; Crohn's disease; neurological disorder; epilepsy; cancer;  
 KW Huntington's disease; Alzheimer's disease; Creutzfeldt-Jakob disease;  
 KW multiple sclerosis; Parkinson's disease; cell proliferative disorder;  
 KW anti-inflammatory; immunosuppressive; neuroprotective; nontropic;  
 KW neuroleptic; anticonvulsant; cytostatic; antiparkinsonian; anxiolytic;  
 KW antipsoriatic; anti-anaemic; anti-HIV; human immunodeficiency virus;  
 KW secretory polynucleotide; secretory protein.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200283876-A2.  
 PN  
 XX 24-OCT-2002.  
 PD  
 XX 27-MAR-2002; 2002WO-US009921.  
 PF  
 XX 29-MAR-2001; 2001US-0280067P.  
 PR

PR 29-MAR-2001; 2001US-0280068P.  
 PR 16-MAY-2001; 2001US-0291280P.  
 PR 17-MAY-2001; 2001US-0291829P.  
 PR 17-MAY-2001; 2001US-0291849P.  
 PR 19-JUN-2001; 2001US-0299428P.  
 PR 20-JUN-2001; 2001US-0299776P.  
 PR 20-JUN-2001; 2001US-030001P.  
 XX (INCY-) INCYTE GENOMICS INC.  
 XX  
 XX Daffo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;  
 PI Dufour GE, Hillman JL, Yu JY, Tuason O, Yap PE, Anshey SR;  
 PI Dauthery SC, Dam TC, Liu TF, Nguyen DA, Kleefeld Y, Gerstin EH;  
 PI Peralta CH, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B;  
 PI Flores V, Marwaha R, Lo A, Lan RY, Urashka ME;  
 XX WPI; 2003-075543/07.  
 DR N-PSDB; ABZ36375.  
 DR XX  
 XX New human secretory proteins and polynucleotides, useful for diagnosing,  
 PT treating or preventing autoimmune/inflammatory disorders (e.g. AIDS),  
 PT neurological disorders (e.g. Alzheimer's), or cell proliferations or  
 PT cancers.  
 XX  
 XX Claim 27; SEQ ID NO 1117; 458pp + Sequence Listing; English.  
 PS  
 XX The invention relates to a secretory polynucleotide (designated sptm)  
 CC comprising any of 567 polynucleotide sequences (ABZ35837-ABZ36403), a  
 CC naturally occurring polynucleotide sequence at least 90 % identical to  
 CC the polynucleotide sequence, a polynucleotide complementary to them or an  
 CC RNA equivalent of them. The polypeptide or polynucleotide are useful for  
 CC treating, preventing or diagnosing a disease or condition associated with  
 CC the expression of functional SPTM. These are particularly useful for  
 CC diagnosing, treating or preventing autoimmune/inflammatory disorders  
 CC (e.g. acquired immunodeficiency syndrome, anaemia, asthma or Crohn's  
 CC disease), neurological disorders (e.g. epilepsy, Huntington's disease,  
 CC dementia, stroke, Alzheimer's disease, Creutzfeldt-Jakob disease,  
 CC multiple sclerosis, cerebral palsy, Parkinson's disease, anxiety,  
 CC schizophrenia or amnesia), or cell proliferative disorders (e.g.  
 CC psoriasis, polycythemia vera, or cancers including adenocarcinoma,  
 CC leukemia, lymphoma, melanoma, myeloma, sarcoma or cancers of the brain,  
 CC breast, cervix or prostate). The present sequence is one of the SPTM  
 CC proteins of the invention (ABP75384-ABP75962). Note: The sequence data  
 CC for this patent did not form part of the printed specification, but was  
 CC obtained in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 XX Sequence 124 AA;  
 SQ  
 Query Match 49.2%; Score 160.5; DB 6; Length 124;  
 Best Local Similarity 57.9%; Pred. No. 1.1e-13;  
 Matches 33; Conservative 6; Mismatches 13; Indels 5; Gaps 1;  
 QY 1 MEPHTVAQAGVQPHDGLGSLQSLPRFRKFSCLILPKIWDYR-----NMNTALIKRNR 52  
 Db 28 MKSHSVAQAGVQWCDLGLSLQPLLPFRKFSCLITPSSWDYRCTPCPVNFICFSRDR 84  
 RESULT 11  
 ADI40596  
 ID ADI40596 standard; protein; 124 AA.  
 XX  
 AC ADI40596;  
 XX  
 XX 22-APR-2004 (first entry)  
 DT  
 XX Human purified secretory polypeptide (SPTM), seq id 289.  
 DE  
 XX Antiartherosclerotic; antipsoriatic; cytostatic; secretory molecule;  
 KW agonist; antagonist; gene therapy; antisense; human; secretory;  
 KW purified secretory polynucleotide; sptm; toxicity; arteriosclerosis;  
 KW psoriasis; cancer.  
 XX

[illegible]



PS Claim 20; Page 496; 765pp; English.  
 XX  
 CC The invention relates to novel human secreted polypeptides. The  
 CC polypeptides and antibodies to the polypeptides are useful for  
 CC determining the presence of or predisposition to a disease associated  
 CC with altered levels of polypeptide. The polypeptides are also useful for  
 CC identifying agents (agonists and antagonists) that bind to them. Cells  
 CC expressing the proteins are useful for identifying a therapeutic agent  
 CC for use in treatment of a pathology related to aberrant expression or  
 CC physiological interactions of the polypeptide. Vectors comprising the  
 CC nucleic acids encoding the polypeptides and cells genetically engineered  
 CC to express them are also useful for producing the proteins. The proteins  
 CC are useful in genetic vaccination, testing and therapy, and can be used  
 CC as nutritional supplements. They may be used to increase stem cell  
 CC proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon  
 CC and/or nerve tissue growth or regeneration; immune suppression and/or  
 CC stimulation; as anti-inflammatory agents; and in treatment of leukaemias.  
 CC AAU29510-AAU3304 represent the amino acid sequences of novel human  
 CC secreted proteins of the invention  
 XX  
 SQ Sequence 134 AA;

Query Match 47.2%; Score 154; DB 4; Length 134;  
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 Qy 2 EPHTVAGVQPHDLSLSLPPKPSCLILPKIWDYR 41  
 Db 58 ESHSVAQAEVQWHDLSLSLPPKPSCLILPSRWYR 97

Search completed: October 11, 2005, 07:11:16  
 Job time : 47.1791 secs

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; Sequence 10, Application US/10146130
; Publication No. US20030004107A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; TITLE OF INVENTION: METHOD OF PREVENTING CELL DEATH USING SEGMENTS OF
; FILE REFERENCE: 59003.000007
; CURRENT APPLICATION NUMBER: US/10/146.130
; CURRENT FILING DATE: 2002-08-06
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-146-130-10

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Db 1 MEHPTVAQAGVQPHDLGSLQSLPRFKRFSCLILPKIWDYRNMMNTALIKENRYTPETGRK 60
Qy 61 S 61
Db 61 S 61

RESULT 3
US-10-092-934-9
; Sequence 9, Application US/10092934
; Publication No. US20030054990A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; TITLE OF INVENTION: METHODS OF USING NEURAL THREAD PROTEINS TO TREAT TUMORS
; FILE REFERENCE: 018792-0199
; CURRENT APPLICATION NUMBER: US/10/092.934
; CURRENT FILING DATE: 2002-06-05
; PRIOR FILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-092-934-9

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Db 61 S 61

RESULT 4
US-10-153-334-9
; Sequence 9, Application US/10153334
; Publication No. US20030096350A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; FILE REFERENCE: 59003.000006
; CURRENT APPLICATION NUMBER: US/10/153.334
; CURRENT FILING DATE: 2002-05-24
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-153-334-9

Query Match      100.0%; Score 326; DB 14; Length 61;
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RESULT 5
US-10-198-069-9
; Sequence 9, Application US/10198069
; Publication No. US20030096756A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; FILE REFERENCE: 59003.000009
; CURRENT APPLICATION NUMBER: US/10/198.069
; CURRENT FILING DATE: 2002-07-19
; PRIOR FILING DATE: 2001-07-19
; PRIOR FILING DATE: 2001-07-19
; PRIOR FILING DATE: 2001-07-19
; PRIOR FILING DATE: 2001-07-19
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-198-069-9

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Qy 61 S 61
Db 61 S 61

RESULT 6
US-10-198-070-9
; Sequence 9, Application US/10198070
; Publication No. US20030109437A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; APPLICANT: GEMMELL, JACK
; FILE REFERENCE: 59003.000006
; CURRENT APPLICATION NUMBER: US/10/198.070
; CURRENT FILING DATE: 2002-05-24
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-198-070-9

Query Match      100.0%; Score 326; DB 14; Length 61;
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Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MEHPTVAQAGVQPHDLGSLQSLPRFKRFSCLILPKIWDYRNMMNTALIKENRYTPETGRK 60
Qy 61 S 61
Db 61 S 61
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; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 59003.000008
; CURRENT APPLICATION NUMBER: US/10/198,070
; CURRENT FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/306,161
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/306,150
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/331,477
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-198-070-9

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Db 1 MEPHTVAQGVPOHDLGSLQSLPRFKRFSCLILPKIWDYRNMTALIKRNRYTPETGRK 60

Qy 61 S 61
Db 61 S 61

RESULT 7
US-10-294-891-7
; Sequence 7, Application US/10294891
; Publication No. US20030168569A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; APPLICANT: GEMMEL, JACK
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF CELLS
; FILE REFERENCE: 59003.000010
; CURRENT APPLICATION NUMBER: US/10/294,891
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: 60/331,447
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-294-891-7

Query Match      100.0%; Score 326; DB 14; Length 61;
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Qy 61 S 61
Db 61 S 61

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US-10-920-313-7
; Sequence 7, Application US/10920313
; Publication No. US20050032704A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; APPLICANT: GEMMEL, JACK
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF CELLS
; FILE REFERENCE: 59003.000010
; CURRENT APPLICATION NUMBER: US/10/920,313
; CURRENT FILING DATE: 2004-08-18
; PRIOR APPLICATION NUMBER: 60/331,447
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-920-313-7

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Qy 61 S 61
Db 61 S 61

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US-10-108-260A-4222
; Sequence 4222, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20040005560A1e1 full length cDNA
; FILE REFERENCE: HI-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
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; SEQ ID NO 4222
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-108-260A-4222

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; Publication No. US20040005560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20040005560A1e1 full length cDNA
; FILE REFERENCE: HI-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4725
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-108-260A-4725
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APPLICANT: Gurney, Austin L.	PRIOR FILING DATE: 1998-09-01
APPLICANT: Watanabe, Colin K.	PRIOR APPLICATION NUMBER: 60/099741
APPLICANT: Wood, William I.	PRIOR FILING DATE: 1998-09-10
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC	PRIOR APPLICATION NUMBER: 60/099763
TITLE OF INVENTION: ACIDS ENCODING THE SAME	PRIOR FILING DATE: 1998-09-10
FILE REFERENCE: P3230R1C1	PRIOR APPLICATION NUMBER: 60/099792
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; PRIOR APPLICATION NUMBER: 60/199397  
; PRIOR FILING DATE: 2000-04-25  
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; PRIOR APPLICATION NUMBER: 09/311832  
; PRIOR FILING DATE: 1999-05-14  
; PRIOR APPLICATION NUMBER: 09/380137  
; PRIOR FILING DATE: 1999-08-25  
; PRIOR APPLICATION NUMBER: 09/380138  
; PRIOR FILING DATE: 1999-08-25  
; PRIOR APPLICATION NUMBER: 09/380142

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Job time : 103.265 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 11, 2005, 06:57:19 ; Search time 13.9452 Seconds  
(without alignments)  
326.535 Million cell updates/sec

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Perfect score: 326  
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Total number of hits satisfying chosen parameters: 513545

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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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4	132.5	40.6	397	5	PCT-US95-17111A-121
5	131	40.2	103	4	US-09-513-999C-5327
6	130.5	40.0	375	2	US-08-454-557C-121
7	130.5	40.0	375	2	US-08-340-426D-121
8	130.5	40.0	375	2	US-08-450-673C-121
9	130.5	40.0	375	4	US-09-872-968-2
10	128	39.3	64	4	US-09-513-999C-4425
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17	124	38.0	132	4	US-09-679-426-573
18	124	38.0	132	4	US-09-759-143-573
19	124	38.0	132	4	US-09-651-236-573
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35	121	37.1	54	4	US-09-513-999C-7068
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37	117	35.9	121	4	US-09-513-999C-7874
38	115.5	35.4	91	4	US-09-621-976-5929
39	115	35.3	66	4	US-09-621-976-5606
40	115	35.3	87	4	US-09-205-258-342
41	115	35.3	111	4	US-09-513-999C-8159
42	114.5	35.1	119	4	US-09-513-999C-7867
43	114	35.0	65	4	US-09-513-999C-6665
44	114	35.0	70	4	US-09-513-999C-6561
45	114	35.0	118	4	US-09-663-600A-114

ALIGNMENTS

RESULT 1  
US-09-513-999C-7519  
; Sequence 7519, Application US/09513999C  
; Patent No. 6783961  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Duclert, A.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
; FILE REFERENCE: 59.US2.REG  
; CURRENT APPLICATION NUMBER: US/09/513.999C  
; CURRENT FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/122,487  
; PRIOR FILING DATE: 1999-02-26  
; NUMBER OF SEQ ID NOS: 36681  
; SOFTWARE: Patent.pm  
; SEQ ID NO 7519  
; LENGTH: 54  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-513-999C-7519

Query Match 42.9%; Score 140; DB 4; Length 54;  
Best Local Similarity 65.9%; Pred. No. 4.2e-13;  
Matches 27; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

Qy 1 MEHPTVAQGVPOHDLGSLQSLPRFKFSCILIPKIDYR 41  
|||:|||||:|||||:|||||:|||||:|||||  
Db 12 MESRLAQAGLQWNLGSLQPLPPGFKRFSCLSPSSWDYR 52

RESULT 2  
US-09-621-976-4553  
; Sequence 4553, Application US/09621976  
; Patent No. 6639063  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Jobert, S.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.  
; FILE REFERENCE: GENSET.054PR2  
; CURRENT APPLICATION NUMBER: US/09/621.976  
; CURRENT FILING DATE: 2000-07-21  
; NUMBER OF SEQ ID NOS: 19335  
; SOFTWARE: Patent.pm  
; SEQ ID NO 4553  
; LENGTH: 63  
; TYPE: PRT  
; ORGANISM: Homo sapiens

US-09-621-976-4553

Query Match 41.4%; Score 135; DB 4; Length 63;  
Best Local Similarity 70.7%; Pred. No. 2.7e-12;  
Matches 29; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 MEPTVAQAGVPOHDLGSLQSLPRPKRFSCLILPKIWDYR 41  
Db 15 MESCVAQAGVRWCHLGLSLQPLPRPKRFSCLILPSSWDYR 55

## RESULT 3

US-09-513-999C-4581  
; Sequence 4581, Application US/09513999C  
; Patent No. 6783961  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Duclert, A.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
; FILE REFERENCE: 59.US2.REG  
; CURRENT APPLICATION NUMBER: US/09/513,999C  
; CURRENT FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/122,487  
; PRIOR FILING DATE: 1999-02-26  
; NUMBER OF SEQ ID NOS: 36681  
; SOFTWARE: Patent.pm  
; SEQ ID NO 4581  
; LENGTH: 61  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SIGNAL  
; LOCATION: -16..-1  
; OTHER INFORMATION: score 7.5  
; OTHER INFORMATION: seq LFCLSVCLFEVES/HS  
US-09-513-999C-4581

Query Match 40.8%; Score 133; DB 4; Length 61;  
Best Local Similarity 61.9%; Pred. No. 5.2e-12;  
Matches 26; Conservative 3; Mismatches 13; Indels 0; Gaps 0;

QY 1 MEPTVAQAGVPOHDLGSLQSLPRPKRFSCLILPKIWDYR 42  
Db 14 VESHVTQAGVQVHSLGPLNSLPPGPKRFSCLSLSSWDYR 55

## RESULT 4

PCT-US95-17111A-121  
; Sequence 121, Application PC/TUS9517111A  
; GENERAL INFORMATION:  
; APPLICANT: de la Monte, Suzanne  
; APPLICANT: Wands, Jack R.  
; TITLE OF INVENTION: Neural Thread Protein Gene Expression and  
; TITLE OF INVENTION: Detection of Alzheimer's Disease  
; NUMBER OF SEQUENCES: 121  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.  
; STREET: 1100 New York Avenue, Suite 600  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/17111A  
; FILING DATE:  
; CLASSIFICATION:

; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/340,426  
; FILING DATE: 14-NOV-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ludwig, Steven R.  
; REGISTRATION NUMBER: 36,203  
; REFERENCE/DOCKET NUMBER: 0609.3840002  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 371-2600  
; TELEFAX: (202) 371-2540  
; INFORMATION FOR SEQ ID NO: 121:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 397 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
PCT-US95-17111A-121

Query Match 40.6%; Score 132.5; DB 5; Length 397;  
Best Local Similarity 59.2%; Pred. No. 6.4e-11;  
Matches 29; Conservative 5; Mismatches 14; Indels 1; Gaps 1;

QY 1 MEPTVAQAGVPOHDLGSLQSLPRPKRFSCLILPKIWDYRNM-NTALI 48  
Db 305 MESHVTQAGVQVNPGLSLQPLPPGPKRFSCLSLPSSWDYGHLLHTPLI 353

## RESULT 5

US-09-513-999C-5327  
; Sequence 5327, Application US/09513999C  
; Patent No. 6783961  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Duclert, A.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
; FILE REFERENCE: 59.US2.REG  
; CURRENT APPLICATION NUMBER: US/09/513,999C  
; CURRENT FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/122,487  
; PRIOR FILING DATE: 1999-02-26  
; NUMBER OF SEQ ID NOS: 36681  
; SOFTWARE: Patent.pm  
; SEQ ID NO 5327  
; LENGTH: 103  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: UNSURE  
; LOCATION: 78  
; OTHER INFORMATION: Xaa=His or Gln  
; FEATURE:  
; NAME/KEY: UNSURE  
; LOCATION: 88  
; OTHER INFORMATION: Xaa=Lys or Asn or Arg or Ser  
US-09-513-999C-5327

Query Match 40.2%; Score 131; DB 4; Length 103;  
Best Local Similarity 70.3%; Pred. No. 2e-11;  
Matches 26; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 5 TVAQAGVPOHDLGSLQSLPRPKRFSCLILPKIWDYR 41  
Db 6 SVTQAGVQWHDGLSLQPLPPGPKRFSCLSLPSSWDYR 42

## RESULT 6

US-08-454-557C-121  
; Sequence 121, Application US/08454557C  
; Patent No. 5830670  
; GENERAL INFORMATION:  
; APPLICANT: de la Monte, Suzanne

APPLICANT: Wands, Jack R.  
TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection  
TITLE OF INVENTION: of Alzheimer's Disease  
NUMBER OF SEQUENCES: 121  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.  
STREET: 1100 New York Avenue, Suite 600  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/454,557C  
FILING DATE: 30-MAY-1995  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Ludwig, Steven R.  
REGISTRATION NUMBER: 36,203  
REFERENCE/DOCKET NUMBER: 0609.3840003  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 371-2600  
TELEFAX: (202) 371-2540  
INFORMATION FOR SEQ ID NO: 121:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 375 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-454-557C-121

Query Match 40.0%; Score 130.5; DB 2; Length 375;  
Best Local Similarity 48.3%; Pred. No. 1.2e-10;  
Matches 29; Conservative 6; Mismatches 20; Indels 5; Gaps 1;

QY 1 MEHPTVAAGVPQHDLGSLQSLPRFRKFSCLILPKIWDYRNM-----NTALIKRNYTP 55  
DB 304 MESHVTOAGVQWPNLGSLOPLPGLKRFCSLSLPSSWDYGHLPHPANFCIFIRGGVSP 363

RESULT 7  
US-08-340-426D-121  
Sequence 121, Application US/08340426D  
Patent No. 5948634  
GENERAL INFORMATION:  
APPLICANT: Wands, Jack R.  
REGISTRATION NUMBER: 36,203  
REFERENCE/DOCKET NUMBER: 0609.3840004  
TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection  
TITLE OF INVENTION: of Alzheimer's Disease  
NUMBER OF SEQUENCES: 121  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.  
STREET: 1100 New York Avenue, Suite 600  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/340,426D  
FILING DATE: 14-NOV-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Ludwig, Steven R.  
REGISTRATION NUMBER: 36,203

REFERENCE/DOCKET NUMBER: 0609.3840002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 371-2600  
TELEFAX: (202) 371-2540  
INFORMATION FOR SEQ ID NO: 121:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 375 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-340-426D-121

Query Match 40.0%; Score 130.5; DB 2; Length 375;  
Best Local Similarity 48.3%; Pred. No. 1.2e-10;  
Matches 29; Conservative 6; Mismatches 20; Indels 5; Gaps 1;

QY 1 MEHPTVAAGVPQHDLGSLQSLPRFRKFSCLILPKIWDYRNM-----NTALIKRNYTP 55  
DB 304 MESHVTOAGVQWPNLGSLOPLPGLKRFCSLSLPSSWDYGHLPHPANFCIFIRGGVSP 363

RESULT 8  
US-08-450-673C-121  
Sequence 121, Application US/08450673C  
Patent No. 5948888  
GENERAL INFORMATION:  
APPLICANT: de la Monte, Suzanne  
REGISTRATION NUMBER: 36,203  
REFERENCE/DOCKET NUMBER: 0609.3840004  
TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection  
TITLE OF INVENTION: of Alzheimer's Disease  
NUMBER OF SEQUENCES: 121  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.  
STREET: 1100 New York Avenue, Suite 600  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/450,673C  
FILING DATE: 30-MAY-1995  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Ludwig, Steven R.  
REGISTRATION NUMBER: 36,203  
REFERENCE/DOCKET NUMBER: 0609.3840004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 371-2600  
TELEFAX: (202) 371-2540  
INFORMATION FOR SEQ ID NO: 121:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 375 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-450-673C-121

Query Match 40.0%; Score 130.5; DB 2; Length 375;  
Best Local Similarity 48.3%; Pred. No. 1.2e-10;  
Matches 29; Conservative 6; Mismatches 20; Indels 5; Gaps 1;

QY 1 MEHPTVAAGVPQHDLGSLQSLPRFRKFSCLILPKIWDYRNM-----NTALIKRNYTP 55  
DB 304 MESHVTOAGVQWPNLGSLOPLPGLKRFCSLSLPSSWDYGHLPHPANFCIFIRGGVSP 363

RESULT 9  
US-09-872-968-2

; Sequence 2, Application US/09872968  
; Patent No. 6770797  
; GENERAL INFORMATION:  
; APPLICANT: Wands, Jack R  
; APPLICANT: de la Monte, Suzanne M  
; TITLE OF INVENTION: Inhibition of Neurodegeneration  
; FILE REFERENCE: 21486-047  
; CURRENT APPLICATION NUMBER: US/09/872,968  
; CURRENT FILING DATE: 2001-06-01  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 375  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-872-968-2

Query Match 40.0%; Score 130.5; DB 4; Length 375;  
Best Local Similarity 48.3%; Pred. No. 1.2e-10;  
Matches 29; Conservative 6; Mismatches 20; Indels 5; Gaps 1;  
QY 1 MEPHTVAQGVPOHDLGSLQSLPRKFRFSCILIPKIDYRNM-----NTALIKRNYTP 55  
Db 304 MESHVTAQGVQVNPNGSLQPLPGLKRFSCLSLPSSWDYGHLPHPANPCIFIRGVSP 363

RESULT 10  
US-09-513-999C-4425  
; Sequence 4425, Application US/09513999C  
; Patent No. 6783961  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Duclert, A.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
; Patent No. 6783961  
; FILE REFERENCE: 59.US2.REG  
; CURRENT APPLICATION NUMBER: US/09/513,999C  
; CURRENT FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/122,487  
; PRIOR FILING DATE: 1999-02-26  
; NUMBER OF SEQ ID NOS: 36681  
; SOFTWARE: Patent.pm  
; SEQ ID NO 4425  
; LENGTH: 64  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SIGNAL  
; LOCATION: -14...-1  
; OTHER INFORMATION: score 4.4  
; OTHER INFORMATION: seq HIFFLSPFIETDS/HS  
; FEATURE:  
; NAME/KEY: UNSURE  
; LOCATION: 10  
; OTHER INFORMATION: Xaa= \* or Trp  
; FEATURE:  
; NAME/KEY: UNSURE  
; LOCATION: 29  
; OTHER INFORMATION: Xaa=Leu or Val  
; FEATURE:  
; NAME/KEY: UNSURE  
; LOCATION: 41  
; OTHER INFORMATION: Xaa=Pro or Ser  
US-09-513-999C-4425

Query Match 39.3%; Score 128; DB 4; Length 64;  
Best Local Similarity 62.5%; Pred. No. 3e-11;  
Matches 25; Conservative 3; Mismatches 12; Indels 0; Gaps 0;

QY 2 EPHTVAAQGVPOHDLGSLQSLPRKFRFSCILIPKIDYR 41  
Db 13 DSHSVAQGVQVXRDLGSLQAPLPGFTPFSCXSLPSSWDYR 52

RESULT 11  
US-09-513-999C-6611  
; Sequence 6611, Application US/09513999C  
; Patent No. 6783961  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Duclert, A.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
; Patent No. 6783961  
; FILE REFERENCE: 59.US2.REG  
; CURRENT APPLICATION NUMBER: US/09/513,999C  
; CURRENT FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/122,487  
; PRIOR FILING DATE: 1999-02-26  
; NUMBER OF SEQ ID NOS: 36681  
; SOFTWARE: Patent.pm  
; SEQ ID NO 6611  
; LENGTH: 64  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-513-999C-6611

Query Match 38.7%; Score 126; DB 4; Length 64;  
Best Local Similarity 64.1%; Pred. No. 5.8e-11;  
Matches 25; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 1 MEPHTVAQGVPOHDLGSLQSLPRKFRFSCILIPKID 39  
Db 1 MGSHSVTAQDMQLDGLSLQPLPRKQFSRLSLPRSD 39

RESULT 12  
US-09-621-976-6572  
; Sequence 6572, Application US/09621976  
; Patent No. 6639063  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Jobert, S.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.  
; FILE REFERENCE: GENSET.054PR2  
; CURRENT APPLICATION NUMBER: US/09/621,976  
; CURRENT FILING DATE: 2000-07-21  
; NUMBER OF SEQ ID NOS: 19335  
; SOFTWARE: Patent.pm  
; SEQ ID NO 6572  
; LENGTH: 68  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: UNSURE  
; LOCATION: 29  
; OTHER INFORMATION: Xaa = His,Asn  
US-09-621-976-6572

Query Match 38.2%; Score 124.5; DB 4; Length 68;  
Best Local Similarity 61.4%; Pred. No. 1e-10;  
Matches 27; Conservative 4; Mismatches 10; Indels 3; Gaps 1;

QY 1 MEPHTVA---QAGVPOHDLGSLQSLPRKFRFSCILIPKIDYR 41  
Db 12 VEPWSLALLPEAGVRWCXIGSLQPLPRKFRFSCILIPSSWDYR 55

RESULT 13  
US-09-513-999C-6065  
; Sequence 6065, Application US/09513999C  
; Patent No. 6783961  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.



```
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 6065
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-513-999C-6065

Query Match      38.0%; Score 124; DB 4; Length 96;
Best Local Similarity 65.8%; Pred. No. 1.9e-10;
Matches 25; Conservative 2; Mismatches 11; Indels 0; Gaps 0;

Qy 6 VAQAGVQPHDGLGSLQSLPRFKRFSCLILPKIWDYRNM 43
    ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 6 VAQAGVQWRDLGSPQPLPPGFKRFSCLSPSSWDYRHV 43
    ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 14
US-09-621-976-5592
; Sequence 5592, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 5592
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -105...-1
US-09-621-976-5592

Query Match      38.0%; Score 124; DB 4; Length 120;
Best Local Similarity 41.9%; Pred. No. 2.5e-10;
Matches 31; Conservative 8; Mismatches 19; Indels 16; Gaps 3;

Qy 3 PHTVAQ-----AGVPQHDGLGSLQSLPRFKRFSCLILPKIWDYRN-----MNTAL 47
    ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 9 PEVIAQLENAAKVLMAGVQWHDLSLPPPPPGFKRFSCLSPSSWDYRHHLPWSIMNNAS 68
    ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 48 IKRNYTPETGRKS 61
    : : : : :
Db 69 M-QSTYSYHLGNQN 81

RESULT 15
US-09-636-215-573
; Sequence 573, Application US/09636215
; Patent No. 6620922
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
```

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; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, William
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.42171C17
; CURRENT APPLICATION NUMBER: US/09/636,215
; CURRENT FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 852
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 573
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-636-215-573

Query Match      38.0%; Score 124; DB 4; Length 132;
Best Local Similarity 65.0%; Pred. No. 2.9e-10;
Matches 26; Conservative 2; Mismatches 12; Indels 0; Gaps 0;

Qy 2 EPHTVAQAGVPPQHDGLGSLQSLPRFKRFSCLILPKIWDYR 41
    ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 34 ESGPVAQAGVQWHDLSLQPLPHRFKQFSCLSLSPHSWDHR 73
    ||||| ||||| ||||| ||||| ||||| ||||| |||||

Search completed: October 11, 2005, 07:42:52
Job time : 13.9452 secs
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